

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:33:17 ; Search time 380.684 Seconds  
(without alignments)  
3996.417 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRYQYRQLGVDPGNLTC 257

Scoring table:

	BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5		
Fgapop 6.0 , Fgapext 7.0		
Delop 6.0 , Delext 7.0		

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US10692367/runat 20052005 172254 19994/app query.fasta_1.846
-DB=N Geneseq 16Dec04 -OPMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US10692367 @CGN 1 1 468 @runat 20052005 172254 19994 -NCPUS=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : N Geneseq 16Dec04:\*

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2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004as:*
13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1452	100.0	774	13	ADS92627
2	1435	98.8	774	13	ADS92645
3	1435	98.8	774	13	ADS92649
4	1405	96.8	774	13	ADS92687
5	1382.5	95.2	771	13	ADS92675

6	1382	95.2	774	13	ADS92661	Ads92661 Chitinase
7	1377	94.8	774	13	ADS92681	Ads92681 Chitinase
8	1373.5	94.6	771	13	ADS92677	Ads92677 Chitinase
9	1366.5	94.1	771	13	ADS92663	Ads92663 Chitinase
10	1363	93.9	774	13	ADS92679	Ads92679 Chitinase
11	1361.5	93.8	771	13	ADS92689	Ads92689 Chitinase
12	1361	93.7	774	13	ADS92639	Ads92639 Chitinase
13	1361	93.7	774	13	ADS92653	Ads92653 Chitinase
14	1356.5	93.4	765	13	ADS92683	Ads92683 Chitinase
15	1353.5	93.2	753	13	ADS92659	Ads92659 Chitinase
16	1351.5	93.1	771	13	ADS92699	Ads92699 Chitinase
17	1342	92.4	780	13	ADS92655	Ads92655 Chitinase
18	1339	92.2	780	13	ADS92691	Ads92691 Chitinase
19	1338.5	92.2	753	13	ADS92697	Ads92697 Chitinase
20	1333.5	91.8	765	13	ADS92641	Ads92641 Chitinase
21	1333	91.8	840	11	ADJ112126	ADJ112126 Maize cDN
22	1332	91.7	774	13	ADS92623	Ads92623 Chitinase
23	1323.5	91.2	753	13	ADS92667	Ads92667 Chitinase
24	1318.5	90.8	753	13	ADS92685	Ads92685 Chitinase
25	1318.5	90.8	771	13	ADS92657	Ads92657 Chitinase
26	1315.5	90.6	753	13	ADS92651	Ads92651 Chitinase
27	1315.5	90.6	777	13	ADS92631	Ads92631 Chitinase
28	1305.5	89.9	753	13	ADS92693	Ads92693 Chitinase
29	1304.5	89.8	753	13	ADS92671	Ads92671 Chitinase
30	1300.5	89.6	777	13	ADS92619	Ads92619 Chitinase
31	1299	89.5	750	13	ADS92695	Ads92695 Chitinase
32	1297.5	89.4	1094	3	AAA96222	AAA96222 cDNA enco
33	1295.5	89.2	753	13	ADS92665	Ads92665 Chitinase
34	1294.5	89.2	753	13	ADS92673	Ads92673 Chitinase
35	1292.5	89.0	753	13	ADS92637	Ads92637 Chitinase
36	1290.5	88.9	753	13	ADS92647	Ads92647 Chitinase
37	1282.5	88.3	753	13	ADS92669	Ads92669 Chitinase
38	1273.5	87.7	753	13	ADS92643	Ads92643 Chitinase
39	1220	84.0	756	13	ADS92629	Ads92629 Chitinase
40	1218	83.9	756	13	ADS92621	Ads92621 Chitinase
41	1212	83.5	756	13	ADS92625	Ads92625 Chitinase
42	1071	73.8	843	8	ADA70140	Ada70140 Rice gene
43	1071	73.8	843	11	ADJ11575	Adj11575 Rice cDNA
c 44	1071	73.8	906	11	ADJ11773	Adj11773 Rice cDNA
c 45	1071	73.8	909	11	ADJ11435	Adj11435 Rice cDNA

#### ALIGNMENTS

RESULT 1  
ADS92627  
ID ADS92627 standard; DNA; 774 BP.  
XX  
XX ADS92627;  
AC  
DT 02-DEC-2004 (first entry)  
XX  
XX Chitinase variant polynucleotide #5.  
DE  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
XX Synthetic.  
XX  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
PD  
XX 22-OCT-2003; 2003WO-US033588.  
PF  
XX 22-OCT-2002; 2002US-0420666P.  
PR  
XX 06-NOV-2002; 2002US-00290086.  
PR  
XX 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;

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XX WPI; 2004-365417/34.
DR P-PSDB; ADS92628.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Disclosure; SEQ ID NO 11; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 774 BP; 139 A; 251 C; 278 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.89e-114 Length: 774
Score: 1452.00 Matches: 257
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92627 (1-774)

QY 1 SerMetGlnAnCysGlyCysGlnProAnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGTCGAGCAAGTTTGGCTACTGCGGC 60

QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCCAGTCCGCGCGTCCGCGCGCGGT 120

QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 61 ValThrAspAlaPhePheAsnGlyTyrLeuValAsnGlnAlaGlySerGlyCysGlyCysGly 80
DB 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACCAAGCGCGGAGCGGTGCGAGGCGAAG 240

QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaAlaAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGAGCGCGTCTCTCGAGGCCATCGCGCGGTACCGCGGCTTCGCGCAT 300

QY 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCCGAGTCCGAGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCGCACGCG 360

QY 121 GluThrGlyHisPheCysTyrLeuSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGCGCATTTCTGTCTACATCGAGCGAGGTCAACAGAGACCGCTACTGCGACCCG 420

QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGCGCGCGCGAGAGTACTACGCGCGCGCGCGCGCGCG 480

QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaAlaGlyPheAspGlyLeuGly 180
DB 481 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
DB 541 GACCCCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaAlaLeu 220
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGTCGAGCAAGTTTGGCTACTGCGGC 60
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DB 601 ATGAACAACATGTCACCGTGTGATGTCGCGCGCGTTCGCGCGCCACCATCAGCGCCATCAAC 660
QY 221 GlyAlaLeuGluCysAsnGlyAsnAspProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
DB 661 GCGCGCTCCGAGTGCAGCGGAAACACCCCGCCAGATGAAACGCGCGTTCGCGTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
DB 721 AGGCAGTACTGCGCGCGAGTCCGCGTGCAGCCCGCGGCAACCACTCACCCTGC 771

RESULT 2
ADS92645
ID ADS92645 standard; DNA; 774 BP.
XX
AC ADS92645;
XX
DT 02-DEC-2004 (first entry)
XX
DB Chitinase variant polynucleotide #12.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
PA PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Valpani N;
XX
XX WPI; 2004-365417/34.
DR P-PSDB; ADS92646.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 29; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 774 BP; 137 A; 251 C; 279 G; 107 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.35e-112 Length: 774
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92645 (1-774)

QY 1 SerMetGlnAnCysGlyCysGlnProAnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGTCGAGCAAGTTTGGCTACTGCGGC 60
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QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCGCGCGTCCGCTCGCGGCGCGT 120  
 QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 121 GCG 180  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysSerGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 181 GTCACCGACGCGTCTTCAACCGCATCAAGAACAGCGCGCGCGCGCGCGCGCGCG 240  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAla 100  
 DB 241 AACTTCTACACCGCGAGCGGTCTCTCGAGGCCATCGCGCGGTACCGCGGCTTCGCGCAT 300  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHieAlaThrHis 120  
 DB 301 GCGCGCTCCGAGGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAlaAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 361 GAGACCGCGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCG 420  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160  
 DB 421 ACCAAGAGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 481 ATCTCGTGAACATACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB 541 GACCCCGCGAGGTGGCGCGCGAGCGCGTGTGGCTTCAAGCGCGCGCGTCTGGTCTCG 600  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 601 ATGAACAACGTCACCGGTGTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAlaProAlaGlnMetAsnAlaArgValGlyTyr 240  
 DB 661 GCGCGCTCTGAGTGGCGCGCGAGCAACCCCGCGCGCGCGCGCGCGCGCGCGCG 720  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB 721 AAGCAGTACTGCGCGAGTCTGCGGTGCGACCCAGCGCGCGCGCGCGCGCGCGCG 771

## RESULT 3

ADS92649

ID ADS92649 standard; DNA; 774 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

XX AC

XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX

PI Muller ML, True T, Simmons CR, Valpani N;  
 XX

XX WPI; 2004-365417/34.  
 DR P-PSDB; ADS92650.  
 XX

XX New chitinase polynucleotides and polypeptides, useful in producing  
 plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 33; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
 encoding them. A method of enhancing plant resistance to a fungus or  
 nematode comprises introducing into a plant a recombinant expression  
 cassette comprising a promoter operably linked to a chitinase  
 polynucleotide of the invention. The plant is maize or soybean. The  
 fungus is from the genus *Fusarium*. The nematode is from the genus  
*Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 plant resistance to a fungus or nematode. This sequence represents a  
 chitinase variant polynucleotide of the invention.

XX Sequence 774 BP; 138 A; 251 C; 278 G; 107 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.35e-112 Length: 774  
 Score: 1435.00 Matches: 254  
 Percent Similarity: 99.22% Conservative: 1  
 Best Local Similarity: 98.83% Mismatches: 2  
 Query Match: 98.83% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92649 (1-774)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGCGAAGTCTGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
 QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACAACCGACGAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
 QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 121 GCG 180  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 181 GTACACCGCGGTCTTCTCAACCGCGCATCAAGAACCGCGCGCGCGCGCGCGCG 240  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
 DB 241 AACTTCTACACCGCGAGCGGTCTCTCGAGGCCATCGCGCGGTACCGCGGCTTCGCGCAT 300  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHieAlaThrHis 120  
 DB 301 GCGCGCTCCGAGGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAlaAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 361 GAGACCGCGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCG 420  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 421 ACCAAGAGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 481 ATCTCGTGAACATACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200

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Db 541 GACCCCGCAGGCTGGCGCGGAGCGCGTGTGGCTTCAAGCGCGGCTCTGTTCTGG 600
Qy 201 MetAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACAACGTCACCGTGTATCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 660
Qy 221 GlyAlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GGCGCCCTCGAGTGGCGGGGAGACACCCCGCCAGATGAACGGCGGCTCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
Db 721 AAGCAGTACTGCCGAGCTCGCGTGCAGCCAGGCGCCCACTTGC 771

```

## RESULT 4

AD92687  
ID ADS92687 standard; DNA; 774 BP.

AC ADS92687;

XX 02-DEC-2004 (first entry)

DT Chitinase variant polynucleotide #33.

DE Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

OS WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR P-PSDB; ADS92688.

XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 71; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4.72e-110	Length:	774
Score:	1405.00	Matches:	245
Percent Similarity:	98.44%	Conservative:	8
Best Local Similarity:	95.33%	Mismatches:	4
Query Match:	96.76%	Indels:	0
DB:	13	Gaps:	0

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US-10-692-367-12 (1-257) x ADS92687 (1-774)
Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACATCGCGCTGCCAGCCAAAGATATGCTGCAGCAAGTTCCGCTACTCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCCAGCAGTACTCGCGCGCAGCGGTGCGAGTCCGCGCGCGCTCGCGCGCGCGGT 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ValThrAspAlaPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCCGACGGTCTTCAACGGCNTCAAGCGCACGCCGCGGAGCGGTGCGAGGSCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCGGAGCGCGTTCCTGAGCGCGCTCAAGCGCTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 301 GGCGGGTCAAGGTGCGAGGCAAGCGGAGATCGCGCTTCCTTCGCGCGCGCGCGCGCG 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAenAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCTACTCGGACCCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGAGTGGCGCGTGCAGCGCGGCGAGAGTACTACGCGCGCGCGCGCGCTGCAG 480
Qy 161 IleSerTrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGAACATAACAACCTACGGCGCGCGGGAGGCGCATCGCTTCGAGCGGCTCGG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrp 200
Db 541 GACCCCGCAGGGTGGCGCGGAGCGCGTGGTGGCGTTCAAGGCGCGCTCTGGTCTGG 600
Qy 201 MetAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACAACGTCACCGTGTATCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 660
Qy 221 GlyAlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GGCGCGCTCGAGTGGCGGGAGCAACCCCGCCAGATGAACGGCGGCTCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
Db 721 AAGCAGTACTGCCGAGCTCGCGTGCAGCCAGGCGCCCACTTGC 771

```

## RESULT 5

AD92675

ID ADS92675 standard; DNA; 771 BP.

XX ADS92675;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #27.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX



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PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92676.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 59; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.8e-108 Length: 771
Score: 1382.50 Matches: 244
Percent Similarity: 96.89% Conservative: 5
Best Local Similarity: 94.94% Mismatches: 7
Query Match: 95.21% Indels: 1
DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92675 (1-771)

Qy 1 SerMetGlnAanCysGlyCysGlnProAanValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACTCGCGCTGCAGCCAACTTCCTGCTCAGCAAGATTTGGCTACTCGCGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGCTACTCGCGCGAGCGGGTGCAGTCCGCGCGCTCG---GGCGGC 117
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 118 GGTGGCGCGGTGGCGCGGAGCGCGCGGAGCGAGTGGCGGTGCGAACTGGCTAATGTG 177
Qy 61 ValThrAspAlaPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 178 GTACCCGACGGCTTCTTCAACGGCATCAAGAACCCAGCCGCGAGCGGTGCGAGCGCAG 237
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIaIaIaIaIaIaIaIaIaIaIa 100
Db 238 AACTTCTACACCCGAGCGGTCTCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCAT 297
Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPhePheAlaHiAlaThrHis 120
Db 298 GCGCGGTTCACAGGTGCAGGGCAAGCGGAGATTGCGGCTTCTTTCGCGCATGTCAACGAC 357
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAanLysSerAanAlaTyrCysAspPro 140
Db 358 GAGACCGGGCATTTCTGTATCATACGCGATCAACAGAGCAACGCCCTACTGCGACCCG 417
Qy 141 ThrLysArgGlnTrrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGCGAGTGGCGGTGCGCGCGGCGGAGAGTACTACGGCGCGGCGCGCTGCGAG 477

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Qy 161 IleSerTrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 478 ATCTCGTGGAACTACAATACGGGCCCGGGGAGGCCCATCGGCTTCGACGGGCTCGGG 537
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTriPheTriP 200
Db 538 GACCCCGCAGGGTGGCGGGACGCCGTGGTGGGCTTCAAGGGCGGCTCTGGTTCGG 597
Qy 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 598 ATGAACAACGTCACCGCTGTGATCGCGAGGCTTCGCGCCACCATCAGGGCCATCAAC 657
Qy 221 GlyAlaLeuGluCysAenGlyAanProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 658 GGCCTCCCTCGAGTGCAGCGGAAACAACCCGCCAGATGAACGGCGCGCTCGGCTACTAC 717
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAanLeuThrCys 257
Db 718 AGGCAGTACTGCCCGCAGCTCGGCTCGACCCAGGCCCACTCCTCCTTGC 768

RESULT 6
ADS92661
ID ADS92661 standard; DNA; 774 BP.
XX
AC ADS92661;
XX
DT 02-DEC-2004 (first entry)
XX
DB Chitinase variant polynucleotide #20.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92662.
XX
PS New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 45; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 774 BP; 139 A; 249 C; 282 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.21e-108 Length: 774
Score: 1382.00 Matches: 241

```

```
Percent Similarity: 97.28% Conservative: 9
Best Local Similarity: 93.77% Mismatches: 7
Query Match: 95.18% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92661 (1-774)

Qy 1 SerMetGlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGAGAACTCGCGTGCAGCCAAACGATATGCTGCAGCGGTTCGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGGACGCGGTTCGGCTGCAGCGGTTCGGCTACTGCGGC 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGAGGCGGAGGCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 180
Qy 61 ValThrAspAlaPhePheAsnGlyIleAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCAACCGAGCGGTTCCTCAACCGGATCAAGAACCGAGCGCGGAGCGGTGCAGGCGCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCGGAGCGGTTCCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgLysArgLysArgLysArgLysArgLysArgLys 120
Db 301 GCGCGGTTCGAGTGCAGGCGAGGCGAGATCGCGCTTCCTTCGCGGCGAGCGCGCAC 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGCGATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCTCTCTCGACCCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGCAGCGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCAG 480
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGAATCAACTACGCGCGCGCGGAGGCGCATCGCGCTTTGACGCGCTCGGG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTrp 200
Db 541 GACCCCAACAGGCTGCGCGGAGCGCGCTGTGTGGCTTCAAGCGCGCGCTCTGTTCTGG 600
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAGCGTGCAGCGGTGTGTGCGCGAGGCGGTTCGCGCGCACCCAGGCGCATCAAC 660
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
Db 661 GCGCGCTTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTCGCGCGAGCTCGGCTGCAGCCAGGCGCCCACTCACTTGC 771

RESULT 7
ADS92681
ID ADS92681 standard; DNA; 774 BP.
XX
AC ADS92681;
XX
DT 02-DEC-2004 (first entry)
DE Chitinase variant polynucleotide #30.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX Heterodera.
OS Synthetic.
```

QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 421 ACCAAGAGGAGTGGCGTGGCGCGCGGAGAGTACTACGGCGGTGGCGCGTGCAG 480  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 481 ATCTGTGGAACTACACTACGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTGCC 540  
 QY 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB 541 GACCCCAACAGGTGGCGCAGGACCGCGTGGCTTCAAGCGCGGCTCTGTGTCTGG 600  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 601 ATGAACAACAGTGCACCGGTGTATCCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 660  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB 661 GGCGCCCTTCGAGTGGCGGCGGGAACAACCCCGCCAGATGAACGCGCGGTCTGCTACTAC 720  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB 721 AAGCAGTACTGCGCGCAGCTCGCGTGCAGCCAGGCGCCCACTTGC 771

## RESULT 8

ADS92677  
 ID ADS92677 standard; DNA; 771 BP.

XX AC ADS92677;

XX DT 02-DEC-2004 (first entry)

XX CC Chitinase variant polynucleotide #28.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 XX KW Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX XX 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR P-PSDB; ADS92678.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 61; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 XX CC encoding them. A method of enhancing plant resistance to a fungus or  
 XX CC nematode comprises introducing into a plant a recombinant expression  
 XX CC cassette comprising a promoter operably linked to a chitinase  
 XX CC polynucleotide of the invention. The plant is maize or soybean. The  
 XX CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 XX CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 XX CC plant resistance to a fungus or nematode. This sequence represents a  
 XX CC chitinase variant polynucleotide of the invention.

SQ Sequence 771 BP; 139 A; 255 C; 272 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2.2e-107 Length: 771  
 Score: 1373.50 Matches: 242  
 Percent Similarity: 97.28% Conservative: 8  
 Best Local Similarity: 94.16% Mismatches: 6  
 Query Match: 94.59% Indels: 1  
 DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92677 (1-771)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGCAAGTACGGCTGCCAGCAAGATATGCTGCAGCAAGTTTCGGCTACTCGGGC 60  
 QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACGACCGACGAGTACTCCGGGACGGGTGCAGTTCGGGCCCGTCCGCCCG---GGCGGC 117  
 QY 41 Gly 60  
 DB 118 GCGCGCGTGGCGCGCGCGAGCGCGGAGGCGAGTGGCGTGCAGAACTGGCTAGGTC 177  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 178 GTCACCGGCTCTTTCTTCAACGGCATCAAGAGCGAGCGCGGAGCGGTGCGAGGGCAAG 237  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
 DB 238 AACTTCTACACCGGAGCGGCTTCTGAGCGCGCTCAAGGGCTACCCAGGGCTTCGCCAT 297  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120  
 DB 298 GCGCGCTCCGAGTTCGAGCGCAAGCGGAGATTGCCGCTTCTTCGCGCAGCGCACGCGC 357  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 358 GAGACCGGGCATTTCTGTATCATCAACGAGATCAACAGAGCAACACGCTTACTGCGACCCG 417  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 418 ACCAAGAGGAGTGGCGTGGCGCGCGCGGCGAGAGTACTACGGGCGCGGCGGCTGCGAG 477  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 478 ATCTGTGGAACTACAACTACGGCGCGCGGAGGCGCATCGCTTCGACGGGCTCGCC 537  
 QY 181 AspProGlyArgValAlaAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB 538 GACCCCGCAGGGTGGCGCGGACGCGGTTCGCGTTCGAGGCGGCGCTCTGGTTCCTGG 597  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 598 ATGAACAACGTGCACCGCTGTATGCCCGGAGGCTTCGGCGCCACCATCAGGGCCATCAAC 657  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB 658 GCGCGCTTCAGTTCGACGGGAGAACACCCCGCCAGATGAACGCGCGGTCTGCTACTAC 717  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB 718 AAGCAGTACTGCGCGCAGCTCGCGTGCAGCCAGGCGCCCACTTGC 768

## RESULT 9

ADS92663

ID ADS92663 standard; DNA; 771 BP.

XX AC ADS92663;

XX AC ADS92663;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #21.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 XX  
 OS Synthetic.  
 XX W02004037194-A2.  
 XX  
 XX 06-MAY-2004.  
 XX  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX  
 XX 22-OCT-2002; 2002US-0420666P.  
 XX  
 XX 06-NOV-2002; 2002US-00290086.  
 XX  
 XX 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 XX P-PSDB; ADS92664.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 XX Claim 4; SEQ ID NO 47; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.  
 XX  
 XX SQ Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.64e-107 Length: 771  
 Score: 1366.50 Matches: 243  
 Percent Similarity: 96.50% Conservative: 5  
 Best Local Similarity: 94.55% Mismatches: 8  
 Query Match: 94.11% Indels: 1  
 DB: 13 Gaps: 1  
 US-10-692-367-12 (1-257) x ADS92663 (1-771)  
 QY 1 SerMetGlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGCAGAACTCGCGTGCAGCCAAACGTATGCTGCAGCAAGTTTCGGCTACTCGCGC 60  
 QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACGACCGACGAGTACTCGCGGCGAGCGGTCGAGTCGCGGCCCGCTCG---GCGCGC 117  
 QY 41 Gly 60  
 DB 118 GC 177  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 178 GTACCGGCTCTCTTCAACGGCATCAAGAACCAAGCGCGCGAGCGCGGTGCGAGGCGCAAG 237  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
 DB 238 AACTTCTACCCCGAGCGGCTTCTGAGCCCGTCAAGGCGTACCCAGGCTTCGCCCAT 297  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHis 120

DB 298 GCGGGTTCACAGGTGCAGGCGCAAGCGCAGATCGCGCCCTTCTTGGCGCATGTACACGAC 357  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 358 GAGACCGGGCATTTCCGCTACATCAGCGAGGTCAACAAGAGCAACGCTTACTTGGACCCG 417  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 418 ACCAAGAGGAGTGGCGTGGCGCGCGCGCGGAGTACTACGCGCGCGCGCTGCAG 477  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 478 ATCTCGTGAACATACAACTACGCGCGCGCGCGGAGGCCATCGCTTTGACGGGCTCGGG 537  
 QY 181 AspProGlyValAlaAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrp 200  
 DB 538 GACCCGCGAGGTGGCGCGCGCGCGCGCGCTGGTGGCTTCAAGGCGCGCTCTGGTTCTGG 597  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 598 ATGAACAACGTCACCGTGTGATGCGCGCGCGCTTCGGCGCCACCATCAGGGCCATCAAC 657  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB 658 GCGCGCTTCGAGTGCAGCGCGGAAACACCCGCGCCAGATGAACGCGCGCTCGGCTACTAC 717  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
 DB 718 AGGAGTACTTCCGCCAGCTCGCGCTGCACCCAGGGCCCAACTCATTGCG 768  
 RESULT 10  
 ADS92679  
 ID ADS92679 standard; DNA; 774 BP.  
 XX  
 AC ADS92679;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polynucleotide #29.  
 XX  
 KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 OS Synthetic.  
 XX W02004037194-A2.  
 XX  
 XX 06-MAY-2004.  
 XX  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX  
 XX 22-OCT-2002; 2002US-0420666P.  
 XX  
 XX 06-NOV-2002; 2002US-00290086.  
 XX  
 XX 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 XX P-PSDB; ADS92680.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 XX Claim 4; SEQ ID NO 63; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 144 A; 256 C; 269 G; 105 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.72e-106 Length: 774  
 Score: 1363.00 Matches: 237  
 Percent Similarity: 96.11% Conservative: 10  
 Best Local Similarity: 92.22% Mismatches: 10  
 Query Match: 93.87% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92679 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGGCGTGCAGCAAACTTCTGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
 Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACAACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGCGCTGCGCGCGCGGC 120  
 Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 121 GCG 180  
 Qy 61 ValThrAspAlaPhePheAsnGlyLysGlnAlaGlySerGlyCysGluGlyLys 80  
 Db 181 GTCAACCGACGGTCTTTCACGGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 240  
 Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaTyrProGlyPheAlaHis 100  
 Db 241 AACTTCTACACCGCGAGCGTCTCTGAGCGCGTCAAGGCGTACCGAGGCTTCGCCAT 300  
 Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaPheAlaPheAlaHis 120  
 Db 301 GCGCGGTACAGGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 Qy 121 GluThrGlyHisPheCysTyrLysSerGluValAlaLysSerAlaTyrCysAspPro 140  
 Db 361 GAGACCGGCGCATTTCTGCTACTCAGCGAGATCAACAGAACCGCTCTCGCGACCG 420  
 Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 Db 421 ACCAAGAGGCGAGTGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaLysGlyPheAspGlyLeuGly 180  
 Db 481 CTGTGCTGGAACTCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyr 200  
 Db 541 GACCCCAACAGGTGGCGCGGAGACCCCGTGTGGCGTTCAAGGCGCGCGCTCTGTCTCG 600  
 Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaAlaAsn 220  
 Db 601 ATGAACAACGTGCACCGTGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
 Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 Db 661 GCGCGCTTCAAGTGGCGGGAACAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
 Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
 Db 721 AAGCAGTACTGCCCGCAGCTCGGCGTGCACCGCGCGCGCGCGCGCGCGCGCGCG 771

RESULT 11

ADS92689

ID ADS92689 standard; DNA; 771 BP.

XX

AC ADS92689;  
 DT 02-DEC-2004 (first entry)  
 XX Chitinase variant polynucleotide #34.  
 DB Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
 XX *Heterodera*.  
 KW Synthetic.  
 XX WO2004037194-A2.  
 PN 06-MAY-2004.  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA Muller ML, True T, Simmons CR, Valpani N;  
 XX WPI; 2004-365417/34.  
 DR P-PSDB; ADS92690.  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX Claim 4; SEQ ID NO 73; 197pp; English.  
 PS The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.  
 XX SQ Sequence 771 BP; 140 A; 249 C; 275 G; 107 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 2.29e-106 Length: 771  
 Score: 1361.50 Matches: 237  
 Percent Similarity: 96.89% Conservative: 12  
 Best Local Similarity: 92.22% Mismatches: 7  
 Query Match: 93.77% Indels: 1  
 DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92689 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGGCGTGCAGCAAACTTCTGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
 Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCGCGCGCTGCGCGCGCG 117  
 Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 118 GCGCGCGGTGGCG 177  
 Qy 61 ValThrAspAlaPhePheAsnGlyLysGlnAlaGlySerGlyCysGluGlyLys 80  
 Db 178 GTCAACCGACCTCTTCTTCAACGGCATCAAGACCGCGCGCGCGCGCGCGCGCG 237  
 Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaTyrProGlyPheAlaHis 100

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Db 238 AACTTCTACACCCGAGCGCTTCTGAGCGCGCTCAAGGGTACCCAGGCTTCGCCCAT 297
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120
Db 298 GCGGGTCCGAGGTGCAGGCAAGCGGAGATCCCGCTTCTTCGGCGCATGTCAACGCAC 357
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAlaPheAlaHisAlaThrHis 140
Db 358 GAGACCGGGCATTTCTGTCTACATCAACGAGATCAACAGAGCAACGCCCTACTCGCACCCG 417
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGCGAGTGGCGCTGCGCGCGGGCAGAGGTACTACGGGCGTGGCCCGCTGCAG 477
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 478 ATCTCGTGAACACTCACTACGGGCGCGCGGGAGGCGCATCGGCTTCGACGGGCTCGGG 537
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 538 GACCCCGGCGAGGTGGCGGGAGCGCGCTGTGGTGGGTTCAGAGCGCGCTCTGGTTCGTG 597
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 598 ATGAACAACGTGCACCGTGTGTGTCGCGCAGCGGCTTCGGCGCCACCATCAGGGCCATCAAC 657
Qy 221 GlyAlaLeuGluCysAsnGlyAsnValProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 658 GCGCGCTTCGAGTGCAGGGAACAACCCCGCCAGATGAACGCGCGCATCGGCTACTAC 717
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 718 AAGCAGTACTCGCCGCTCGCGTGCACCCAGGCGCCCAACCTCATTGC 768

RESULT 12
ADS92639
ID ADS92639 standard; DNA; 774 BP.
AC ADS92639;
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DT 02-DEC-2004 (first entry)
DE Chitinase variant polynucleotide #9.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92640.
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PT New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 23; 197pp; English.
XX
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CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention..
XX
SQ Sequence 774 BP; 146 A; 246 C; 271 G; 111 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,54e-106 Length: 774
Score: 1361.00 Matches: 237
Percent Similarity: 95.72% Conservative: 9
Best Local Similarity: 92.22% Mismatches: 11
Query Match: 93.73% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92639 (1-774)
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATGCTGCAGCAAGTTTGGCTACTCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGGCGAGGGTGCAGTTCGGGCGCGCTCGCGTTCGGGCGGC 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GGCAGCAGTGGCGCGCGCGGAGCGCGGAGCGAGTGGCGTGCAGACGTGGCTAATGTG 180
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGly 80
Db 181 GTCAACCGCGCTTCTTCAACGCGCATCAAGAACCGAGCCGCGAGCTGGTCGAGGGGCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCCGAGCGGTCTTCTGAGCGCGCTCAAGGGTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGTTCGAGGTGCAGGCGAGCGAGATCGCGCTTCTTCGCGCATGTCAACGCAC 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAlaPheAlaHisAlaThrHis 140
Db 361 GAGACCGGGCATTTTGTGTCTACATCAACGAGGTCAACAGAGCAACGCCCTACTCGCACCCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGGCGCTGCGCGCGGGCAGAGTACTACGGGCGGCGCGCTCGAG 480
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGAACACTCACTACGGGCGCGGAGGCGCATCGGCTTCGACGGGCTGGGA 540
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCGACAGACTGGCGCGAGGACCCCGTGTGTTCAGTCCGCGCTCGGCTTCGG 600
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACGTGCACCGTGTGTGTCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660
Qy 221 GlyAlaLeuGluCysAsnGlyAsnValProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGCAGGCGGAAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 721 AAGCAGTACTCGCGCTCGAGCTCGCGTGCACCCGCGCAACACCTCACCCTGC 771
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The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention..









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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:37:22 ; Search time 3056.63 Seconds

(without alignments)  
4074.095 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :

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4: gb.on:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1320	90.9	843	8 MZECHITA	M84164 Zea mays ch
2	1297.5	89.4	1094	6 AR321624	AR321624 Sequence
3	1291	88.9	1128	8 AY532740	AY532740 Zea diplo
4	1287	88.6	810	8 MZECHITB	M84165 Zea mays ch

5	1274	87.7	1094	8 AY532775	AY532775 Zea mays
6	1273	87.7	1123	8 AY532726	AY532726 Zea mays
7	1273	87.7	1131	8 AY532780	AY532780 Zea mays
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15	1269	87.4	1110	8 AY532787	AY532787 Zea diplo
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21	1262	86.9	1140	8 AY532731	AY532731 Zea mays
22	1260.5	86.8	1122	8 AY532771	AY532771 Zea mays
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#### ALIGNMENTS

RESULT 1	MZECHITA	Zea mays chitinase A	843 bp	DNA	linear	PLN 27-APR-1993
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ACCESSION	M84164	chitinase A.				
VERSION	M84164.1	GI:168440				
KEYWORDS						
SOURCE						
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AUTHORS						
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Best Local Similarity: 90.20% Mismatches: 16
Query Match: 90.91% Indels: 0
DB: 8 Gaps: 0

US-10-692-367-12 (1-257) x MZECHITA (1-843)

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Db 76 CAGAACTCGCGTCTCCAGCAAACTTCTGTCGAGCAAGTTTCGGCTACTCGCGCAGCAGC 135
Qy 23 AspGluTyrCysGlyAspGlnSerGlyProCysArgSerGlyGlyGlyGlyGly 42
Db 136 GACGCCTACTCGCGGACGGGTGCGAGTCGGGCGCGTCCGCTCGGGCGGGCGGGCGGC 195
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
Db 196 GCGCGCGCGCGGAGGGCGGGGAGGCGAGTGGCGGTGCGAAGTGGCTAATGTGGTCAAC 255
Qy 63 AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 256 GACGGCTTCTTCAACGGCATCAAGAACAGCGCGGAGCGGTGCGAGGCAAGAACTTC 315
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Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 376 ACGGAGGTGGAGGCAAGCGGAGATCGCGCTTCTTCGGCGAGTCAACGACGAGAC 435
Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142
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RESULT 2
AR321624 LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6563020.
ACCESSION AR321624
VERSION AR321624.1 GI:33706864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1094)
AUTHORS Simmons,C.R. and Valpani,N.
TITLE Maize chitinases and their use in enhancing disease resistance in
crop plants
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;
FEATURES Location/Qualifiers
source 1..1094
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ORIGIN
Alignment Scores:
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Score: 1297.50 Matches: 229
Percent Similarity: 93.33% Conservative: 9
Best Local Similarity: 89.80% Mismatches: 10
Query Match: 89.36% Indels: 7
DB: 6 Gaps: 1

US-10-692-367-12 (1-257) x AR321624 (1-1094)

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Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
Db 270 AGTGGCGGC-----GGTGGTGGCAACGTGGCTAGCGTCTCGTCAAC 308
Qy 63 AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 309 GGCTCTCTTCTTCAACGGCATCAAGAGCCGAGCGCGGAGCGGTGCGAGGGCAAGACTTC 368
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 429 TCGCAGGTGCAAGCAAGCGGAGATCGCGCTTCTTCGGCGCACGCCACGACGAGAC 488
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Db 489 GGGCATTTCTGTATCATCAGCGAGATCAACAGAGCAACGCTACTTGGACCCGACCAAG 548
Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162
Db 549 AGGAGTGGCGGTGGCGCGGGGCGAGAACTACTACGGGCGGGCGGCTCGAGATCTCG 608
Qy 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db 609 TGGAACTACACTACGGGCGCGGGAGGGCCATCGGCTTCGAGCGGGCTCGGGGACCCC 668
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 QY 203 AenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 222  
 Db 729 ACCTGTACACGGGGTGGTCCGAGGGGTTCGCGCCACACAGGGCCCATCAACGGCGCC 788  
 QY 223 LeuGluCysAenGlyAsnAsnProAlaGlnMetAenAlaArgValGlyTyrTyrArgGln 242  
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## RESULT 3

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 LOCUS  
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 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

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 AY532740.1 GI:48093261  
 Zea diploperennis  
 Zea diploperennis  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 1128)  
 Tiffin,P.  
 Comparative evolutionary histories of chitinase genes in the genus  
 Zea and family poaceae  
 Genetics 167 (3), 1331-1340 (2004)  
 15280246  
 2 (bases 1 to 1128)  
 Tiffin,P.  
 Direct Submission  
 Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
 1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
 Location/Qualifiers

## FEATURES

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## ORIGIN

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 Percent Similarity: 81.76% Conservative: 9  
 Best Local Similarity: 78.72% Mismatches: 13  
 Query Match: 88.91% Indels: 41  
 DB: 8 Gaps: 1

US-10-692-367-12 (1-257) x AY532740 (1-1128)  
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 QY 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu--- 121  
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## RESULT 4

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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

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 M84165  
 M84165.1 GI:168442  
 chitinase B.  
 Zea mays  
 Zea mays  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 810)  
 Huynh, O.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R.  
 and Shah, D.M.  
 Antifungal proteins from plants. Purification, molecular cloning,  
 and antifungal properties of chitinases from maize seed  
 J. Biol. Chem. 267 (10), 6635-6640 (1992)  
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 MEDLINE  
 PUBMED  
 COMMENT  
 Original source text: Zea mays (library: Lamda GT 10 corn seed  
 (imibed)) seed DNA.

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gene

CDS

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## ORIGIN

US-10-692-367-12 (1-257) x MZECHITB (1-810)  
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 181 GCGAGTGTGGC-----GGTGTGCGAAGTTCGGCTAGCGTCTGCTCACC 222  
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 LOCUS Zea mays subsp. parviglumis isolate p9 chitinase (chia) gene,  
 DEFINITION complete cds.

ACCESSION AV532775

VERSION AV532775.1 GI:48093331

KEYWORDS

SOURCE

ORGANISM

Zea mays subsp. parviglumis  
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 1094)

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

2 (bases 1 to 1094)

Tiffin, P.

Direct Submission

Submitted (23-JAN-2004) Plant Biology, University of Minnesota,

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

Location/Qualifiers

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gene

mRNA

CDS

## ORIGIN

Alignment Scores:  
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 Query Match: 87.74% Indels: 32  
 DB: 8 Gaps: 1

US-10-692-367-12 (1-257) x AY532775 (1-1094)

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## RESULT 6

AY532726

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

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Best Local Similarity: 77.44% Mismatches: 10

Query Match: 87.67% Indels: 48

DB: 8 Gaps: 2

US-10-692-367-12 (1-257) x AY532726 (1-1123)

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DEFINITION Zea mays subsp. parviglumis isolate p1 chitinase (chia) gene,  
complete cds.  
ACCESSION AY532768  
VERSION AY532768.1 GI:48093317  
KEYWORDS  
SOURCE Zea mays subsp. parviglumis  
ORGANISM Zea mays subsp. parviglumis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1115)  
AUTHORS Tiffin,P.  
TITLE Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
JOURNAL Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
REFERENCE 2 (bases 1 to 1115)  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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ORIGIN

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Best Local Similarity: 79.72% Mismatches: 16  
Query Match: 87.50% Indels: 33  
DB: 8 Gaps: 2  
US-10-692-367-12 (1-257) x AY532768 (1-1115)  
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QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
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Db 213 GCGCGCGCAGTGGCGCGGAGCGCGAGTGGCGGTAACGAGTGGCTTAAACGTGGTCAACC 272  
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Db 693 AGGACATCGGCTTCAACGGGCTCGCGACCCCAACAGGCTGGCGAGCGCGGTGATC 752  
QY 192 AlaPheIysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMetProGlnGly 211  
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RESULT 9  
AY532733  
LOCUS AY532733 1127 bp DNA linear PLN 29-JUL-2004

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DEFINITION Zea mays subsp. parviglumis isolate p12 chitinase (chiB) gene,
complete cds.
ACCESSION AY532733
VERSION AY532733.1 GI:48093247
KEYWORDS
ORGANISM
Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
Zealand family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORGANISM Zea diploperennis  
REFERENCE  
AUTHORS Tiffin,P.  
TITLE Comparative evolutionary histories of chitinase genes in the genus  
zealand family poaceae  
JOURNAL Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
REFERENCE  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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RESUL II  
AY532783

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ORGANISM	Zea diploperennis	
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	clade: Panicoideae; Andropogoneae; Zea	

REFERENCE	1 (bases 1 to 1110)		
AUTHORS	Tiffin,P.		
TITLE	Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae		
JOURNAL	Genetics 167 (3), 1331-1340 (2004)		
PUBMED	15280246		
REFERENCE	2 (bases 1 to 1110)		
AUTHORS	Tiffin,P.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA		
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Best Local Similarity:	78.82%	Mismatches:	14
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Alignment Scores:	
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Length:	1110
Matches:	227
Conservative:	11
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Indels:	36

	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
	Tiffin,P. Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae
	Genetics 167 (3), 1331-1340 (2004)
	PUBMED 15280246
	JOURNAL Tiffin,P.
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	1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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clade; Panicoideae; Andropogoneae; Zea.
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Tiffin,P.
REFERENCE Comparative evolutionary histories of chitinase genes in the genus
AUTHORS ze and family poaceae
TITLE Genetics 167 (3), 1331-1340 (2004).
JOURNAL PUBMED 15280246
REFERENCE 2 (bases 1 to 1110)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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US-10-692-367-12 (1-257) x AY532785 (1-1110)
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            Tiffin,P.
REFERENCE 1 (bases 1 to 1110)
TITLE      Comparative evolutionary histories of chitinase genes in the genus
            Zea and family poaceae
JOURNAL    Genetics 167 (3), 1331-1340 (2004)
PUBMED     15280246
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AUTHORS    Tiffin,P.
TITLE      Direct Submission
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Qy      83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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Qy      190 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro 209
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ACCESSION AY532787
VERSION    AY532787.1 GI:48093355
KEYWORDS
SOURCE
ORGANISM   Zea diploperennis
            Zea diploperennis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 1110)
            Tiffin,P.
REFERENCE 1 (bases 1 to 1110)
TITLE      Comparative evolutionary histories of chitinase genes in the genus
            Zea and family poaceae
JOURNAL    Genetics 167 (3), 1331-1340 (2004)

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PUBMED 15280246  
REFERENCE 2 (bases 1 to 1110)  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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/db\_xref="GI:48093356"  
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"

## ORIGIN

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Percent Similarity: 82.64% Conservative: 11  
Best Local Similarity: 78.82% Mismatches: 14  
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US-10-692-367-12 (1-257) x AY532787 (1-1110)

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QY 123 GlyHis-----124
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QY 190 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMetPro 209
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Db 747 GTGATCGCGTTCAAGACGCGCGCTCTGCTGATGAACAACAGTGCACCGCTGTGATGCCG 806
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QY 210 GlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAenGlyAenAen 229
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Job time : 3062.63 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2005, 12:21:21 ; Search time 116.081 Seconds  
(without alignments)  
1133.730 Million cell updates/sec

Title: US-10-692-367-12  
Perfect score: 1452  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1316	90.6	280	Q6JBQ2	Q6jbq2 zea mays (s
5	1316	90.6	284	2 Q6JBQ9	Q6jbq9 zea mays (s
6	1313	90.4	282	2 Q6JBQ3	Q6jbq3 zea mays (s
7	1312	90.4	280	2 Q6JBQ7	Q6jbq7 zea mays (s
8	1310	90.2	280	2 Q6JBK9	Q6jbk9 zea mays (s
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11	1306	89.9	282	2 Q6JBQ6	Q6jbq6 zea mays (s
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15	1302.5	89.7	281	2 Q6JB11	Q6jb11 zea mays (s
16	1302	89.7	280	2 Q6JBQ8	Q6jbq8 zea mays (s
17	1301.5	89.6	278	2 Q6JBK4	Q6jbk4 zea mays (s
18	1301	89.6	278	2 Q6JB13	Q6jb13 zea mays (s
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26	1294.5	89.2	279	2 Q6JB10	Q6jb10 zea mays (s
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28	1292	89.0	278	2 Q6JB15	Q6jb15 zea diplo
29	1291.5	88.9	279	2 Q6JB05	Q6jb05 zea mays (s
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ALIGNMENTS

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DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
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OX NCBI\_TaxID=4576;  
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RP SEQUENCE FROM N.A.  
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
RA Tiffin P.;  
RT "Comparative evolutionary histories of chitinase genes in the genus  
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RL Genetics 167:1331-1340(2004).  
DR EMBL; AV532740; AAT40009.1; -.  
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 DB 86 SFFNGIKNAGSGCEGKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFAHATHET 145

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 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
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 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
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 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532774; AAT40043.1; -.  
 DR HSSP; P10969; 1K7V.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; F:chitinase activity; IEA.  
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 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
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 DR InterPro; IPR000726; Glyco\_hydro\_19.  
 DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR ProDom; PD354900; Glyco\_hydro\_19; 1.  
 DR SMART; SM00270; ChtBD1; 1.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE; PS00026; CHIT\_BIND\_1; 1.  
 DR PROSITE; PS00941; CHIT\_BIND\_1\_2; 1.  
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 SQ SEQUENCE 280 AA; 29256 MW; DC908138098DE0A3 CRC64;

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DB 28 QNCGQPNVCCSKFGYCGTTDAYCGDGCQSGPCRS--GGGGGGGGGGGGGGGGANVANVT 85

QY 63 DAFNGIKNAGSGCEGKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFAHATHET 122  
 DB 86 DAFNGIKNAGSGCEGKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFAHATHET 145

QY 123 GHFCYISEVKNNAVCPTKQWPCAAQKYYGRGLOISWNNYGPAGRAIGPDGLGDP 182  
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 DB 206 GRVARDVAVFAKALWFMNNVHVRVMPQGFATIRAINGALECGNPNPAQNNARVGYRQ 265

QY 243 YCRLGVDPGNLTC 257  
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 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
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 GN Name=chiA;  
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 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 ze and family poaceae.";  
 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532780; AAT40049.1; -.  
 DR HSSP; P10969; 1K7V.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; F:chitinase activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
 DR InterPro; IPR001002; Chitin binding 1.  
 DR InterPro; IPR000726; Glyco\_hydro\_19.  
 DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
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 DR SMART; SM00270; ChtBD1; 1.  
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QY 63 DAFNGIKNAGSGCEGKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFAHATHET 122  
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Qy 243 YCROLGVDPGNNLTC 257
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Db 266 YCQLRVDPGPNLTC 280

RESULT 2
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C;Date: 12-Mar-1993 #sequence_revision 03-Feb-1994 #text_change 10-Jul-1998
C;Accession: B42424
R;Huyh, Q.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.
J. Biol. Chem. 267, 6635-6640, 1992
A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifungal
A;Reference number: A42424; MUID:92202208; PMID:1551872
A;Accession: B42424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <HUY>
A;Cross-references: GB:M84165
A;Note: the authors translated the codon AAG for residue 104 as Asn, GGC for residue 105
0 as Ile, CAA for residue 231 as Asn and CGC for residue 232 as Gly
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;20-55/Domain: hevein chitin-binding domain homology <HCB>
F;70-268/Domain: plant chitinase homology <PCH>

Query Match 88.6%; Score 1287; DB 2; Length 268;
Best Local Similarity 89.0%; Pred. No. 1.2e-94;
Matches 227; Conservative 9; Mismatches 13; Indels 6; Gaps 1;

Qy 3 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANVT 62
|||||
Db 20 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVASVT 73
|||||

Qy 63 DAFENGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFPAHATHET 122
:|||||
Db 74 SSFENGINKQAGSGCEGKNFYTRSAFLSAVKGYPGFAHGGSQVQCKREIAAFPAHATHET 133
:|||||

Qy 123 GHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGRAIGFDGLDP 182
|||||
Db 134 GHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGRAIGFDGLDP 193
|||||

Qy 183 GRVARDAVAFKALWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARVGYTRQ 242
|||||
Db 194 GRVARDAVAFKALWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARVGYTRQ 253
|||||

Qy 243 YCROLGVDPGNNLTC 257
|||||
Db 254 YCROLGVDPGPNLTC 268
|||||

RESULT 3
S51678
chitinase (EC 3.2.1.14) class I - European elder (fragment)
N;Alternate names: pathogenesis-related protein PR-3 type
C;Species: Sambucus nigra (European elder)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51678
R;Coupe, S.A.; Taylor, J.E.; Roberts, J.A.
submitted to the EMBL Data Library, December 1994
A;Description: Characterisation of mRNAs that encode pathogenesis-related proteins that
A;Reference number: S51645
A;Accession: S51678
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <COU>
A;Cross-references: UNIPROT:Q43150; EMBL:246948; NID:G603881; PID:CAA87072.1; PID:G6038
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;16-51/Domain: hevein chitin-binding domain homology <HCB>
F;61-261/Domain: plant chitinase homology <PCH>
```

```
Query Match 60.0%; Score 870.5; DB 2; Length 261;
Best Local Similarity 59.6%; Pred. No. 1e-61;
Matches 155; Conservative 30; Mismatches 60; Indels 15; Gaps 4;

Qy 1 SMQNCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANV 60
|||||
Db 14 SGQNCQCAPNLCCSQFGYCGSDAAYCGEGRSGFCY-----GSPFGSSASSAVNI 62
|||||

Qy 61 VTDAFENGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFPAHATH 120
|||||
Db 63 VTNNFFNGLISPNQ-GCAGSGFYTRDAFLAASFPYPAFGTTGSDNEDRRREIAAFATHSH 121
|||||

Qy 121 ETGHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGRAIGFDGL 179
|||||
Db 122 ETGHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGQSIGFDGL 181
|||||

Qy 180 GDPGRVARDAVAFKALWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARV 237
|||||
Db 182 GDPGIVARDPVISFRASLWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARV 241
|||||

Qy 238 GYTRYQYCRQLGVDPGNNLTC 257
|||||
Db 242 NYTQFCNQLSVPPGGNLRC 261
|||||

RESULT 4
S25311
chitinase (EC 3.2.1.14) precursor - rape
C;Species: Brassica napus (rape)
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C;Accession: S25311
R;Raamsen, U.; Bojse, K.; Collinge, D.B.
Plant Mol. Biol. 20, 277-287, 1992
A;Title: Cloning and characterization of a pathogen-induced chitinase in Brassica napus.
A;Reference number: S25311; MUID:93004480; PMID:1391771
A;Accession: S25311
A;Molecule type: mRNA
A;Residues: 1-268 <RAS>
A;Cross-references: UNIPROT:Q06209; EMBL:X61488; NID:G17798; PID:CAA43708.1; PID:G17799
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-24/Domain: signal sequence #status predicted <Sig>
F;25-268/Product: chitinase #status predicted <MAT>
F;25-60/Domain: hevein chitin-binding domain homology <HCB>
F;74-268/Domain: plant chitinase homology <PCH>

Query Match 59.4%; Score 862.5; DB 2; Length 268;
Best Local Similarity 60.2%; Pred. No. 4.5e-61;
Matches 154; Conservative 30; Mismatches 59; Indels 13; Gaps 4;

Qy 3 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGANVANVT 62
|||||
Db 25 QNCGCAPNLCCSQFGYCGSDAAYCGEGRSGFCY-----IVT 77
|||||

Qy 63 DAFENGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFPAHATHET 122
|||||
Db 78 QAFENGINKQAGSGCGAGKNFYTRDSFNAANTPFNFANSVT----RREIATMFAHATHET 133
|||||

Qy 123 GHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGD 181
|||||
Db 134 GHFCYISEVNVKSNAYCDPTKQWPQCAAGQKYGRGLQISWNYNYPAGQSIGFDGLGD 193
|||||

Qy 182 PGRVARDAVAFKALWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARVGYTR 241
|||||
Db 194 PELVSSNPTVAFRGLFWFMMNVHVRVMPQGFATIRAINGALECGNPNPAQNNARVGYTR 252
|||||

Qy 242 QYCRQLGVDPGNNLTC 257
|||||
Db 253 DYCCQLGVDPGPNLSC 268
|||||

RESULT 5
T47601
```

QY 49 -GGSGGANVANVVTDAFFNGIKNAGSGGEGKNTFTSRSAFLSAIAAYPGFAHGSGSEVER 107  
 DB 78 PGTGGGSSVSDIVSQAFDFGIIGQAASCPGKNFTYRAAFLSAVD--PKFGNEGSSDDN 135  
 QY 108 KRIIAFAFAHATHETGHFCYISE--VNKSNAYCDPTK-ROMPCAAGOKYYGRGPLOISWN 164  
 DB 136 KRIIAFAFAHISHETNLCHIERDGVGDYCDQKAAQYPCAAHGKYYGRGPLOISWN 195  
 QY 165 YNYGPAGRAITGFDGLGDPGRVARDVAVFAKALWFWMNNVHRYVMQFGGATIRAINGALE 224  
 DB 196 YNYALAGALGFDGLGNPKERKATDVNTSPKAAWFWMTNVHVSVMNQFGGATIRAINGALE 255  
 QY 225 CNGNPPAQMNAVGVYTRYQYCRQLGVDPGNLTC 257  
 DB 256 CNGQNDQANDRIQFYKKYCADEGVAPGDNLTC 288

RESULT 7  
 A84868  
 probable endochitinase [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: A84868  
 R;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,  
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; T  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;  
 Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalian  
 A;Reference number: A84420, MUID:20083487; PMID:10617197  
 A;Accession: A84868  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-264 <STO>  
 A;Cross-references: UNIPROT:O24658; GB:AE002093; NID:g2281111; PIDN:AAB64047.1;  
 C;Genetics:  
 A;Gene: At2g43590  
 A;Map position: 2  
 C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain hom

Query Match 56.8%; Score 824.5; DB 2; Length 264;  
 Best Local Similarity 57.0%; Pred. No. 4.5e-58;  
 Matches 146; Conservative 32; Mismatches 61; Indels 17; Gaps 4;

QY 3 QNCGCPNVCCSKFPGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGGGANVANVT 62  
 DB 25 QNCGCAPNLCCSQFGYCGTDDAYCGVGCRRGPKR-----GSGTPTGSGVGSIVT 73  
 QY 63 DAFNGIKNAGSGGCGKNTFTSRSAFLSAIAAYPGFAHGSGSEVERKRIIAFAHATHET 122  
 DB 74 QGFNNIIINQAGNCGACGKGFYTRDSFVNAAANTPPFNANSVT----RRIEATMFHFHET 129  
 QY 123 GHFCYISEVN-KSNAYCDPTKROMPCAAGOKYYGRGPLOISWNVYGPAGRAITGFDGLG 181  
 DB 130 GHFCYILEEINGATNTYCCSNTQYPCAPGKGYFGRGPLOISWMNYNGACQSGLDLRLR 189  
 QY 182 PGRVARDVAVFAKALWFWMNNVHRYVMQFGGATIRAINGALECNGNPPAQMNAVGVYR 241  
 DB 190 PELVGSNPVAFPTGLFWFNNVSRPVLNQFGGATIRAING-MECNGNSGAVNARIGYR 248  
 QY 242 QYCRQLGVDPGNLTC 257  
 DB 249 DYCGQLGVDPGNLSC 264

RESULT 8  
 S16579  
 chitinase (EC 3.2.1.14) precursor - kidney bean  
 C;Species: Phaseolus vulgaris (kidney bean)  
 C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C;Accession: S16579  
 R;Margis-Finheiro, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.  
 Plant Mol. Biol. 17, 243-253, 1991  
 A;Title: Isolation of a complementary DNA encoding the bean PR4 chitinase: an

A;Reference number: S16579; MUID:91322521; PMID:1863776

A;Accession: S16579

A;Molecule type: mRNA

A;Residues: 1-270 <MAR>

A;Cross-references: UNIPROT:P27054; EMBL:X57187

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;24-59/Domain: hevein chitin-binding domain homology <HCB>

F;70-270/Domain: plant chitinase homology <PCH>

Query Match 56.2%; Score 816; DB 2; Length 270;

Best Local Similarity 57.9%; Pred. No. 2.2e-57;

Matches 150; Conservative 32; Mismatches 65; Indels 12; Gaps 4;

Qy 1 SMQNGCPNVCCKSFYCGTDDYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60

Db 22 SAQNGCGAEGLCSSQYCGTGGEDYCGTGGCGGCTT-----ASPPPSNNVN-ADI 71

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVERKREIAAFAHATH 120

Db 72 LTADFLNGIIDQADSGCGKGFYTRDAFLSALNSYTDGFRVGSDDSKREIAAFAHATH 131

Qy 121 ETGHFCYISEVN-KSNAYCDPTK-RQWPCAAQKQYGRGPIQISWNNYGPAGRAIGPDG 178

Db 132 ETGHFCYIEEDGASKDYCDDESIAQYPCSSSKGYHGRGPIQLSWNNFYGPAGSANNPDG 191

Qy 179 LGDPCRVARDAAVFAKALWFMNNVHVRVMPQGFATIRANGALECNGNPPAQMNAVVG 238

Db 192 LGAPETVSNVSVFKAALWFMNNVHVRVMPQGFATIRANGALECNGNPPAQMNAVVG 251

Qy 239 YYRYCQQLGVDGNNLTC 257

Db 252 YYTEYCRQLGVDGNNLTC 270

RESULT 9

S57476

chitinase class 4 - cowpea (fragment)

C;Species: Vigna unguiculata (cowpea)

C;Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S57476

R;Vo, L.T.T.; Broughton, W.; Krause, A.

A;Reference number: S57468

A;Accession: S57476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-249 <VOL>

A;Cross-references: UNIPROT:Q43686; EMBL:X88803; NID:G871767; PID:G8717

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

F;4-39/Domain: hevein chitin-binding domain homology <HCB>

F;70-249/Domain: plant chitinase homology <PCH>

Query Match 56.0%; Score 812.5; DB 2; Length 249;

Best Local Similarity 58.3%; Pred. No. 3.8e-57;

Matches 151; Conservative 30; Mismatches 65; Indels 13; Gaps 4;

Qy 1 SMQNGCPNVCCKSFYCGTDDYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60

Db 2 SAQNGCGAEGLCSSQYCGTGGEDYCGTGGCGGCTT-----SSSLNNVNVAADI 51

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVERKREIAAFAHATH 120

Db 52 VTDAFFNGIIDQADSGCGKGFYTRDAFLSALDSYTDGFRVGSDDSKREIAAFAHATH 111

Qy 121 ETGHFCYISEVN-KSNAYCDPTK-RQWPCAAQKQYGRGPIQISWNNYGPAGRAIGPDG 178

Db 112 ETGHFCYIEEDGASKDYCDDESIAQYPCSS-SRGYTVVPIQLSWNNFYGPAGSANNPDG 170

Qy 179 LGDPCRVARDAAVFAKALWFMNNVHVRVMPQGFATIRANGALECNGNPPAQMNAVVG 238

Db 171 LGPPETVSNVSVFKAALWFMNNVHVRVMPQGFATIRANGALECNGNPPAQMNAVVG 230

Qy 239 YYRYCQQLGVDGNNLTC 257

Db 231 YYTEYCRQLGVDGNNLTC 249

RESULT 10

T03405

probable chitinase (EC 3.2.1.14) IIB - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C;Accession: T03405

R;Tuong, N.; Itoh, Y.

A;Description: Nucleotide sequence of rice class II chitinase cDNA.

A;Reference number: Z14936

A;Accession: T03405

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-229 <TRU>

A;Cross-references: UNIPROT:O04138; EMBL:AB003194

A;Experimental source: cv. Nipponbare

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;30-229/Domain: plant chitinase homology <PCH>

Query Match 55.8%; Score 809.5; DB 2; Length 229;

Best Local Similarity 58.1%; Pred. No. 6.1e-57;

Matches 141; Conservative 26; Mismatches 39; Indels 1; Gaps 1;

Qy 52 SGGANVANVVTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVERKREI 111

Db 23 AAGVSVESVVTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVERKREI 82

Qy 112 AAPFAHATHETGHFCYISEVNKSA-YCDPTKRWPCAAQKQYGRGPIQISWNNYGP 170

Db 83 AAPFAHATHETGHFCYISEVNKSA-YCDPTKRWPCAAQKQYGRGPIQISWNNYGP 142

Qy 171 GRAIGPDGLDPCRVARDAAVFAKALWFMNNVHVRVMPQGFATIRANGALECNGNPP 230

Db 143 GKNGFGDGLDPCRVARDAAVFAKALWFMNNVHVRVMPQGFATIRANGALECNGNPP 202

Qy 231 AQMNARVYRYQYCRQLGVDGNNLTC 257

Db 203 GAVNARVYRYQYCRQLGVDGNNLTC 229

RESULT 11

H84867

probable endochitinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: H84867

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, D.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-265 <STO>

A;Cross-references: UNIPROT:O24598; GB:AB020993; NID:G2281112; PIDN:AA64048.1; GSPDB:GN

C;Genetics:

A;Map position: 2

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 54.7%; Score 794; DB 2; Length 265;

Best Local Similarity 55.9%; Pred. No. 1.2e-55;

Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 4;

Qy 3 QNCGQPNVCCSKFGYCGTDDYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 62

```
Db 25 QNDCAPNLCSSQFGYCGTTADYCGSTCQSGPCRVGPGPTGAG-----LVGNIVT 74
Qy 63 DAPFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATHET 122
Db 75 QIFFNNIINOAGNGCAGKSFYTRDSFINATNTPFSFAN----TVTRREIATMFHAFTYET 130
Qy 123 GHFCYIIEVW-KSNAYCDPTKRWPCAAQGYKYGRLQIISWNNYNGPAGRAIGFDGLGD 181
Db 131 GHFCYIEBINGASRVCMQDNNRQYPCAPAKSYHGRGPLLLSWNFNYGACGSLGLDLRLQ 190
Qy 182 PGRVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGYR 241
Db 191 PELVSSNPFVAFRTALWFMKSVRVINQGFATIRALSG-FDCGRNLGWNARIGYR 249
Qy 242 QYRCQLGVDPGNNLTC 257
Db 250 DYCGQLGDPGANITC 265

RESULT 12
Ti4345
chitinase (EC 3.2.1.14) EP3-3/ET, class IV - carrot
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4345
R:Kragh, K.; De Vries, S.C.
submitted to the EMBL Data Library, March 1996
A:Reference number: 217995
A:Accession: Ti4345
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-266 <KRA>
A:Cross-references: UNIPROT:Q96410; EMBL:U52847; NID:g1549332; PID:g1549333
A:Experimental source: strain sg766 trophy
C:Genetics:
A:Gene: EP3
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami-
A:Pathway: polysaccharide degradation
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-56/Domain: hevein chitin-binding domain homology <HCB>
F:69-266/Domain: plant chitinase homology <PCH>

Query Match 54.2%; Score 786.5; DB 2; Length 266;
Best Local Similarity 55.8%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYCGEGCQAGPCTNTAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYIEVW-KSNAYCDPTKRWPCAAQGYKYGRLQIISWNNYNGPAGRAIGFDGL 179
Db 131 ETGYFCHKEETNGDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYIDAGKSNEDFGL 189
Qy 180 GPGREVARDAVAFKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFKTALWYKVKVQSVTQGFATIRAIN-SIECNGGSPDAVNSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266

RESULT 13
Ti4348
chitinase (EC 3.2.1.14) EP3B/E6, class IV - carrot
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4348
R:Kragh, K.; De Vries, S.C.
submitted to the EMBL Data Library, March 1996
A:Reference number: 217995
A:Accession: Ti4348
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-268 <KRA>
A:Cross-references: UNIPROT:Q96409; EMBL:U52846; NID:g1549330; PID:g1549331
A:Experimental source: strain sg766 trophy
C:Genetics:
A:Gene: EP3
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami-
A:Pathway: polysaccharide degradation
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:23-58/Domain: hevein chitin-binding domain homology <HCB>
F:71-268/Domain: plant chitinase homology <PCH>

Query Match 53.5%; Score 777.5; DB 2; Length 268;
Best Local Similarity 55.2%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYCGEGCQAGPCTNTAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYIEVW-KSNAYCDPTKRWPCAAQGYKYGRLQIISWNNYNGPAGRAIGFDGL 179
Db 131 ETGYFCHKEETNGDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYIDAGKSNEDFGL 189
Qy 180 GPGREVARDAVAFKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFKTALWYKVKVQSVTQGFATIRAIN-SIECNGGSPDAVNSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266
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C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4348
R:Kragh, K.; De Vries, S.C.
submitted to the EMBL Data Library, March 1996
A:Reference number: 217995
A:Accession: Ti4348
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-266 <KRA>
A:Cross-references: UNIPROT:Q96411; EMBL:U52848; NID:g1549334; PID:g1549335
A:Experimental source: strain sg766 trophy
C:Genetics:
A:Note: EP3
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami-
A:Pathway: polysaccharide degradation
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-56/Domain: hevein chitin-binding domain homology <HCB>
F:69-266/Domain: plant chitinase homology <PCH>

Query Match 54.1%; Score 785.5; DB 2; Length 266;
Best Local Similarity 56.2%; Pred. No. 5.5e-55;
Matches 145; Conservative 33; Mismatches 69; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCTAGLCCSKHGYCGTTSYCGEGCQAGPCTNTAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYIEVW-KSNAYCDPTKRWPCAAQGYKYGRLQIISWNNYNGPAGRAIGFDGL 179
Db 131 ETGYFCHKEETNGDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYIDAGKSNEDFGL 189
Qy 180 GPGREVARDAVAFKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFKTALWYKVKVQSVTQGFATIRAIN-SIECNGGSPDAVNSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266

RESULT 14
Ti4344
chitinase (EC 3.2.1.14) EP3-2/H1, class IV - carrot
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti4344
R:Kragh, K.; De Vries, S.C.
submitted to the EMBL Data Library, March 1996
A:Reference number: 217995
A:Accession: Ti4344
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-268 <KRA>
A:Cross-references: UNIPROT:Q96409; EMBL:U52846; NID:g1549330; PID:g1549331
A:Experimental source: strain sg766 trophy
C:Genetics:
A:Gene: EP3
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami-
A:Pathway: polysaccharide degradation
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:23-58/Domain: hevein chitin-binding domain homology <HCB>
F:71-268/Domain: plant chitinase homology <PCH>

Query Match 53.5%; Score 777.5; DB 2; Length 268;
Best Local Similarity 55.2%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYCGEGCQAGPCTNTAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYIEVW-KSNAYCDPTKRWPCAAQGYKYGRLQIISWNNYNGPAGRAIGFDGL 179
Db 131 ETGYFCHKEETNGDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYIDAGKSNEDFGL 189
Qy 180 GPGREVARDAVAFKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFKTALWYKVKVQSVTQGFATIRAIN-SIECNGGSPDAVNSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266
```



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 24, 2005, 12:54:28 ; Search time 91.7495 Seconds  
(without alignments)  
936.991 Million cell updates/sec

Title: US-10-692-367-12  
Perfect score: 1452  
Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRYQYRQLGVDPGNLTC 257

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1452	100.0	257	17	US-10-692-367-12
2	1435	98.8	257	17	US-10-692-367-30
3	1435	98.8	257	17	US-10-692-367-34
4	1405	96.8	257	17	US-10-692-367-72
5	1382.5	95.2	256	17	US-10-692-367-60
6	1382	95.2	257	17	US-10-692-367-46
7	1377	94.8	257	17	US-10-692-367-66
8	1373.5	94.6	256	17	US-10-692-367-62
9	1366.5	94.1	256	17	US-10-692-367-48
10	1365.5	94.0	256	17	US-10-692-367-74
11	1363	93.9	257	17	US-10-692-367-64
12	1361	93.7	257	17	US-10-692-367-24
13	1361	93.7	257	17	US-10-692-367-38

14	1356.5	93.4	254	17	US-10-692-367-68
15	1353.5	93.2	250	17	US-10-692-367-44
16	1351.5	93.1	256	17	US-10-692-367-84
17	1342	92.4	259	17	US-10-692-367-40
18	1339	92.2	259	17	US-10-692-367-76
19	1338.5	92.2	250	17	US-10-692-367-82
20	1333.5	91.8	254	17	US-10-692-367-26
21	1333	91.8	255	17	US-10-692-367-1
22	1333	91.8	303	15	US-10-425-114-57156
23	1332	91.7	257	17	US-10-692-367-8
24	1327	91.4	280	17	US-10-692-367-19
25	1323.5	91.2	250	17	US-10-692-367-52
26	1320	90.9	280	17	US-10-692-367-17
27	1318.5	90.8	250	17	US-10-692-367-70
28	1318.5	90.8	256	17	US-10-692-367-42
29	1315.5	90.6	250	17	US-10-692-367-36
30	1315.5	90.6	258	17	US-10-692-367-16
31	1305.5	89.9	250	17	US-10-692-367-78
32	1304.5	89.8	250	17	US-10-692-367-56
33	1300.5	89.6	258	17	US-10-692-367-4
34	1299.5	89.5	301	15	US-10-425-114-63860
35	1299.5	89.5	302	15	US-10-425-114-71741
36	1299	89.5	249	17	US-10-692-367-80
37	1297.5	89.4	248	17	US-10-692-367-2
38	1297.5	89.4	281	14	US-10-304-928-2
39	1295.5	89.2	250	17	US-10-692-367-50
40	1294.5	89.2	250	17	US-10-692-367-58
41	1294.5	89.2	293	15	US-10-425-114-64209
42	1294.5	89.2	298	15	US-10-425-114-52906
43	1292.5	89.0	250	17	US-10-692-367-22
44	1290.5	88.9	250	17	US-10-692-367-32
45	1287	88.6	269	17	US-10-692-367-18

## ALIGNMENTS

## RESULT 1

US-10-692-367-12  
; Sequence 12, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-12

Query Match 100.0%; Score 1452; DB 17; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.2e-112;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180

Qy 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

Qy 241 ROYCRQLGVDPPGNLTC 257
Db 241 ROYCRQLGVDPPGNLTC 257

RESULT 2
US-10-692-367-30
; Sequence 30, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-30

Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180

Qy 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

Qy 241 ROYCRQLGVDPPGNLTC 257
Db 241 ROYCRQLGVDPPGNLTC 257

RESULT 3
US-10-692-367-34
; Sequence 34, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-34

Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180

Qy 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

Qy 241 ROYCRQLGVDPPGNLTC 257
Db 241 ROYCRQLGVDPPGNLTC 257

RESULT 4
US-10-692-367-72
; Sequence 72, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-72

Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAAYPGFAHGSSEVERKREIAAFPAHATH 120

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRWPCAGOKYGRGPLQISWNYNYPAGRAIGFDGLG 180

Qy 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

Qy 241 ROYCRQLGVDPPGNLTC 257
Db 241 ROYCRQLGVDPPGNLTC 257
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Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 121 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 181 DPNRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Qy 241 ROYCRQLGVDPGNNLTC 257  
Db 241 ROYCRQLGVDPGNNLTC 257

## RESULT 7

US-10-692-367-66  
; Sequence 66, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-66

Query Match 94.8%; Score 1377; DB 17; Length 257;  
Best Local Similarity 93.4%; Pred. No. 8.2e-106;  
Matches 240; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGG 60  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGG 60  
Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
Db 61 VTDFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFHATH 120  
Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 121 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLA 180  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 181 DPNRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Qy 241 ROYCRQLGVDPGNNLTC 257  
Db 241 ROYCRQLGVDPGNNLTC 257

## RESULT 8

US-10-692-367-62

; Sequence 62, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-62

Query Match 94.6%; Score 1373.5; DB 17; Length 256;  
Best Local Similarity 94.2%; Pred. No. 1.6e-105;  
Matches 242; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGG 60  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCR-GGGGGGGGGGGGGG 59  
Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
Db 60 VTGSFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFHATH 119  
Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 120 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLA 179  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 180 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 239  
Qy 241 ROYCRQLGVDPGNNLTC 257  
Db 240 ROYCRQLGVDPGNNLTC 256

## RESULT 9

US-10-692-367-48  
; Sequence 48, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06

```
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-48

Query Match          94.1%; Score 1366.5; DB 17; Length 256;
Best Local Similarity 94.6%; Pred. No. 6e-105;
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVASV 59

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGGSEVERKREIAAPFAHATH 120
Db 60 VTGSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHVTH 119

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 120 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 179

Qy 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 240
Db 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 239

Qy 241 ROYCRQLGVDGPNLTC 257
Db 240 ROYCRQLGVDGPNLTC 256

RESULT 10
US-10-692-367-74
; Sequence 74, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-64

Query Match          93.9%; Score 1363; DB 17; Length 257;
Best Local Similarity 92.2%; Pred. No. 1.2e-104;
Matches 237; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGGSEVERKREIAAPFAHATH 120
Db 60 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHATH 120

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 120 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180

Qy 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 240
Db 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 240

Query Match          94.0%; Score 1365.5; DB 17; Length 256;
Best Local Similarity 92.6%; Pred. No. 7.3e-105;
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVASV 59

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGGSEVERKREIAAPFAHATH 120
Db 60 VTGSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHVTH 119

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 120 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 179

Qy 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 240
Db 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 239

Qy 241 ROYCRQLGVDGPNLTC 257
Db 240 ROYCRQLGVDGPNLTC 256

RESULT 10
US-10-692-367-74
; Sequence 74, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-74

Query Match          94.0%; Score 1365.5; DB 17; Length 256;
Best Local Similarity 92.6%; Pred. No. 7.3e-105;
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVASV 59

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGGSEVERKREIAAPFAHATH 120
Db 60 VTGSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHVTH 119

Qy 121 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 120 ETGHFCYISEVNKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 179

Qy 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 240
Db 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNNPQMMARVGY 239

Qy 241 ROYCRQLGVDGPNLTC 257
Db 240 ROYCRQLGVDGPNLTC 256
```

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Db 181 DPNRVARDPVLAFAKALWFNNVHRVMPQFGATIRAINGALKCGNNPAQMDARVGY 240
Qy 241 RQYCRQLGVDPGNNLTC 257
:|||||
Db 241 RQYCRQLGVDPGNNLTC 257

RESULT 12
US-10-692-367-24
; Sequence 24, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-24

Query Match 93.7%; Score 1361; DB 17; Length 257;
Best Local Similarity 92.2%; Pred. No. 1.7e-104;
Matches 237; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCGPCRCGCGGGGGGGGGGGGGGGANV 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCGPCRCGCGGGGGGGGGGGGGGGANV 60

Qy 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
Db 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAFFAHATH 120

Qy 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNNYGPAGRAIGFDGLG 180
Db 121 ETGHLCTINEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNNYGPAGRAIGFDGLG 180

Qy 181 DPNRVARDAVFAKALWFNNVHRVMPQFGATIRAINGALKCGNNPAQMDARVGY 240
Db 181 DPNRVARDAVFAKALWFNNVHRVMPQFGATIRAINGALKCGNNPAQMDARVGY 240

Qy 241 RQYCRQLGVDPGNNLTC 257
Db 241 RQYCRQLGVDPGNNLTC 257

RESULT 13
US-10-692-367-38
; Sequence 38, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
```

```
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-38

Query Match 93.7%; Score 1361; DB 17; Length 257;
Best Local Similarity 92.6%; Pred. No. 1.7e-104;
Matches 238; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCGPCRCGCGGGGGGGGGGGGGGGANV 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCGPCRCGCGGGGGGGGGGGGGGGANV 60

Qy 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFFAHATH 120
Db 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAFFAHATH 120

Qy 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNNYGPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNNYGPAGRAIGFDGLG 180

Qy 181 DPNRVARDAVFAKALWFNNVHRVMPQFGATIRAINGALKCGNNPAQMDARVGY 240
Db 181 DPNRVARDAVFAKALWFNNVHRVMPQFGATIRAINGALKCGNNPAQMDARVGY 240

Qy 241 RQYCRQLGVDPGNNLTC 257
Db 241 RQYCRQLGVDPGNNLTC 257

RESULT 14
US-10-692-367-68
; Sequence 68, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
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; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68

Query Match          93.4%; Score 1356.5; DB 17; Length 254;
Best Local Similarity 93.0%; Pred. No. 4e-104;
Matches 239; Conservative 9; Mismatches 6; Indels 3; Gaps 1;

Qy 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRSGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGGGGGGGGGGGGGGGANVASV 57

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 120
Db 58 VTGSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFFAHATH 117

Qy 121 ETGHFCYIISEVKNKNAYCDPTKRWPCAAAGOKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 118 ETGHFCYIISEINKSNAYCDPTKRWPCAAAGOKYYGRGPLQISWNYNYPAGRAIGFDGLG 177

Qy 181 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 240
Db 178 DPNRVAQDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 237

Qy 241 QYCRQLGVDPGNNLTC 257
Db 238 QYCRQLGVDPGNNLTC 254
```

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RESULT 15
US-10-692-367-44
; Sequence 44, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-44

Query Match          93.2%; Score 1353.5; DB 17; Length 250;
Best Local Similarity 93.4%; Pred. No. 7e-104;
Matches 240; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

Qy 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRSGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRSGGGGGGGGGGGGGGANVANV 53

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 120
```

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Db 54 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 113
Qy 121 ETGHFCYIISEVKNKNAYCDPTKRWPCAAAGOKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 114 ETGHFCYIISEINKSNAYCDPTKRWPCAAAGOKYYGRGPLQISWNYNYPAGRAIGFDGLG 173
Qy 181 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 240
Db 174 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 233
Qy 241 QYCRQLGVDPGNNLTC 257
Db 234 QYCRQLGVDPGNNLTC 250
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Search completed: May 24, 2005, 13:12:27  
Job time : 92.7495 secs

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ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/704,288C  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: protein  
MOLECULE TYPE: protein  
US-07-704-288C-8

Query Match 43.9%; Score 637; DB 1; Length 330;  
Best Local Similarity 43.9%; Pred. No. 1.1e-46;  
Matches 130; Conservative 36; Mismatches 80; Indels 50; Gaps 9;  
Qy 3 QNCG-----CQNVCSKFGYCTTDEYCGDCGCGPCRSQGGGGGGGGGGGGGGA 55  
Db 27 QNCGSQGGKACASGQCCKFGWCNTNDYCG----SGNCQSQCPGGGPGPGDGLGSA 82  
Qy 56 NVANVVTDAFNGIKNOAGSCGCKNFYTRSAFLAIAVPGPAHGGSEVERKEIAAFA 115  
Db 83 -ISMSFDM---LKHRENSCQGNFYSAFNARSPFGFTSGDINARKKEIAAFA 138  
Qy 116 AHATHET-----GHFCYISEVKNKSNAYCDPTKRWPCAAQKTYGRGPLQIS 162  
Db 139 AQTSHETGGWASAPDGPYANGYCFLERGNGPYDPCPSS--QWPCAPGRKYFGRGPIQIS 197  
Qy 163 WNYNGPAGRAIGDGLDGPGRVADAVAFKALWFMMN-----NVHRVM-----PQ- 210  
Db 198 HNYNGPCGRAIADVLNPNLVDTPVISEKTALWFMMTPQSPKPSCHDVIIGRWNPSS 257  
Qy 211 -----GFGATIRANGALECNGNPNQMNARVGYROYCRQLGVDPGNLTC 257  
Db 258 ADRAANRLPGFVITNIINGLECGRTDNRVQDRIGFYRRYCSILGVTGPDNLDC 313

RESULT 6  
US-08-379-259-8  
Sequence 8, Application US/08379259  
Patent No. 585939  
GENERAL INFORMATION:  
APPLICANT: LAMB, CHRISTOPHER J.  
APPLICANT: ZHU, QUN  
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT  
TITLE OF INVENTION: DEFENSE REGULATORY  
TITLE OF INVENTION: ELEMENTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,259  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/704,288  
FILING DATE: 22-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: protein  
MOLECULE TYPE: protein  
US-08-379-259-8

Query Match 43.9%; Score 637; DB 1; Length 330;  
Best Local Similarity 43.9%; Pred. No. 1.1e-46;  
Matches 130; Conservative 36; Mismatches 80; Indels 50; Gaps 9;  
Qy 3 QNCG-----CQNVCSKFGYCTTDEYCGDCGCGPCRSQGGGGGGGGGGGGGGA 55  
Db 27 QNCGSQGGKACASGQCCKFGWCNTNDYCG----SGNCQSQCPGGGPGPGDGLGSA 82  
Qy 56 NVANVVTDAFNGIKNOAGSCGCKNFYTRSAFLAIAVPGPAHGGSEVERKEIAAFA 115  
Db 83 -ISMSFDM---LKHRENSCQGNFYSAFNARSPFGFTSGDINARKKEIAAFA 138  
Qy 116 AHATHET-----GHFCYISEVKNKSNAYCDPTKRWPCAAQKTYGRGPLQIS 162  
Db 139 AQTSHETGGWASAPDGPYANGYCFLERGNGPYDPCPSS--QWPCAPGRKYFGRGPIQIS 197  
Qy 163 WNYNGPAGRAIGDGLDGPGRVADAVAFKALWFMMN-----NVHRVM-----PQ- 210  
Db 198 HNYNGPCGRAIADVLNPNLVDTPVISEKTALWFMMTPQSPKPSCHDVIIGRWNPSS 257  
Qy 211 -----GFGATIRANGALECNGNPNQMNARVGYROYCRQLGVDPGNLTC 257  
Db 258 ADRAANRLPGFVITNIINGLECGRTDNRVQDRIGFYRRYCSILGVTGPDNLDC 313

RESULT 7  
US-08-475-427-13  
Sequence 13, Application US/08475427  
Patent No. 5859340  
GENERAL INFORMATION:  
APPLICANT: DUBOIS, Michel  
APPLICANT: GRISON, Rene  
APPLICANT: LEGUAY, Jean-Jacques  
APPLICANT: PIGNARD, Annie  
APPLICANT: TOPPAN, Alain  
TITLE OF INVENTION: Recombinant gene coding for a protein  
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

**us-10-692-367-12.rail**

STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/842,165  
FILING DATE: 19920501  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-842-165-13

Query Match	43.1%	Score 626.5	DB 2	Length 329
Best Local Similarity	44.1%	Pred. No. 8.5e-46		
Matches 132	Conservative 38	Mismatches 76	Indels 53	Gaps 12
Qy	3	QNCG-----CQPNVCCSKFYGGTTDXYCGDG-CQSGPCRSGGGGGGGGGGGGSGG	54	
Db	25	QNCSGGGKVCASGGCCSKFGWCGNTDCHSGNCQS-QCPGGGPGPVPVTGGDLS--	81	
Qy	55	ANVANVTDAPFNG-INKQAGSCGEK-NPYTSAFLEATAANPGPAHGGSEVERKEIA	112	
Db	82	-----VISNSMFPQMLKHRNENSCQGNKYSYNAFITAARSPFGTSGDINARKKEIA	136	
Qy	113	APFAAHATHET-----GHF-----CYISEVNKSNAYCDPTTKQWPCAAQKYTYGRPL	159	
Db	137	APFAQTSHETTGWPSAPDGPFAWGYCFLRERGNPGDYCSPSS-QWPCAPGRKYFGRGPI	195	
Qy	160	QISWNNYGPAGRAIGPDGLGDCPRVARDAAVFAKALWFMN-----NVHRVM-----	208	
Db	196	QISHNNYGPGRRAIGVDLLNNPDLVATDPVISFKTAIWFMTTQSPKPSCHDVIIRGN	255	
Qy	209	PQ-----GFGATIRAINGALECGNNPQAQMARVGTYRQYRQLGVDGPGNNLTC	257	
Db	256	PSAGDRSANRLPGFGVITNIINGLECGRGNDNRVODRIGFYRRYCGILVYSGPDNLDG	314	

RESULT 9  
US-07-704-288C-6  
; Sequence 6, Application US/07704288C  
; Patent No. 5399680  
; GENERAL INFORMATION:  
; APPLICANT: LAMB, CHRISTOPHER J.  
; APPLICANT: ZHU, QUN  
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY  
; TITLE OF INVENTION: ELEMENTS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States  
; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-704-288C-6.

Query Match 42.9%; Score 623; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 1.6e-45;
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 SAQCQSQAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVTDAPFNG-INKQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSSEVERKREI 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GGGDLGSISSSMFQDMLKHRNDNACQKGKGFYSYNAFINAARSPPGFGTSGDTTARKREI 117

QY 112 AAPFAHATHET-----GHFCYISVKNKNAYCDPTKQWPCAAQCKYGRGP 158
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 AAPFAQTSHTTGGWATAPDGPYAWGYCWLREQSGPDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWMN-----NVHRVM--- 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 IQISHNYNGPCGALGVLDLNNPDVATDPVISFKSALWFMTQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRAINGALCEGNNPAQNNARVGYRYQYCRQLGVDPGNNLTC 257
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 237 PSSADRAANRLPGFGVITNIINGGLECGRGTDSDRQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 10
US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-704-288C-6.

Query Match 42.9%; Score 623; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 1.6e-45;
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
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Db 9 SAQCQSQAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVTDAPFNG-INKQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSSEVERKREI 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GGGDLGSISSSMFQDMLKHRNDNACQKGKGFYSYNAFINAARSPPGFGTSGDTTARKREI 117

QY 112 AAPFAHATHET-----GHFCYISVKNKNAYCDPTKQWPCAAQCKYGRGP 158
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Db 118 AAPFAQTSHTTGGWATAPDGPYAWGYCWLREQSGPDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWMN-----NVHRVM--- 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 IQISHNYNGPCGALGVLDLNNPDVATDPVISFKSALWFMTQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRAINGALCEGNNPAQNNARVGYRYQYCRQLGVDPGNNLTC 257
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Db 237 PSSADRAANRLPGFGVITNIINGGLECGRGTDSDRQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 11
US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-07-791-931-6

Query Match 42.9%; Score 622.5; DB 3; Length 310;
Best Local Similarity 41.0%; Pred. No. 1.7e-45;
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 SAQCQSQAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC-----PGGPTPP 56

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-704-288C-6.

Query Match 42.9%; Score 623; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 1.6e-45;
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 SAQCQSQAGGARCASGLCCSFGWCGTNDYCGPNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVTDAPFNG-INKQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSSEVERKREI 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 58 GGGDLGSISSSMFQDMLKHRNDNACQKGKGFYSYNAFINAARSPPGFGTSGDTTARKREI 117

QY 112 AAPFAHATHET-----GHFCYISVKNKNAYCDPTKQWPCAAQCKYGRGP 158
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 118 AAPFAQTSHTTGGWATAPDGPYAWGYCWLREQSGPDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWMN-----NVHRVM---- 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 177 IQISHNYNGPCGALGVLDLNNPDVATDPVISFKSALWFMTQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRAINGALCEGNNPAQNNARVGYRYQYCRQLGVDPGNLTC 257
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DB 237 PSSADRAANRLPGFGVITNIINGGLECGRGTDSDRQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 10
US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-704-288C-6.

Query Match 42.9%; Score 623; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 1.6e-45;
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 SAQCQSQAGGARCASGLCCSFGWCGTNDYCGPNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVTDAPFNG-INKQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSSEVERKREI 111
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DB 58 GGGDLGSISSSMFQDMLKHRNDNACQKGKGFYSYNAFINAARSPPGFGTSGDTTARKREI 117

QY 112 AAPFAHATHET-----GHFCYISVKNKNAYCDPTKQWPCAAQCKYGRGP 158
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DB 118 AAPFAQTSHTTGGWATAPDGPYAWGYCWLREQSGPDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWMN-----NVHRVM---- 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 177 IQISHNYNGPCGALGVLDLNNPDVATDPVISFKSALWFMTQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRAINGALCEGNNPAQNNARVGYRYQYCRQLGVDPGNLTC 257
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DB 237 PSSADRAANRLPGFGVITNIINGGLECGRGTDSDRQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 11
US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-07-791-931-6

Query Match 42.9%; Score 622.5; DB 3; Length 310;
Best Local Similarity 41.0%; Pred. No. 1.7e-45;
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 8 SAQCQSQAGGARCASGLCCSFGWCGTNDYCGPNCQS-QC-----PGGPTPP 56

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QY 53 GGANVANVTDAPFNG-1KNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111  
DB 57 GGGDLGSLISSMFDQMLKRNNDNACQKGFYSNAFINARSPFGTSGDITTKARKREI 116  
QY 112 AAFPAHATHET------GHFCYISEVKNKNAYCDPTKROWPCAGQKYGRGP 158  
DB 117 AAFPAQTSHTTGGWATAPDGPYAWGYCWLREQSGPGDYCTPS-GQWPCAPGRKYFGRP 175  
QY 159 LQISWNNYNYGPAGRAIGDGLGDPGRVARDVAFAKALWFMWN------VHRV 207  
DB 176 IQISHNNYNYGPCRAIGVLDLNNPDLVATDPVIFSKSALWFMWTPQSPKPSCHDVIIGRW 235  
QY 208 MPQ------GFGATIRAINGALCNGNPNQAMNARVGYRYOYCRQLGVDPPGNLTC 257  
DB 236 QPSSADRAANRLPGFGVITNIINGLECGRGTDSRVQDRIGFYRYCSILGVSGDNLDC 295

RESULT 12  
US-08-047-413-11  
; Sequence 11, Application US/08047413  
; Patent No. 5670706  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS. PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL-RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/047,413  
; FILING DATE: 19-APR-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-047-413-11

Query Match 42.7%; Score 619.5; DB 1; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMONCG------CQPNVCCSKFYCGTDTDEYCGDG-CQSGPCRSGGGGGGGGGGGGS 52  
DB 22 SASQCSQAGARCARGLCCSKFGWCGNTNDYCGPNCQS-QC-----PGGTPP 70  
QY 53 GGANVANVTDAPFNG-1KNQAGSGCEGKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111  
DB 71 GGGDLGSLISSMFDQMLKRNNDNACQKGFYSNAFINARSPFGTSGDITTKARKREI 130  
QY 112 AAFPAHATHET------GHFCYISEVKNKNAYCDPTKROWPCAGQKYGRGP 158  
DB 131 AAFPAQTSHTTGGWATAPDGPYAWGYCWLREQSGPGDYCTPS-GQWPCAPGRKYFGRP 189  
QY 159 LQISWNNYNYGPAGRAIGDGLGDPGRVARDVAFAKALWFMWN------VHRV 207  
DB 190 IQISHNNYNYGPCRAIGVLDLNNPDLVATDPVIFSKSALWFMWTPQSPKPSCHDVIIGRW 249  
QY 208 MPQ------GFGATIRAINGALCNGNPNQAMNARVGYRYOYCRQLGVDPPGNLTC 257  
DB 250 QPSSADRAANRLPGFGVITNIINGLECGRGTDSRVQDRIGFYRYCSILGVSGDNLDC 309

RESULT 13  
US-08-229-050-11  
; Sequence 11, Application US/08229050  
; Patent No. 6066491  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS. PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,050  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-229-050-11

Query Match	42.7%	Score 619.5	DB 3	Length 324
Best Local Similarity	41.0%	Pred. No. 3.3e-45		
Matches 123	Conservative 43	Mismatches 79	Indels 55	Gaps 9
QY	1	SMQNCG-----CQPNVCCSKFYCGTTDDEYCGDGG-CQSGPCRSRGGGGGGGGGGGGGGS	52	
Db	22	SAEQCSQAGGARCASGLCCSKFCWCGNTNDYCGFGNCQS-QC-----PGGPTTP	70	
QY	53	GGANVANVVDADPFG-IKKQAGSGCGKQNPYTRSAFLAATAAPGFAHGGSEVERKREI	111	
Db	71	GGDGLSGIISSWFQMLKRRNDWACQCKGFYSYNAFINARSFPGTSGDITARKREI	130	
QY	112	AAPFAHAHETH-----GHFCYISEVNKSNAYCDPTTKRQWPCAAQKQYGRGP	158	
Db	131	AAPFAQTSHTTGGWATADPGPYAWGYCWLREQCSPGDYCTPS-GQWPCAPGRKYFKRGCP	189	
QY	159	LQTSWNYNYPAGRAIGFDGLGDPGRVARADAVAFKAALFMMNN-----VHRV	207	
Db	190	IQISHNYNYPGCGRAIGVDLLNNPDLVATDPDVISFKGALFMMTTPQSPKPSCHDVI	249	
QY	208	MPQ-----GFGATIRAINGALCEGNPNPAQMNARVYTYROYCRQLGVDPGNLTC	257	
Db	250	QPSADRAANRLPGFVITMIINGLSCRGRTDSRVQDRIGFYARYCSILGVSPGDNLD	309	

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;          TELEX: 706141
;          INFORMATION FOR SEQ ID NO: 11:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 324 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
US-08-801-563-11

```

Query Match	42.7%	Score	619.5	DB	3	Length	324
Best Local Similarity	41.0%	Pred. No.	3.3e-45				
Matches	123	Conservative	43	Mismatches	79	Indels	55
Gaps	9						
QY	1	SMONCG-----CQPNVCCSKFGYCGTITDEYCGDG-CQSGPCRCSSGGGGGGGGGGGGGS	52				
DB	22	SAEQCSQAGGARCAAGLCCSKFGWCNTINDYCGPNCQS-QC-----PGGPTTP	70				
QY	53	GGANVANVTDAFFNG-IGNQAGSGCEGKNFYTRSAFLAIAAYPCFAHGCSSVERKREI	111				
DB	71	GGDGLSGIISSMFDQMLKHRNDNACQGGFGFSYNAFINAAFSFPGTSGDTTAKREI	130				
QY	112	AAPFAAHATHET-----GHFCYISEVNKSNAYCDPTKRWPCAAAGQKYTCRGP	158				
DB	131	AAFFAQTSHETGGWATAPDGPYAWCYCWLREQCSPGDYCTPS-GQWPCAPGRKYFGRGP	189				
QY	159	LQISWMYNYGPAGRAITFGDLGDPGRVADAVAFKAALWFWMNN-----VHRV	207				
DB	190	IQISHYNYNGPCRAIGVDLLNNPDVATDPVTSFKSALWFWMTPQSPKPSCHDVITGRW	249				
QY	208	MPC-----GFGATIRANGALECNGNPAQMNARVGYRYQYCRQLGVDPGNNLTC	257				
DB	250	QFSSADRAANRLPGFVQITNIINGLECGRGDTRSRVQDRIGFYRRYCSILGVSPGNLDC	309				

RESULT 15  
US-07-704-288C-7  
Sequence 7, Application US/07704288C  
Patent No. 5399680  
GENERAL INFORMATION:  
APPLICANT: LAMB, CHRISTOPHER J.  
APPLICANT: ZHU, QUN  
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY  
TITLE OF INVENTION: ELEMENTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/704,288C  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 314 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown

```

; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-7

Query Match      42.4%; Score 615; DB 1; Length 314;
Best Local Similarity 42.5%; Pred. No. 7.7e-45;
Matches 122; Conservative 41; Mismatches 74; Indels 50; Gaps 9;

Qy 7 CQPNVCCSKFYCGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGGGANVANVVTDAF 65
Db 27 CAPGLCCSKFGWCGNTNDYCGPNCQS-QCPGPGPSGDLGG-----VISNSM 73

Qy 66 FNGIKNOAG-SGCEGK-NFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAPFAHATHET- 122
Db 74 FDQMLNHRNDNACQCKNMFYSYNAFISAGSPGFGTTGDITARKREIAAPFLAQTSHETT 133

Qy 123 -----GHFCYISEYVKNKNAYCDPTKQWPCAAAGQYGRGLQISMNYYGPA 170
Db 134 GGWPSAPDGPVANGVCFLEQSPGDICTPSS-QWPCAPGRKYFGRGPIQISHNYYGPC 192

Qy 171 GRAIGFDGLDPRVARDANVAFKAALWFNN-----NVHRVMP-----Q 210
Db 193 GRAIGVDLLNPNPDVATDSVISFKSAIWFMTPOSPPKPSCHDVITGRWPSGADQANRVP 252

Qy 211 GFQATIRAINGALCNGNPNQMARVGYRYQYCRQLGVDPGNLTC 257
Db 253 GFGVITNIINGLEGCHGSDSRVQDRIGFYRYCGILGVSPGDLDC 299
```

Search completed: May 24, 2005, 12:56:20  
Job time : 33.428 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 24, 2005, 12:19:56 ; Search time 117.095 Seconds  
(without alignment)  
848.864 Million cell updates/sec

Title: US-10-692-367-12  
Perfect score: 1452  
Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRYQYRQLGVDPGNLTC 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A: Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1452	100.0	257	8	ADS92628 Chitinase
2	1435	98.8	257	8	ADS92646 Chitinase
3	1435	98.8	257	8	ADS92650 Chitinase
4	1405	96.8	257	8	ADS92688 Chitinase
5	1382.5	95.2	256	8	ADS92676 Chitinase
6	1382	95.2	257	8	ADS92662 Chitinase
7	1377	94.8	257	8	ADS92682 Chitinase
8	1373.5	94.6	256	8	ADS92678 Chitinase
9	1366.5	94.1	256	8	ADS92664 Chitinase
10	1365.5	94.0	256	8	ADS92690 Chitinase
11	1363	93.9	257	8	ADS92680 Chitinase
12	1361	93.7	257	8	ADS92654 Chitinase
13	1361	93.7	257	8	ADS92640 Chitinase
14	1356.5	93.4	254	8	ADS92684 Chitinase
15	1353.5	93.2	250	8	ADS92660 Chitinase
16	1351.5	93.1	256	8	ADS92700 Chitinase
17	1342	92.4	259	8	ADS92656 Chitinase
18	1339	92.2	259	8	ADS92692 Chitinase
19	1338.5	92.2	250	8	ADS92698 Chitinase
20	1333.5	91.8	254	8	ADS92842 Chitinase
21	1333	91.8	255	8	ADS92617 Maize chi
22	1332	91.7	257	8	ADS92624 Chitinase
23	1327	91.4	280	8	ADS92635 Maize chi
24	1323.5	91.2	250	8	ADS92668 Chitinase
25	1320	90.9	280	8	ADS92633 Maize chi

26	1318.5	90.8	250	8	ADS92686 Chitinase
27	1318.5	90.8	256	8	ADS92658 Chitinase
28	1315.5	90.6	250	8	ADS92652 Chitinase
29	1315.5	90.6	258	8	ADS92632 Chitinase
30	1305.5	89.9	250	8	ADS92694 Chitinase
31	1304.5	89.8	250	8	ADS92672 Chitinase
32	1300.5	89.6	258	8	ADS92620 Chitinase
33	1299	89.5	249	8	ADS92696 Chitinase
34	1297.5	89.4	248	8	ADS92618 Maize chi
35	1297.5	89.4	281	3	RAB18894 A maize c
36	1295.5	89.2	250	8	ADS92666 Chitinase
37	1294.5	89.2	250	8	ADS92674 Chitinase
38	1292.5	89.0	250	8	ADS92638 Chitinase
39	1290.5	88.9	250	8	ADS92648 Chitinase
40	1287	88.6	269	8	ADS92634 Maize chi
41	1282.5	88.3	250	8	ADS92670 Chitinase
42	1275.5	87.8	270	8	ADS92636 Maize chi
43	1273.5	87.7	250	8	ADS92644 Chitinase
44	1220	84.0	251	8	ADS92630 Chitinase
45	1218	83.9	251	8	ADS92622 Chitinase

## ALIGNMENTS

### RESULT 1

ADS92628  
ID ADS92628 standard; protein; 257 AA.

XX ADS92628;

AC ADS92628;

DT 02-DEC-2004 (first entry)

XX

DE Chitinase variant polypeptide #5.

XX

KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX Synthetic.

OS

XX WO2004037194-A2.

FN

XX

XX

PD 06-MAY-2004.

XX

PF 22-OCT-2003; 2003WO-US033588.

XX

PR 22-OCT-2002; 2002US-0420666P.

XX

PR 06-NOV-2002; 2002US-00290086.

XX

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Muller ML, True T, Simmons CR, Yalpani N;

XX

DR WPI; 2004-365417/34.

XX

DR N-PSDB; ADS92627.

XX

PT New chitinase polynucleotides and polypeptides, useful in producing

XX

PT plants with enhanced resistance against a fungus or a nematode.

XX

PS Claim 26; SEQ ID NO 12; 197pp; English.

XX

CC The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.

XX Sequence 257 AA;

SQ

```
Query Match      100.0%; Score 1452; DB 8; Length 257;
Best Local Similarity 100.0%; Pred. No. 4.5e-123; Indels 0; Gaps 0;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60
QY 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLBAIAAAYPGFAHGSGSEVERKRETAAPFAHATH 120
DB 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLBAIAAAYPGFAHGSGSEVERKRETAAPFAHATH 120
QY 121 ETGHFCYISEVNKSNAYCDPTKROWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180
DB 121 ETGHFCYISEVNKSNAYCDPTKROWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
QY 241 RQYCRQLGVDPGNNLTC 257
DB 241 RQYCRQLGVDPGNNLTC 257

RESULT 2
ADS92646
ID ADS92646 standard; protein; 257 AA.
XX AC ADS92646;
XX DT 02-DEC-2004 (first entry)
XX DE Chitinase variant polypeptide #12.
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX OS Synthetic.
XX PN WO2004037194-A2.
XX PD 06-MAY-2004.
XX PF 22-OCT-2003; 2003WO-US033588.
XX PR 22-OCT-2002; 2002US-0420666P.
XX PR 06-NOV-2002; 2002US-00290086.
XX PR 14-MAR-2003; 2003US-00389432.
XX PA (VERD-) VERDIA INC.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX DR WPI: 2004-365417/34.
XX DR N-PSDB; ADS92645.
XX PT New chitinase polynucleotides and polypeptides, useful in producing
XX PT plants with enhanced resistance against a fungus or a nematode.
XX PS Claim 3; SEQ ID NO 30; 197pp; English.
XX CC The invention relates to chitinase polypeptides and the polynucleotides
XX CC encoding them. A method of enhancing plant resistance to a fungus or
XX CC nematode comprises introducing into a plant a recombinant expression
XX CC cassette comprising a promoter operably linked to a chitinase
XX CC polynucleotide of the invention. The plant is maize or soybean. The
XX CC fungus is from the genus Fusarium. The nematode is from the genus
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX CC plant resistance to a fungus or nematode. This sequence represents a
XX CC chitinase variant polypeptide of the invention.

SQ Sequence 257 AA;
Query Match      98.8%; Score 1435; DB 8; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.5e-121; Indels 0; Gaps 0;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60
QY 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLBAIAAAYPGFAHGSGSEVERKRETAAPFAHATH 120
DB 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLBAIAAAYPGFAHGSGSEVERKRETAAPFAHATH 120
QY 121 ETGHFCYISEVNKSNAYCDPTKROWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180
DB 121 ETGHFCYISEVNKSNAYCDPTKROWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240
QY 241 RQYCRQLGVDPGNNLTC 257
DB 241 RQYCRQLGVDPGNNLTC 257

RESULT 3
ADS92650
ID ADS92650 standard; protein; 257 AA.
XX AC ADS92650;
XX DT 02-DEC-2004 (first entry)
XX DE Chitinase variant polypeptide #14.
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX OS Synthetic.
XX PN WO2004037194-A2.
XX PD 06-MAY-2004.
XX PF 22-OCT-2003; 2003WO-US033588.
XX PR 22-OCT-2002; 2002US-0420666P.
XX PR 06-NOV-2002; 2002US-00290086.
XX PR 14-MAR-2003; 2003US-00389432.
XX PA (VERD-) VERDIA INC.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX DR WPI: 2004-365417/34.
XX DR N-PSDB; ADS92649.
XX PT New chitinase polynucleotides and polypeptides, useful in producing
XX PT plants with enhanced resistance against a fungus or a nematode.
XX PS Claim 3; SEQ ID NO 34; 197pp; English.
XX CC The invention relates to chitinase polypeptides and the polynucleotides
XX CC encoding them. A method of enhancing plant resistance to a fungus or
XX CC nematode comprises introducing into a plant a recombinant expression
XX CC cassette comprising a promoter operably linked to a chitinase
XX CC polynucleotide of the invention. The plant is maize or soybean. The
XX CC fungus is from the genus Fusarium. The nematode is from the genus
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX CC plant resistance to a fungus or nematode. This sequence represents a
XX CC chitinase variant polypeptide of the invention.
```



XX Sequence 257 AA;  
XX Query Match 98.8%; Score 1435; DB 8; Length 257;  
XX Best Local Similarity 98.8%; Pred. No. 1.5e-121;  
XX Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAPFAHATH 120  
DB 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAPFAHATH 120  
QY 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPNQMNARVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPNQMNARVGY 240  
QY 241 ROYCRQLGVDPGNLTC 257  
DB 241 ROYCRQLGVDPGNLTC 257

RESULT 4  
ADS92688  
ID ADS92688 standard; protein; 257 AA.  
XX AC ADS92688;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #33.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92687.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 72; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polypeptide of the invention.  
XX Sequence 257 AA;

Query Match 96.8%; Score 1405; DB 8; Length 257;  
Best Local Similarity 95.3%; Pred. No. 8e-119;  
Matches 245; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANVANV 60  
QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAPFAHATH 120  
DB 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAPFAHATH 120  
QY 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPNQMNARVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPNQMNARVGY 240  
QY 241 ROYCRQLGVDPGNLTC 257  
DB 241 ROYCRQLGVDPGNLTC 257

RESULT 5  
ADS92676  
ID ADS92676 standard; protein; 256 AA.  
XX AC ADS92676;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #27.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92675.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 60; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing

CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 256 AA;

Query Match 95.2%; Score 1382.5; DB 8; Length 256;  
 Best Local Similarity 94.9%; Pred. No. 8.7e-117; Indels 1; Gaps 1;  
 Matches 244; Conservative 5; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 SMQCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCQPNVCCSKFGYCGTTDAYCGDGCQSGPCRS-GGGGGGGGGGGGGGGANVANV 59  
 QY 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAFFAHATH 120  
 DB 60 VTDAFFNGIKNOAGSCGCKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHVTH 119  
 QY 121 ETGHFCYI SEVNKSNAYCDPTKROWPCAAGQKYGRGPLQISWNYNYPAGRAIGFDGLG 180  
 DB 120 ETGHFCYI SEINKSNAYCDPTKROWPCAAGQKYGRGPLQISWNYNYPAGRAIGFDGLG 179  
 QY 181 DPGRVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALECNNGNPPAQMNAVGY 240  
 DB 180 DPGRVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALECNNGNPPAQMNAVGY 239  
 QY 241 ROYCRQLGVDPPGNLTC 257  
 DB 240 ROYCRQLGVDPPGNLTC 256

# RESULT 6

ADSS2662  
 ID ADSS2662 standard; protein; 257 AA.

XX AC ADSS2662;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #20.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR N-PSDB; ADSS2661.

XX XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 46; 197pp; English.  
 CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus

CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 257 AA;

Query Match 95.2%; Score 1382; DB 8; Length 257;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-117; Indels 0; Gaps 0;  
 Matches 241; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SMQCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAFFAHATH 120  
 DB 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATH 120  
 QY 121 ETGHFCYI SEVNKSNAYCDPTKROWPCAAGQKYGRGPLQISWNYNYPAGRAIGFDGLG 180  
 DB 121 ETGHFCYI SEINKSNAYCDPTKROWPCAAGQKYGRGPLQISWNYNYPAGRAIGFDGLG 180  
 QY 181 DPGRVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALECNNGNPPAQMNAVGY 240  
 DB 181 DPGRVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALECNNGNPPAQMNAVGY 240  
 QY 241 ROYCRQLGVDPPGNLTC 257  
 DB 241 ROYCRQLGVDPPGNLTC 257

# RESULT 7

ADSS2682  
 ID ADSS2682 standard; protein; 257 AA.

XX AC ADSS2682;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #30.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR N-PSDB; ADSS2681.

XX XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 66; 197pp; English.  
 CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

SQ Sequence 257 AA;

Query Match 94.8%; Score 1377; DB 8; Length 257;  
 Best Local Similarity 93.4%; Pred. No. 2.8e-116;  
 Matches 240; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 SMQCGCPNVCCSKFGYCGTTDEYCGDCGSCGCRSGGGGGGGGGGGGGGANNV 60  
 DB 1 SMQCGCPNVCCSKFGYCGTTDEYCGDCGSCGCRSGGGGGGGGGGGGGGANNV 60  
 QY 61 VTDAFFNGIKNOAGSGCEGKGFYTRSAFLAIAAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 DB 61 VTDSFFNGIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGGSQVGKREIAAFPAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLA 180  
 QY 181 DPGVARDAVAFKAALWFNNVHRVMPQGFATIRAINGALCEGNGNPAQMNAVGY 240  
 DB 181 DENVAQDAVAFKAALWFNNVHRVMPQGFATIRAINGALCEGNGNPAQMNAVGY 240  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 241 KQYCRQLGVDPGNNLTC 257

#### RESULT 8

ADS92678  
 ID ADS92678 standard; protein; 256 AA.  
 XX  
 AC ADS92678;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Chitinase variant polypeptide #28.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 XX  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92677.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 62; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

SQ Sequence 256 AA;

Query Match 94.6%; Score 1373.5; DB 8; Length 256;  
 Best Local Similarity 94.2%; Pred. No. 5.7e-116;  
 Matches 242; Conservative 8; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 SMQCGCPNVCCSKFGYCGTTDEYCGDCGSCGCRSGGGGGGGGGGGGGGANNV 60  
 DB 1 SMQCGCPNVCCSKFGYCGTTDEYCGDCGSCGCRSGGGGGGGGGGGGGGANNV 59  
 QY 61 VTDAFFNGIKNOAGSGCEGKGFYTRSAFLAIAAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 DB 60 VTGSFFNGIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFPAHATH 119  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
 DB 120 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLA 179  
 QY 181 DPGVARDAVAFKAALWFNNVHRVMPQGFATIRAINGALCEGNGNPAQMNAVGY 240  
 DB 180 DPGVARDAVAFKAALWFNNVHRVMPQGFATIRAINGALCEGNGNPAQMNAVGY 239  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 240 KQYCRQLGVDPGNNLTC 256

#### RESULT 9

ADS92664  
 ID ADS92664 standard; protein; 256 AA.  
 XX  
 AC ADS92664;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Chitinase variant polypeptide #21.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92663.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 48; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
XX  
SQ Sequence 256 AA;

Query Match 94.1%; Score 1366.5; DB 8; Length 256;  
Best Local Similarity 94.6%; Pred. No. 2.4e-115;  
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANNV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRS- GGGGGGGGGGGGGGANNV 59  
QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
DB 60 VTGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFHATH 119  
QY 121 ETGHFCYISEVKNKNAYCDPTKQWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180  
DB 120 ETGHFRYISEVKNKNAYCDPTKQWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 179  
QY 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECGNPNPAQMNARVGY 240  
DB 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECGNPNPAQMNARVGY 239  
QY 241 RQYCRQLGVDPGNNLTC 257  
DB 240 RQYCRQLGVDPGNNLTC 256

RESULT 10  
ADS92690  
ID ADS92690 standard; protein; 256 AA.  
XX  
XX ADS92690;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Chitinase variant polypeptide #34.  
XX  
XX Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
XX Synthetic.  
XX  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
XX  
XX 06-NOV-2002; 2002US-00290086.  
XX  
XX 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
XX N-ESDB; ADS92689.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 3; SEQ ID NO 74; 197pp; English.  
XX  
XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
XX  
SQ Sequence 256 AA;

Query Match 94.0%; Score 1365.5; DB 8; Length 256;  
Best Local Similarity 92.6%; Pred. No. 3e-115;  
Matches 238; Conservative 12; Mismatches 6; Indels 1; Gaps 1;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANNV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRP- GGGGGGGGGGGGGGANNV 59  
QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
DB 60 VTDSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFHATH 119  
QY 121 ETGHFCYISEVKNKNAYCDPTKQWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180  
DB 120 ETGHFCYINEINKSNAYCDPTKQWPCAAQORYYGRGPLQISWNYNGPAGRAIGFDGLG 179  
QY 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECGNPNPAQMNARVGY 240  
DB 180 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECGNPNPAQMNARVGY 239  
QY 241 RQYCRQLGVDPGNNLTC 257  
DB 240 RQYCRQLGVDPGNNLTC 256

RESULT 11  
ADS92680  
ID ADS92680 standard; protein; 257 AA.  
XX  
XX ADS92680;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Chitinase variant polypeptide #29.  
XX  
XX Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
XX Synthetic.  
XX  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
XX  
XX 06-NOV-2002; 2002US-00290086.  
XX  
XX 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
XX N-ESDB; ADS92679.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 3; SEQ ID NO 64; 197pp; English.  
XX  
XX The invention relates to chitinase polypeptides and the polynucleotides

CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprising introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 93.9%; Score 1363; DB 8; Length 257;  
 Best Local Similarity 92.2%; Pred. No. 5.1e-115; Indels 0; Gaps 0;  
 Matches 237; Conservative 10; Mismatches 10;  
 QY 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 DB 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNGPAGRDIGFNGLA 180  
 QY 181 DPGVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNVGVY 240  
 DB 181 DPNRVARDVLAFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNDARVGY 240  
 QY 241 QYCRQLGVDGPNLTC 257  
 DB 241 QYCRQLGVDGPNLTC 257

RESULT 12  
 ADS92654  
 ID ADS92654 standard; protein; 257 AA.  
 XX  
 AC ADS92654;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #16.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PP 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 FI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92653.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 38; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprising introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 93.7%; Score 1361; DB 8; Length 257;  
 Best Local Similarity 92.6%; Pred. No. 7.7e-115;  
 Matches 238; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 DB 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAIAAYPGFAHGGSEVERKREIAAFPAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNGPAGRDIGFNGLA 180  
 QY 181 DPGVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNVGVY 240  
 DB 181 DPNRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNVGVY 240  
 QY 241 QYCRQLGVDGPNLTC 257  
 DB 241 QYCRQLGVDGPNLTC 257

RESULT 13  
 ADS92640  
 ID ADS92640 standard; protein; 257 AA.  
 XX  
 AC ADS92640;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #9.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PP 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 FI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92639.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 24; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

SQ Sequence 257 AA;

Query Match 93.7%; Score 1361; DB 8; Length 257;  
 Best Local Similarity 92.2%; Pred. No. 7.7e-115;  
 Matches 237; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60  
 Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSVERKREIAAPFAHATH 120  
 Db 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHATH 120

Qy 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGOKYGRGLQISWNYNGPAGRAIGFDGLG 180  
 Db 121 ETGHLCYINEVKNKNAYCDPTKRWPCAAAGOKYGRGLQISWNYNGPAGRAIGFDGLG 180

Qy 181 DPGRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCEGNNPAQMNARVGY 240  
 Db 181 DPDLAQDPLVLSFKSALFWNNVHVRVMPQGFATIRAINGALCEGNNPAQMNARVGY 240

Qy 241 QYCRQLGVDPGNNLTC 257  
 Db 241 QYCRQLGVDPGNNLTC 257

RESULT 14

ADSD2684  
 ID ADS2684 standard; protein; 254 AA.  
 XX AC ADS2684;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Chitinase variant polypeptide #31.  
 XX KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX OS Synthetic.  
 XX FN WO2004037194-A2.  
 XX PD 06-MAY-2004.  
 XX PF 22-OCT-2003; 2003WO-US033588.  
 XX PR 22-OCT-2002; 2002US-0420666P.  
 XX PR 06-NOV-2002; 2002US-00290086.  
 XX PR 14-MAR-2003; 2003US-00389432.  
 XX PA (VERD-) VERDIA INC.  
 XX PA (PION-) PIONEER HI-BRED INT INC.  
 XX FI Muller ML, True T, Simmons CR, Yalpani N;  
 XX DR WPI; 2004-365417/34.  
 XX DR N-PSDB; ADS2683.  
 XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 XX plants with enhanced resistance against a fungus or a nematode.

PS Claim 3; SEQ ID NO 68; 197pp; English.  
 XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

SQ Sequence 254 AA;

Query Match 93.4%; Score 1356.5; DB 8; Length 254;  
 Best Local Similarity 93.0%; Pred. No. 1.9e-114;  
 Matches 239; Conservative 9; Mismatches 6; Indels 3; Gaps 1;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60  
 Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRS--GGGGGGGGGGGGGGGGANVASV 57

Qy 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSVERKREIAAPFAHATH 120  
 Db 58 VTGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAPFAHATH 117

Qy 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGOKYGRGLQISWNYNGPAGRAIGFDGLG 180  
 Db 118 ETGHFCYISEINKSNAYCDPTKRWPCAAAGOKYGRGLQISWNYNGPAGRAIGFDGLG 177

Qy 181 DPGRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCEGNNPAQMNARVGY 240  
 Db 178 DPNEVADAVAVFAKALFWNNVHVRVMPQGFATIRAINGALCEGNNPAQMNARVGY 237

Qy 241 QYCRQLGVDPGNNLTC 257  
 Db 238 QYCRQLGVDPGNNLTC 254

RESULT 15

ADSD2660  
 ID ADS2660 standard; protein; 250 AA.  
 XX AC ADS2660;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Chitinase variant polypeptide #19.  
 XX KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX OS Synthetic.  
 XX FN WO2004037194-A2.  
 XX PD 06-MAY-2004.  
 XX PF 22-OCT-2003; 2003WO-US033588.  
 XX PR 22-OCT-2002; 2002US-0420666P.  
 XX PR 06-NOV-2002; 2002US-00290086.  
 XX PR 14-MAR-2003; 2003US-00389432.  
 XX PA (VERD-) VERDIA INC.  
 XX PA (PION-) PIONEER HI-BRED INT INC.  
 XX FI Muller ML, True T, Simmons CR, Yalpani N;  
 XX DR WPI; 2004-365417/34.  
 XX DR N-PSDB; ADS2659.  
 XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 XX plants with enhanced resistance against a fungus or a nematode.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:20:11 ; Search time 2216.06 Seconds  
(without alignments)  
13294.634 Million cell updates/sec

Title: US-10-692-367-11  
Perfect score: 774  
Sequence: 1 tcgatgcagactgcggctg.....gcaacaacctcacctgtgta 774

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsei:  
9: gb\_gsei2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	691.8	89.4	1179	3	AY103546 Zea mays
2	607.6	78.5	958	4	BG837479 Zea mays
3	597.6	77.2	855	4	BG837663 Zea mays
4	553.4	71.5	767	7	COS24416 3530_1_16
5	543.4	70.2	737	6	CD435649 EL01N0364
6	530.4	68.5	625	5	BM895383 952073H05
7	529.2	68.4	716	7	COS20138 3530_1_13
8	525.6	67.9	628	4	BM736454 952051A06
9	519.4	67.1	837	7	CN133023 952051A06
10	503	65.0	647	6	CA197556 SCBFAD106
11	502	64.9	710	6	CD43492 EL01N0427
12	501	64.7	820	6	CD995497 QB255f07
13	498.2	64.4	578	6	CD994454 QB15f08
14	497.2	64.2	741	6	CD994869 QB18d07
15	497.2	64.2	753	6	CD994885 QB18e05
16	497	64.2	578	6	CD994156 QB13f07
17	495.6	64.0	575	6	CD994132 QB13e04
18	485.6	62.7	567	5	BU050046 111019B0
19	485	62.7	812	7	CN132942 OX1_9_D11
20	483	62.4	754	6	CD995176 QB20H11
21	481.2	62.2	550	6	CF001565 QB4f06.x
22	481.2	62.2	559	6	CD999920 QB10a02
23	481.2	62.2	562	6	CF000010 QB11a02
24	481.2	62.2	562	6	CF000028 QB13e12

25	481.2	62.2	562	6	CF000357	QB15b09.
26	481.2	62.2	562	6	CF000565	QB17b11.
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28	481.2	62.2	573	6	CF000161	QB12g06.
29	481.2	62.2	573	6	CF000412	QB15g11.
30	481.2	62.2	574	6	CD999947	QB10c07.
31	481.2	62.2	574	6	CF000325	QB14g11.
32	481.2	62.2	587	6	CF002068	QB18f07.x
33	481.2	62.2	587	6	CF002109	QB18h11.x
34	481.2	62.2	606	6	CF001250	QB2a02.x
35	481.2	62.2	606	6	CF001262	QB2b02.x
36	481.2	62.2	606	6	CF001900	QB2c09.x
37	481.2	62.2	742	6	CF001316	QB2e05.p
38	480.2	62.0	573	6	CF000017	QB11a12.
39	479.6	62.0	603	6	CF001775	QB6c07.x
40	479.6	62.0	627	6	CF001901	QB7c10.x
41	479.6	62.0	641	6	CF011507	QB7h11.x
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44	477.6	61.7	688	6	CA281399	SCAGSD104
45	477	61.6	626	6	CF001317	QB2e05.x

ALIGNMENTS

RESULT 1  
AY103546

LOCUS AY103546 1179 bp mRNA linear HTC 16-OCT-2002

DEFINITION Zea mays PC0155066 mRNA sequence.

ACCESSION AY103546

VERSION AY103546.1 GI:21206624

KEYWORDS HTC.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1179)  
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

TITLE Unpublished (2002)

JOURNAL 2 (bases 1 to 1179)  
Coe,E.H.

REFERENCE 1 (bases 1 to 1179)  
Coe,E.H.

AUTHORS Direct Submission

TITLE Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

JOURNAL If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
Location/Qualifiers  
1..1179  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="MaizeDB:638921"  
/db\_xref="taxon:4577"  
Library="Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes"

Query Match 89.4%; Score 691.8; DB 3; Length 1179;

Best Local Similarity 93.9%; Pred. No. 9.8e-131;  
Matches 720; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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QY 66 CGACGAGTACTGCGGCGAGCGGTCAGTCCGGCCCGTCCGCTCGGGCGGGGTGGCG 125  
Db 208 CGACGCCCTACTGCGGCGAGCGGTCAGTCCGGCCCGTCCGCTCGGGCGGGGTGGCG 267

QY 126 CGGCGCGCGCGCGAGCGCGCGAGGAGTGGCGGTCGCAACGCTGGCTAATGTGGTCA 185  
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QY 186 CGACGCGTTCTTCAACGCGCATCAAGAACACAGCGCGGAGCGGGTCGAGGCGAAGAACTT 245  
Db 328 CGACGCGTTCTTCAACGCGCATCAAGAACACAGCGCGGAGCGGGTCGAGGCGAAGAACTT 387

QY 246 CTACACCGGAGCGGTTCTCGAGGCCATCGCGCGTACCGGGCTTCGGCGCATGGCGG 305  
Db 388 CTACACCGGAGCGGTTCTCGAGGCCGTCAACGCGTACCGGGCTTCGGCGCATGGCGG 447

QY 306 CTCCGAGTCCAGCGCAAGCGGAGATTGCGGCTTCTTCGCGCACGCGCACGACGAC 365  
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QY 366 CGGCGATTCTGCTACATCAGCGAGTCAACAGAGCAACGCTACTCGACCGACCAA 425  
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QY 426 GAGCGAGTGGCGGCGCGCGGCGGAGAGTACTACGGGCGCGCGCTGCGAGATCTC 485  
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QY 486 GTGGAATACAACTACCGGCGCGCGGAGGCGCATCGGCTTCAACGCGCTCGGGACCC 545  
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QY 546 CGGCGAGGTGGCGGCGAGCGCGTGGTGGTTCAGGCGGGGCTCTGGTCTCGATGAA 605  
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RESULT 2  
BG837479 958 bp mRNA linear EST 25-MAY-2001  
LOCUS Zm10\_10h09 A Zm10\_AAPC\_ECORC\_Fusarium graminearum\_corn\_silk Zea  
DEFINITION Zea mays clone Zm10\_10h09, mRNA sequence.

ACCESSION BG837479  
VERSION BG837479.1 GI:14203802  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A., Sprout,D. and Tinker,N.A.

TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum  
JOURNAL Unpublished (2001)  
COMMENT Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,  
CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-8566  
Email: harrislj@agr.gc.ca.  
Location/Qualifiers  
1. 958  
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/clone="Zm10\_10h09"  
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/clone\_lib="Zm10\_AAPC\_ECORC\_Fusarium\_graminearum\_corn\_silk"

FEATURES  
source

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI;  
Site\_2: XhoI; Field-grown corn was silk channel-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."

## ORIGIN

Query Match 78.5%; Score 607.6; DB 4; Length 958;  
Best Local Similarity 89.7%; Pred. No. 1.3e-113;  
Matches 681; Conservative 6; Mismatches 61; Indels 11; Gaps 3;

QY 6 GCAGAACTGCGGCTGCCAGCAACAGTATGCTGAGCAAGTTTGCTACTCGGCACGCA 64  
Db 31 GCAGAACTGCGGCTGCCAGCAACAACTTCTGCTGAGCAAGTTTGCTACTCGGCACGCA 90

QY 65 CCGACGAGTACTGCGGCGAGCGGGTCAGTCCGCGCCGCTCGCGGCGGGGTGGCG 124  
Db 91 CCGACGACTACTGCGGCGAGCGGGTCAGTCCGCGCCCGCTCGCTCG-----GGCG 141

QY 125 CGGCGCGGCGGCGGAGCGGCGGAGCGAGTGGCGGTGCGAAGTGGTCA 184  
Db 142 CGGCGCGGCGGCGGAGCGGCGGAGCGAGTGGCGGTGCGAAGTGGTCA 201

QY 185 CCGACGCGTTCTTCAACGCGCATCAAGAACACAGGCGCGGAGCGGGTGGCGGCGCAAGAACT 244  
Db 202 CGGACGCGTTCTTCAACGCGCATCAAGAACACAGGCGCGGAGCGGGTGGCGGCGCAAGAACT 261

QY 245 TCTACACCGGAGCGGTTCTTCGAGGCGCATCGCGCGGTACCCGGGCTTCGCGCATGGCG 304  
Db 262 TCTACACCGGAGCGGTTCTTCGAGGCGCGGTCAACAAAGTACCCGCTTCGCGCATGGCG 320

QY 305 GCTCGAGTTCGAGCGCAAGCGGAGATTGCGCGCTTCTTCGCGCACGCGCACGACGAGA 364  
Db 321 GGACGAGGTGGAGGCGCAAGCGGAGTTCGCGCGCTTCTTCGCGCACGCTCAGCACGAGA 380

QY 365 CCGGCGCATTTCTGCTACATCAGCGAGGTCAACAAAGAGCAACGCTACTTCGCGACCGGACCA 424  
Db 381 CCGGACATTTCTGCTACATCAGCGAGTCAACAAAGAGCAACGCTACTTCGCGACGCA 440

QY 425 AGAGCGAGTGGCGCGCGCGCGGCGGAGAGTACTACGCGGCGGCGCGCGCTCGCATCT 484  
Db 441 ACAGCGAGTGGCGCGCGCGGCGGAGAGTACTACGCGGCGGCGCGCGCTCGCATCT 500

QY 485 CGTGGAACTACAACTACGCGGCGCGGCGGAGGCGCATCGGCTTCGAGCGGCTCGGGGACC 544  
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Db 561 CAAACAGGGTGGCGAGGACCGCGTGGTGGCGTTCAAGACGCGCTCTGGTTCTGGATGA 620
QY 605 ACAAGTGCACCGTGTGATGCGCGCAGGGCTTCGGCGCCACCATCAGGCGCATCAACGGCG 664
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Db 681 CCTCGAGTGAACGGGAAACACCCCGCCAGATGAACGCGCGTCTCGGCTACTACAGGC 740
QY 725 AGTACTGCGCGCAGTTCGGCTGCGTCCAGCCGGGCAACACC 763
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RESULT 3
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LOCUS Zm10_01e10_A Zm10_AAFRC_ECORC_Fusarium graminearum_corn_silk Zea
DEFINITION may's cDNA clone Zm10_01e10, mRNA sequence.
ACCESSION BG837663
VERSION BG837663.1 GI:14203986
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 855)
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2001)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrielj@agr.gc.ca.
FEATURES
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/clone="Zm10_01e10"
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/clone_lib="Zm10_AAFRC_ECORC_Fusarium graminearum_corn_silk
"
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Site 2: XhoI; Field-grown corn was silk channel-inoculated
in the morning (~10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."

ORIGIN
Query Match 77.2%; Score 597.6; DB 4; Length 855;
Best Local Similarity 90.3%; Pred. No. 1.5e-111;
Matches 670; Conservative 0; Mismatches 49; Indels 23; Gaps 2;

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Db 794 CAGTCGGGCGCGT-----CCGCTCGGGCGCGCGCGCAGT 757
QY 151 GGCAGTGGCGGTGGAACGTGGCTAATGTGTGTCAACGACGGCTTCTTCAACGGGNTCAAG 210
Db 756 GCGCGCGGTGTGGGAACGTGGCTAGGCTCGTCAACCGGCTCTCTTCTTCAACGGCATCAAG 697
QY 211 AACCAAGCGCGGAGCGGCTGCGAGGCAAGAACTTCTACACCCGAGCGCGTCTCTCGAG 270
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QY 271 GCCATCGCGGTATACCGGGGCTTCGCGCATGCGCGGCTCCGAGGTGCGAGCGCAAGCGCAG 330
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QY 751 CCGGCGCAACCACTCCTCCTCT 772
Db 157 CCGGCGCAACCACTCCTCCTCT 136

RESULT 4
LOCUS CO524416
DEFINITION 3530_1_161_1_E12.y_1 3530 - Full length cDNA library created by
in vitro from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION CO524416
VERSION CO524416.1 GI:50329290
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 767)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
```

Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 3530\_1161\_1 row: E column: 12.

## FEATURES

Location/Qualifiers  
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/note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSPORT vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Query Match 71.5%; Score 553.4; DB 7; Length 767;  
Best Local Similarity 91.4%; Pred. No. 1.5e-102;  
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DB 705 CAGCGTGCACGGGTGGTGGCGAGGGGTTTCGGCGCGCACCATCAGGCGCATCAACGGCGC 764  
  
QY 666 CCT 668  
DB 765 CCT 767

## RESULT 5

CD435649  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

CD435649 737 bp mRNA linear EST 03-JUN-2003  
E01N0364B04.b Endosperm\_3 Zea mays cDNA, mRNA sequence.  
CD435649  
CD435649.1 GI:31351292  
EST.  
Zea mays  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 737)  
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
Larkins, B., Becraft, P. and Messing, J.  
Characterization of the maize endosperm transcriptome and its  
comparison to the rice genome  
Genome Res. 14 (10), 1932-1937 (2004)  
Contact: Lai, Jinsheng  
Dr. Joachim Messing's lab  
Wakeman Institute, Rutgers University  
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
Tel: 732-445-3801  
Fax: 732-445-5735  
Email: jlai@wakeman.rutgers.edu  
Seq primer: T3.  
Location/Qualifiers  
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/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W22"  
/db\_xref="taxon:4577"  
/tissue\_type="Endosperm of 7-23DAP"  
/clone\_lib="Endosperm 3"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## ORIGIN

Query Match 70.2%; Score 543.4; DB 6; Length 737;  
Best Local Similarity 89.8%; Pred. No. 1.6e-100;  
Matches 619; Conservative 0; Mismatches 36; Indels 34; Gaps 2;

QY 6 GCAGAACTGCGGCTGCCAGCCAAACGATGCTGCGAGCAAGTTTGCTACTGCGGACGAC 65  
DB 126 GCAGAACTGCGGCTGCCAGCCAAACGATGCTGCGAGCAAGTTTGCTACTGCGGACGAC 185

Db 82 GCAGAACTGGCGTCCAGCCAAACGCTCTGCTGACGAAGTTCCGCTACTCGGCGACGAC 141  
Qy 66 CCACAGTACTGCGCGACGCGTGCAGTCCGCGCCCGTGCCTCGGCGCGCGTGGCGG 125  
Db 142 CGACAGTACTGCGCGACGCGTGCAGTCCGCGCCCGTGCCTCGGCGCGCGCGCGC-- 199  
Qy 126 CGGCGCGCGCGCGGCGGCGGAGGCGAGTGGCGGTGCGAACGTGGTGAATATGCTAC 185  
Db 200 -----GGTGGTGCBAACGTTAGCTAGCTCGTCTAC 228  
Qy 186 CGACGCTTCTTCAACGCGCATCAAGAACAGCCCGGAGCGCGGTGCGAGGCGCAAGAACTT 245  
Db 229 CGGCTCTTCTTCAACGCGCATCAAGAACAGCCCGGAGCGGTTGCGAGGCGCAAGAACTT 288  
Qy 246 CTACACCGGAGCGGTTCTCGAGGCGCATCGCCCGGTACCGGGGCTTCGCGCATGGCGG 305  
Db 289 CTACACCGGAGCGGTTCTCGAGGCGGTCAAGGCGGTACCGAGGCTTCGCCCATGGCGG 348  
Qy 306 CTCGAGGTTCGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCACGCCACGACGAGAC 365  
Db 349 GTCCGAGGTGAGGCGCAAGCGCGAGATCGCGCTTCTTCGCGCACGCCACGACGAGAC 408  
Qy 366 CGGCGATTCTCTGCTACATCAGCGGTCAACAGAGCAACGCTACTGCGACCCGACCA 425  
Db 409 CGGCGATTCTCTGCTACATCAGCGAGATCAACAGAGCAACGCTACTGCGACCCGACCA 468  
Qy 426 GAGCGAGTGGCGGTGCGCGCGGCGGAGGAGTACTACGCGGCGCGCCCGCTGCGAGATCTC 485  
Db 469 GAGCGAGTGGCGGTGCGCGCGGCGGAGGAGTACTACGCGGCGCGCCCGCTGCGAGATCTC 528  
Qy 486 GTGGAATCTACACTACGCGGCGCGGAGGCGGCGCATCGGCTTCGACGGGCTTCGCGGACCC 545  
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Qy 546 CGGAGGCTGCGCGGCGCGCGGTGCGCGTTCGAGGCGCGCTCTGTTCTGATGAA 605  
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Qy 606 CAACGTGCAC--CGTGTGATGCGGAGGCGTTCGCGCGCACCATCAAGGCGCATCAACGCGC 664  
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Qy 665 CCCTCGAGTGCACGCGGCAACCCCGCC 693  
Db 709 CCCTCGAGTGGCGGGAACACCCCGCC 737

## RESULT 6

BM895383  
LOCUS 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
DEFINITION mays cDNA, mRNA sequence.

ACCESSION BM895383

VERSION BM895383.1 GI:19350851

KEYWORDS EST.

SOURCE Zea mays

## ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 625)

Walbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952073 row: H column: 05.

FEATURES  
source

Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
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/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
/note="vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size 400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

## ORIGIN

Query Match 68.5%; Score 530.4; DB 5; Length 625;  
Best Local Similarity 92.4%; Pred. No. 7e-98;  
Matches 569; Conservative 0; Mismatches 46; Indels 1; Gaps 1;  
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Db 11 GCGGAGCAGTGGCGGTGCGAACTGCTAATGTGGTCCACGACGCGTCTTCAACGCGCA 69  
Qy 206 TCAAGAACCGAGCGCGGAGCGGTGCGAGGCGAAGAACTTCTACACCGGAGCGGTTC 265  
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Qy 266 TCGAGGCGCATCGCGCGTACCGCGGCTTCGCGCATGGGCTCCGAGGTTCAGCGCGCAGC 325  
Db 130 TGAAGCGCGTCAACAACTACCGCGGCTTCGCGCATGGGCTTCGAGGTTCAGCGCGCAGC 189  
Qy 326 GCGAGATTGCGCGCTTCTTCGCGCACCGCACGAGACCGCGCATTTCTGTCTACATCA 385  
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Qy 386 GCGAGGTCAACAGAGCAACCGCTTCTGCGACCGCACGAGGCGAGTGGCGCGTGGCGCG 445  
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Qy 446 GCGGCGAGAGTACTACGGGCGCGCGCTGCGAGATCTCGTGAACCTACAACTACCGGC 505  
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Db 370 CCGCGGCGAGGCGCATCGGCTTCGACGGGCTTCGCGGAGACCCCGGAGGTTCGCGGAGC 429  
Qy 566 CCGTGTGGGTTCAAGCGCGCGCTCTGTTCTGATGAAACAACTGTCACCGTGTGATGC 625  
Db 430 CCGTGTGGGTTCAAGCGCGCGCTCTGTTCTGATGAAACAACTGTCACCGTGTGATGC 489  
Qy 626 GCGAGGCTTCGCGCGCGCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCACCGGAGCA 685  
Db 490 GCGAGGCTTCGCGCGCGCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCACCGGAGCA 549  
Qy 686 ACCCGCGCGAGATGAACGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTCGCGC 745  
Db 550 ACCCGCGCGAGATGAACGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTCGCGC 609  
Qy 746 TCGACCGCGGCAACAA 761  
Db 610 TCGACCGCGGCGCCAA 625

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RESULT 7
COS20138      3530_1_132_1_F10.Y_1_3530 - Full length cDNA library created by
LOCUS         716 bp      mRNA      linear      EST 15-JUL-2004
DEFINITION   Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION    COS20138
VERSION      COS20138.1 GI:50325012
KEYWORDS     EST.
SOURCE       Zea mays
ORGANISM     Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 716)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530_1_132_1 row: F column: 10.
FEATURES             source
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            /lab_host="DH10B"
            /clone_lib="3530 - Full length cDNA library created by
            Invitrogen from multiple tissues"
            /note="Organ: silks, husks, ears, pollen, shoot tips,
            leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
            6.1; Site:1: EcoRV; Site_2: NotI; Maize Gene Discovery
            Project contracted with Invitrogen to produce a
            normalized, full length library in a pSPORT vector. This
            is a Gateway compatible vector, permitting clone movement
            to new vector backbones for expression in diverse host
            cells using recombination rather than restriction enzymes.
            Details of the vector and sequencing primers are available
            at ZmDB in the EST library description tables. poly(A)+
            mRNA was prepared by Invitrogen, and equimolar amounts of
            RNA from each of the 12 tissue samples were mixed together
            for selection of mRNA with a 5' cap. After synthesis of
            cDNA, a normalization step was conducted against the
            mixture of RNA sources. This step effected a 20X to 80X
            reduction in common transcript types. Tissues prepared: 1.
            just emerging silks; 2. inner husks from ears of sample
            #1; 3. 20 dap aleurone; 4. immature tassels, stages from
            1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
            vegetative shoot tips from 15 day old seedlings; all
            leaves with an expanded or partially expanded sheath
            were removed; 8. mature leaf tissue; 9. 0.5 cm long root
            tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
            12 dap endosperm and embryo; 12. 17 dap endosperm and
            embryo. All of the sequenced clones in project 3530 will
            be archived at the University of Arizona along with the
            Unigene clones from the Maize Gene Discovery EST
            sequencing projects. Clones can be ordered through the
            ZmDB web site or directly from the University of Arizona
            (http://www.genome.arizona.edu/orders/). High density
            filters containing over 18,000 clones can also be ordered
            from the University of Arizona."

Matches 563; Conservative 0; Mismatches 38; Indels 1; Gaps 1;
Qy 6 GCAGAACTGCGGCTGCGCAGCAAAAGTATGCTGCAGCAAGTTTGGCTACTTGCAGCACGAC 65
Db 116 GCAGAACTGCGGCTGCGCAGCAAAAGTATGCTGCAGCAAGTTTGGCTACTTGCAGCACGAC 175
Qy 66 CGACGAGTACTTGCAGCGCGACGCGGTGCACAGTGCAGGCGCGCTCGGCGCGCGGTGCGG 125
Db 176 CGACGCTACTTGCAGCGCGACGCGGTGCACAGTGCAGGCGCGCTCGGCGCGCGGTGCGG 235
Qy 126 CGGCGGCGCGCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185
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Qy 186 CGACGCGTCTTCAACGCGCATCAAGAACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245
Db 296 CGACGCGTCTTCAACGCGCATCAAGAACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 355
Qy 246 CTACACCGCGGAGCGGTTCTCTCGAGGCGCATCGCGCGCTACCGCGGCTTCGCGCATGGCG 305
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Qy 306 CTCCGAGGTGAGCGCAAGCGCGGAGATGCGCGCTTCTTGCAGCGCGCGCGCGCGCGAGAC 365
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Qy 366 CGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTTGCAGCGCGCGCA 425
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Qy 426 GAGCGAGTGGCGCGTGCAGCGCGCGGCGGAGAGTACTACGGGCGCGCGCGCTTGCAGATGTC 485
Db 536 CAGCGAGTGGCGCGTGCAGCGCGCGGCGGAGAGTACTACGGGCGCGCGCGCTTGCAGATGTC 595
Qy 486 GTGGAATACAACTACCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545
Db 596 GTGGAATACAACTACCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 654
Qy 546 CGGCGAGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 605
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Db 715 CA 716

RESULT 8
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LOCUS         952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
DEFINITION   mays cDNA, mRNA sequence.
ACCESSION    BM736454
VERSION      BM736454.1 GI:19057787
KEYWORDS     EST.
SOURCE       Zea mays
ORGANISM     Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 628)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952051 row: A column: 06.

Query Match      68.4%; Score 529.2; DB 7; Length 716;
Best Local Similarity 93.5%; Pred. No. 1.2e-97;
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      /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
      /note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."
    67.9%; Score 525.6; DB 4; Length 628;
    Best Local Similarity 91.9%; Pred. No. 6.7e-97;
    Matches 566; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Qy 157 GCGGTGCGAAGTGGCTTAATGTGTACCGACGGCTTCTTCAACGGCATCAAGACGAG 216
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Qy 217 GCGGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGGTCTCTCGAGGCCATC 276
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Qy 277 GCGGTACCGGGTTCGCGCATGGCGTCCGAGTCCGAGTCCGAGCGGAGATGTC 336
Db 122 AACAAAGTACCGGGTTCGCGCATGGCGGAGCGAGTGGAGGCGAGATGTC 181

Qy 337 GCCTTCTTCGCGCAGCCACGACGAGACCGGGATTTCTGTATCATCAGCGAGTCAAC 396
Db 182 GCCTTCTTCGCGCAGCTACGACGAGACCGGACATTTCTGTATCATCAGCGATCAAC 241

Qy 397 AAGAGCAAGCTTACTGCGACCCGACCAAGAGGCGAGTGGCGCGCGGGGCGAGAG 456
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Qy 457 TACTACGGCGCGCGCGCTGCGATCTCGTGGAACTACACTACGGCGCGCGGGGAGG 516
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Qy 517 GCCATCGGCTTCGAGCGGCTCGGGACCCCGGAGGGTGGCGCGGACCGCGTGTGCG 576
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Qy 577 TTCAAGCGCGCGCTCTGTTCTGGATGAACAACTGCAACCGTGTATGCCGACGGCTTC 636
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Qy 637 GGGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCACGGGACAAACCCCGCCAG 696
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Qy 697 ATGAACGGCGCGCTGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGG 756
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Qy 757 AACAACTCACTGCT 772
Db 602 CCCAACTCACTGCT 617

ORIGIN
  Query Match 67.9%; Score 525.6; DB 4; Length 628;
  Best Local Similarity 91.9%; Pred. No. 6.7e-97;
  Matches 566; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Qy 157 GCGGTGCGAAGTGGCTTAATGTGTACCGACGGCTTCTTCAACGGCATCAAGACGAG 216
Db 3 GGGCGGCGAAGTGGCTTAAGTGG-CAGCGACGGTCTTCAACGGCATCAAGACGAG 61

Qy 217 GCGGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGGTCTCTCGAGGCCATC 276
Db 62 GCGGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGGTCTCTCGAGGCCGTC 121

Qy 277 GCGGTACCGGGTTCGCGCATGGCGTCCGAGTCCGAGTCCGAGCGGAGATGTC 336
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Qy 337 GCCTTCTTCGCGCAGCCACGACGAGACCGGGATTTCTGTATCATCAGCGAGTCAAC 396
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Qy 517 GCCATCGGCTTCGAGCGGCTCGGGACCCCGGAGGGTGGCGCGGACCGCGTGTGCG 576
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Qy 577 TTCAAGCGCGCGCTCTGTTCTGGATGAACAACTGCAACCGTGTATGCCGACGGCTTC 636
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Qy 637 GGGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCACGGGACAAACCCCGCCAG 696
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Qy 697 ATGAACGGCGCGCTGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGG 756
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Qy 757 AACAACTCACTGCT 772
Db 602 CCCAACTCACTGCT 617
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RESULT 9
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DEFINITION
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  OX1_9 D11.g1 A002 Oxidatively-stressed leaves and roots Sorghum
  bicolor cDNA clone OX1_9 D11_A002 5', mRNA sequence.
ACCESSION
  CN133023
VERSION
  CN133023.1 GI:45963543
KEYWORDS
  EST.
SOURCE
  Sorghum bicolor (sorghum)
  Sorghum bicolor
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Sorghum.
  1 (bases 1 to 837)
  Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
  Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
  An EST database from Sorghum: oxidatively stressed leaves and roots
  Unpublished (2003)
  Other ESTs: OX1_9 D11.b1 A002
  Contact: Cordonnier-Pratt MM
  Laboratory for Genomics and Bioinformatics
  The University of Georgia, Department of Plant Biology
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
  the Human Genome Center, University of Tokyo Institute of Medical
  Science; plant material and RNA prepared at Texas A & M University;
  sequencing done in the Laboratory for Genomics and Bioinformatics,
  University of Georgia. Sequence ends have been trimmed to exclude
  vector and regions below Phred quality 16. Three-prime sequences
  are presented as their reverse complement and have been trimmed to
  exclude polyA.
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      XhoI; Site 2: XhoI; The library was prepared from polyA+
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      sorghum seedlings. At 8 days of age, growth medium was
      supplemented with hydrogen peroxide to 0.003% and leaves
      were misted with 10 uM methyl viologen. Leaves and roots
      were harvested at 3, 12 and 27 hr after treatment and all
      tissue pooled. Double-stranded cDNA was cloned
      unidirectionally into different DraIII sites of the
      pME18S-FL3 vector (5-prime DraIII site is CACTGTGTC,
      3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
      insert."
FEATURES
source
  Query Match 67.1%; Score 519.4; DB 7; Length 837;
  Best Local Similarity 84.2%; Pred. No. 1.2e-95;
  Matches 624; Conservative 0; Mismatches 81; Indels 36; Gaps 2;

Qy 6 GCAGAACTCGCGCTGCGAGCAACAGTATGTCGAGCAAGTTTGGCTACTCGGCACGAC 65
Db 133 GCAGAACTACGGCTGCGAGCGAGTTACTGTCGAGCAAGTTTCGGTTACTCGGCACGAC 192

Qy 66 GCAGAGTACTGCGGCGACCGGTCCAGTCCGCGCCCTGCGCTCGGCGCGGCTGCGG 125
Db 193 GCAGAGTACTGCGGCGACCGGTCCAGTCCGCGCCCTGCGCTCGGCGCGGCTGCGG 241

Qy 126 CGGCGCGCGCGCGGAGCGGCGGAGGCGGAGTGGCGGTGGCAACGTCGTCGTCAC 185
Db 242 -----GGCGGCGAGTGGAGGTGGGNAACGTCGTCGTCGTCAC 282
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426 GAGGCGAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGCGGCGCGCGCTTCGAGATCTC 485
427 |||||
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517 CAGGCGAGTGGCGGTGCGCGCGGTGCGAGTACTACGCGGCGCGCGCTTCGAGATCTC 576
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486 GTGGAATTCACATACGCGCGCGGCGAGGCGCATCGGCTTCGAGCGGCTTCGGGAGCC 545
487 |||||
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577 GTGGAATTCACATACGCGCGCGTTCGCGGAGGAGCATCGGCTTCGAGCGGCTTCGGA 636
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546 CGGCGAGGTGCGCGGAGCGCGGTGCGGCTTCGAGCGGCGCGCTTCGAGATCTC 605
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637 GGCACAGGTGCGCGCAAGACGCGGTGCGGCTTCGAGCGGCGCGCTTCGAGATCTC 696
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639 |||||
606 CAACGTGACCGTGTGATGCGCGAGGCTTCGCGCGCGCGCGCGCTTCGAGCGGCGCG 665
607 |||||
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697 CAACGTGACCGGGTGATGCGAGGCGTTCGCGCGCGCGCGCGCTTCGAGCGGCGCG 756
698 |||||
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699 |||||
666 CCTCGAGTGAACCGGAAACACCGCGCGCGAGATGAACCGCGCGTTCGAGCGGCGCG 725
667 |||||
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757 CCTCGAGTGAACCGGAAACATCTGCGCGAGATGAACCGCGCGGTTGCGCTACTACAG 816
758 |||||
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726 GTACTGCGCGCGCTCGCGGT 746
727 |||||
727 |||||
817 GTACTGCGCGAGCTCGCGGT 837
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RESULT 10
CAL197556 647 bp mRNA linear EST 25-SEP-2003
LOCUS SCBFAD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11
DEFINITION 5', mRNA sequence.
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ACCESSION CAL197556
VERSION CAL197556.1 GI:35227930
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KEYWORDS EST.
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SOURCE Saccharum officinarum
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ORGANISM Saccharum officinarum
```

```
REFERENCE 1 (bases 1 to 647)
Vettore, A.L., da Silva, P.R., Kemper, B.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
```

```
COMMENT Contact: Arruda P
```

```
Centro de Biologia Molecular e Engenharia Genetica
```

```
Universidade Estadual de Campinas
```

```
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
```

```
Tel: 55 19 3788 1137
```

```
Fax: 55 19 3788 1089
```

```
Email: parruda@unicamp.br
```

```
Clone distribution: clone distribution information can be found
```

```
through the Brazilian Clone Collection Center (BCCC) at
```

```
http://www.bcccenter.fcav.unesp.br
```

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Plate: 067 row: A column: 11
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Seq primer: T7 Promoter Primer.
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Location/Qualifiers
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## FEATURES

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1..647
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCBFAD1067A11"
/lab_host="DH10B"
/clone_lib="AD1"
/notes="Organ: seedlings inoculated with Gluconacetobacter
diazotrophicans; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Gluconacetobacter
diazotrophicans]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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## ORIGIN

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Query Match 65.08; Score 503; DB 6; Length 647;
Best Local Similarity 86.8%; Pred. No. 2.6e-92;
Matches 567; Conservative 0; Mismatches 80; Indels 6; Gaps 1;
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Qy 164 CGAACGTGGGTAAATGTGGTCAACGACGCGGTTCCTTCAACGGGATCAAGAACGAGCC 223
Db 61 GGAACGTGGGTAGCGTTGTCAACGACGCAATTTCTTCAACGGGATCAAGAACGAGCC 120
Qy 224 CGGGTTCGAGGGCAAGAACTTCTACACCGGAGCGGCTTCTTCCAGGCGCATCGCCGCT 283
Db 121 ACGGTTCGAGGGCAAGAACTTCTACACCGGAGTGGCTTCTTCCAGGCGCGGCGGCT 180
Qy 284 ACCCGGCTTCGCGCATGCGGCGTCCGAGGTTCGAGCGCAAGCGGAGATTGCCGCTTCT 343
Db 181 ACAAGGCTTC-----GGTGGCGGTGGTGGAGGCGAGCGGCGGCGGCGGCTTCT 234
Qy 344 TCGCGACGCGCGACGACGAGACGCGGCAATTTCTGTATCATCAGCGAGGTCAACAGGCA 403
Db 235 TCGCGCACGTCACGACGAGACGCGCAATTTCTGTATCATCAGCGAAATCAACAGGAACA 294
Qy 404 ACGCCTACTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
Db 295 ACGCCTACTCGAGCTCGAGCAACAGGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 354
Qy 464 GCGCGCGCGCGCTGCAGATCTCTGTGGAATACAACTACGCGCGCGCGCGCGCGCGCGCG 523
Db 355 GCGCGCGCGCGCTGCAGATCTCTGTGGAATACAACTACGCGCGCGCGCGCGCGCGCGCG 414
Qy 524 GCTTCGACGCGGCTCGGGGACCGCGCGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 583
Db 415 GCTTCAACGCGGCTCGGGGACCGCGCGAGGTGGCGCGAGGACGCGCGGTGATCGCGTTC 474
Qy 584 CGGCGCTCTGGTCTGTGATGAACACGTCGACCGCTGTGTGATGTCGCGCGCGCGCGCGCG 643
Db 475 CGGCGCTCTGGTCTGTGACGAAACGTCGACCGGTGTGATGTCGAGGGGTTCGAGGCGCA 534
Qy 644 CCATCAGGGCCATCAACCGCGCGCTTCGAGTGCACCGGAAACAAACCGCGCGCGCGCGCG 703
Db 535 CCATCAGGGCTATCAACCGAGCGCTTCGAGTGCACCGGAAACAAACCGCGCGCGCGCGCG 594
Qy 704 CGCGCGTCTGGTCTACTACAGGAGTACTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 756
Db 595 CGCGCGTCTGGTCTACTCAAGCAGTACTGTCTCAGCAGCTCGCGGTTCGACCGCGCGCG 647
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## RESULT 11

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CD443492
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```
LOCUS
```

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DEFINITION EL01N0427B11.b Endosperm_4 Zea mays cDNA, mRNA linear EST 03-JUN-2003
```



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ACCESSION CD443492
VERSION CD443492.1 GI:31359135
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 710)
Larkin, B., Becraft, P. and Messing, J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
1..710
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/cultivar="W22"
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XhoI"

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Best Local Similarity 91.2%; Pred. No. 4.2e-92;
Matches 551; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 6 GCAGAACTCGCGTCCAGCCAAACGATGTCGACGAAAGTTGGCTACTCGGCACGAC 65
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DB 185 CGACGAGTACTGTCGCGAGCGGTGCGAGTCCGCGCCGTCGCGTCCGCGGCGGTGG 244
QY 126 CGCGCGCGCGCGCGGAGCGCGGAGCGAGTGGCGGTGCGAAGTGGCTAATGTTGTCAC 185
DB 245 CGCGAGTGGTGC-----GGTGTGGAAAGTGGCTAGCGTCTGTCAC 286
QY 186 CGACCGGTTCTTCAACGCGCATCAAGAACGAGCCGCGGAGCGGTCGAGGCGCAAGAACTT 245
DB 287 CAGCTCTCTTCAACGCGCATCAAGAACGAGCCGCGGAGCGGTGCGAGGCGCAAGAACTT 346
QY 246 CTACACCGCGAGCGGTCTCTCGAGCCATCGCCCGGTACCGGCGTTCGCGCATGGCG 305
DB 347 CTACACCGCGAGCGGTCTCTGAGCGCGGTCAAGCGGTACCGAGCTTCGCCCAATGGCG 406
QY 306 CTCCGAGGTGAGCGCGAGATTCGCGCTTCTTCGCGCACGCGCCACGCAAGAGAC 365
DB 407 GTCGAGGTGAGCGCGAGATTCGCGCTTCTTCGCGCACGCGCCACGCAAGAGAC 466
QY 366 CGGGCATTTCTGCTCATCATCAGCGAGTCAACAGAGCAACGCTACTCGCACCGGACAA 425
DB 467 CGGGCATTTCTGCTCATCATCAGCGAGATCAACAGAGCAACGCTACTCGCACCGGACAA 526
QY 426 GAGGCACTGCGTCCGCGCGGCGGAGAGTACTACGCGCGCGCGCTGCGATCTC 485
DB 527 GAGGCACTGCGTCCGCGCGGCGGAGAGTACTACGCGCGCGCGCTGCGATCTC 586
QY 486 GTGGAACTACAACTACGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 545
DB 587 GTGGAACTACAACTACGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 646

QY 546 CGGCAGGCTGCGCGGAGACGCCGTGGTGGCTTCAAGCGCGCGCTCTGGTCTCGATGAA 605
DB 647 CGGCAGGCTGCGCGGAGACGCCGTGGTGGCTTCAAGCGCGCGCTCTGGTCTCGATGAA 706
QY 606 CAAC 609
DB 707 CAGC 710

RESULT 12
CD995497
LOCUS CD995497 820 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB25f07.xg QBB Zea mays cDNA clone QBB25f07, mRNA sequence.
ACCESSION CD995497
VERSION CD995497.1 GI:32855816
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 820)
Genopiante.
Genopiante, a major partnership french program in plant genomes
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com
and http://genopiante-info.infobiogen.fr).

FEATURES
Location/Qualifiers
1..820
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ORIGIN
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Best Local Similarity 93.7%; Pred. No. 6.7e-92;
Matches 522; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 216 GCGCGGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGCGGTTCTCGAGGCCAT 275
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QY 276 GCGCGGTACCGGGCTTCGGCATGGCGTCCGAGTCCGAGTCCGAGCGAGCGGAGATTGC 335
DB 105 CAAGCGGTACCGAGCTTCGCGCCACGCGGCTGCGAGTCCGAGCGAGCGAGATCGC 164
QY 336 CGCTCTTCTTCGCGCACGCCACGACGAGACCGGCGCATTTCTGTACATCAGCGAGTCAA 395
DB 165 CGCTCTTCTTCGCGCACGCCACGACGAGACCGGCGCATTTCTGTACATCAGCGAGTCAA 224
QY 396 CAAGAGCAACGCCCTACTTCGCGACCCGACCAAGAGGAGTGGCGGTGCGCGCGGGGAGAA 455
DB 225 CAAGAGCAACGCCCTACTTCGCGACCCGCGCGTGGCGGTGCGCGCGGGGAGAA 284
QY 456 GTACTTACGGGCGCGCGCGTTCGAGATCTCGTGAATCTACAACTACCGGGCCCGGGGAG 515
DB 285 GTACTTACGGGCGCGCGCGTTCGAGATCTCGTGAATCTACAACTACCGGGCCCGGGGAG 344
QY 516 GGCCATCGGCTTCGACGGGCTTCGGGAGCCCGCGGAGGGTGGCGGAGACGCGGTGGTGGC 575
DB 345 GGCCATCGGCTTCGACGGGCTTCGGGAGCCCGCGGAGGGTGGCGGAGACGCGGTGGTGGC 404
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Qy	636	CGGGCCACCATCAGGCGCCATCAACGGCGCCCTCGAGTGCNAACGGGACACACCCCGGCCA	695
Db	465	CGGGCGCCACCAACAGGCGCCATCAACGGCGCCCTCGAGTGCAGCGGGAACAAACCCCGGCCA	524
Qy	696	GATGAACGCGCGCGCTCGGCTACTACAGCAGTACTTGC CGCCAGCTCGCGCTCGACCCCGGG	755
Db	525	GATGAACGCGCGCGCTCGGCTACTACAGCAGTACTTGC CGCCAGCTCGCGCTCGACCCCGGG	584
Qy	756	CAACAACCTCACCTGCT 772	
Db	585	GCCCAACCTCACCTGCT 601	
RESULT 13			
CD994454			
LOCUS			
DEFINITION			
CD994454			
ACCESSION			
VERSION			
CD994454.1			
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Zea mays			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Genoplatte, a major partnership french program in plant genomics			
Unpublished (2003)			
Contact: Genoplatte			
Genoplatte			
93, rue Henri Rochefort 91025 EVRY CEDEX France			
Tel: 33 1 69 47 54 00			
Fax: 33 1 69 47 54 10			
This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' ( <a href="http://www.genoplatte.com">http://www.genoplatte.com</a> ) and <a href="http://genoplatte-info.inbio.gen.fr">http://genoplatte-info.inbio.gen.fr</a> .			
Location/Qualifiers			
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ORIGIN			
Query Match			
Best Local Similarity			
Matches			
518; Conservative			
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34; Indels			
0; Gaps			
0; 21			
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Qy	281	CGTACCGGGCTTCGCGCATCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCT	340
Db	66	CGTACCGAGGTTTCGCCACCGCGGGTTCGAGGTCGAGGCGAAGCGCGAGATTCGCGCT	125
Qy	341	TCCTTCGCGACGCCACGCAACCGGCGCATTTCTGCTCATCAGCGAGTCAACAAGA	400
Db	126	TCCTTCGCGACGCCACGCAACCGGCGCATTTCTGCTCATCAGCGAGTCAACAAGA	185
Qy	401	GCAACGCTACTGCGACCGGCGAAGGCGAGTGGCGCGCGCGGCGAGAGTACT	460
Db	186	GCAACGCTACTGCGACCGGCGAAGGCGAGTGGCGCGCGCGGCGAGAGTACT	245
Qy	461	ACGGGCGCGCGCTGCGAGATCTCGTGGAACTCAAACTACGGGCGCGCGGAGGGCCA	520

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Db 121 TTCGCGACGCCGACGAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGC 180
Qy 403 AACGCTACTGCGACCCGACCAAGAGGAGTGCGCGTGCAGCGCGGGGAGAGTACTTAC 462
Db 181 AACGCTACTGCGACCCGAGCAAGAGGAGTGCGCGTGCAGCGCGGGGAGAGTACTTAC 240
Qy 463 GGGCGGGCGCGCTGAGATCTGCTGGAACTAACAATACGAGGCGCGGGGAGGGCCATC 522
Db 241 GGGCGGGCGCGCTGAGATCTGCTGGAACTAACAATACGAGGCGCGGGGAGGGCCATC 300
Qy 523 GGTCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGCGGAGCGCGTGTGGCGTTCAAG 582
Db 301 GGTCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGGGAGCGCGTGTGGCGTTCAAG 360
Qy 583 GGGCGGCTCTGTTCTGAGTAACAACGTCGACCGTGTGATGCCGAGGGCTTCGGCGCC 642
Db 361 GGGCGGCTCTGTTCTGAGTAACAACGTCGTCAGCGGGTGGTCCGCGAGGGTTCGGCGCC 420
Qy 643 ACCATCAGGGCCATCAACGGCGCCCTCGAGTGCACGGGACAAACCCCGCCAGATGAAC 702
Db 421 ACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAGGGGAAACAACCCCGCCAGATGAAC 480
Qy 703 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGTGCAGCCGGGCAACAAC 762
Db 481 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGTGCAGCCCGGGCCAAAC 540
Qy 763 CTCACCTGCT 772
Db 541 CTCACCTGCT 550
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## RESULT 15

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QBB18e05.xg QBB Zea mays cDNA clone QBB18e05, mRNA sequence.
ACCESSION CD994885
VERSION CD994885.1 GI:32855204
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## KEYWORDS

EST.

Ze mays

Ze mays

ORGANISM

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 753)

Genoplane.

Genoplane, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplane

Genoplane

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'genoplane' (<http://www.genoplane.com>

and <http://genoplane-info.infobiogen.fr>).

Location/Qualifiers

1..753

/organism="Zea mays"

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/db\_xref="taxon:4577"

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## ORIGIN

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Best Local Similarity 94.0%; Pred. No. 4e-91;
Matches 517; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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```
Qy 223 AGCGGTTGCGAGGCAAGAACTTCTACACCGGAGCGGTTCTCGAGGCCATCGCGCG 282
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Db 1 AGCGGTTGCGAGGCAAGAACTTCTACACCGGAGCGGTTCTCGAGGCCATCGAGGCG 60
```

```
Qy 283 TACCGGGCTTCGGGCATGCGGGTCCAGGTCCAGGCGCAAGCGGAGATTGCGCGCTTC 342
Db 61 TACCGAGGCTTCGGCCCAAGCGGGGTGCGAGGTGCAGGGCAAGCGGAGATCGCGCTTC 120
Qy 343 TTCGGCAGCGCCAGCGACGAGACCGGGCATTTCTGTACTACATCAGCGAGGTCAACAAGAGC 402
Db 121 TTCGGCAGCGCCAGCGACGAGACCGGGCATTTCTGTACTACATCAGCGAGATCAACAAGAGC 180
Qy 403 AACGCTACTGCGACCCGACCAAGAGGAGTGCGCGTGCAGCGCGGGGAGAGTACTTAC 462
Db 181 AACGCTACTGCGACCCGAGCAAGAGGAGTGCGCGTGCAGCGCGGGGAGAGTACTTAC 240
Qy 463 GGGCGGGCGCGCTGAGATCTGCTGGAACTAACAATACGAGGCGCGGGGAGGGCCATC 522
Db 241 GGGCGGGCGCGCTGAGATCTGCTGGAACTAACAATACGAGGCGCGGGGAGGGCCATC 300
Qy 523 GGTCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGGGAGCGCGTGTGGCGTTCAAG 582
Db 301 GGTCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGGGAGCGCGTGTGGCGTTCAAG 360
Qy 583 GGGCGGCTCTGTTCTGAGTAACAACGTCGACCGTGTGATGCCGAGGGCTTCGGCGCC 642
Db 361 GGGCGGCTCTGTTCTGAGTAACAACGTCGTCAGCGGGTGGTCCGCGAGGGTTCGGCGCC 420
Qy 643 ACCATCAGGGCCATCAACGGCGCCCTCGAGTGCACGGGAAACAACCCCGCCAGATGAAC 702
Db 421 ACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAGGGGAAACAACCCCGCCAGATGAAC 480
Qy 703 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGTGCAGCCGGGCAACAAC 762
Db 481 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGTGCAGCCCGGGCCAAAC 540
Qy 763 CTCACCTGCT 772
Db 541 CTCACCTGCT 550
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Job time : 2221.06 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 14:20:22 ; Search time 397.391 Seconds  
(without alignments)  
11943.947 Million cell updates/sec

Title: US-10-692-367-11  
Perfect score: 774  
Sequence: 1 tcgatgagaactggcgtg.....gcaacaacctcaacctgtga 774

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
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- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774	100.0	774	19	US-10-692-367-11
2	771	99.6	771	18	US-10-389-432B-11
3	761.2	98.3	774	19	US-10-692-367-29
4	759.6	98.1	774	19	US-10-692-367-33
5	758.2	98.0	771	18	US-10-389-432B-29
6	756.6	97.8	771	18	US-10-389-432B-33
7	727.6	94.0	774	19	US-10-692-367-71
8	714.8	92.4	774	19	US-10-692-367-45
9	711.8	92.0	771	18	US-10-389-432B-45
10	711.6	91.9	774	19	US-10-692-367-23
11	710	91.7	771	19	US-10-692-367-59

12	710	91.7	774	19	US-10-692-367-37	Sequence 37, Appl
13	708.6	91.6	771	18	US-10-389-432B-23	Sequence 23, Appl
14	707	91.3	768	18	US-10-389-432B-59	Sequence 59, Appl
15	707	91.3	771	18	US-10-389-432B-37	Sequence 37, Appl
16	706.8	91.3	771	19	US-10-692-367-61	Sequence 61, Appl
17	706.8	91.3	774	19	US-10-692-367-65	Sequence 65, Appl
18	703.8	90.9	768	18	US-10-389-432B-61	Sequence 61, Appl
19	703.8	90.9	771	18	US-10-389-432B-65	Sequence 65, Appl
20	703.6	90.9	774	19	US-10-692-367-63	Sequence 63, Appl
21	702	90.7	771	19	US-10-692-367-47	Sequence 47, Appl
22	700.6	90.5	771	18	US-10-389-432B-63	Sequence 63, Appl
23	699	90.3	768	18	US-10-389-432B-47	Sequence 47, Appl
24	694	89.7	771	19	US-10-692-367-73	Sequence 73, Appl
25	691.8	89.4	1138	17	US-10-425-114-30480	Sequence 30480, A
26	691.8	89.4	1530	18	US-10-425-115-135817	Sequence 135817, A
27	690.8	89.3	840	15	US-10-259-165-762	Sequence 762, Appl
28	686.8	88.7	765	19	US-10-692-367-67	Sequence 67, Appl
29	686	88.6	771	19	US-10-692-367-83	Sequence 83, Appl
30	682.8	88.2	774	19	US-10-692-367-7	Sequence 7, Appl
31	680.4	87.9	753	19	US-10-692-367-43	Sequence 43, Appl
32	679.8	87.8	845	18	US-10-389-432B-7	Sequence 7, Appl
33	678	87.6	780	19	US-10-692-367-75	Sequence 75, Appl
34	677.4	87.5	750	18	US-10-389-432B-43	Sequence 43, Appl
35	677.2	87.5	765	19	US-10-692-367-25	Sequence 25, Appl
36	676.4	87.4	780	19	US-10-692-367-39	Sequence 39, Appl
37	674.8	87.2	771	19	US-10-692-367-41	Sequence 41, Appl
38	674.6	87.2	777	19	US-10-692-367-15	Sequence 15, Appl
39	674.2	87.1	762	18	US-10-389-432B-25	Sequence 25, Appl
40	673.4	87.0	777	18	US-10-389-432B-39	Sequence 39, Appl
41	671.8	86.8	768	18	US-10-389-432B-41	Sequence 41, Appl
42	671.6	86.8	774	18	US-10-389-432B-15	Sequence 15, Appl
43	669.4	86.5	777	19	US-10-692-367-3	Sequence 3, Appl
44	668.4	86.4	774	18	US-10-389-432B-3	Sequence 3, Appl
45	664.6	85.9	1141	18	US-10-425-115-135807	Sequence 135807, A

#### ALIGNMENTS

RESULT 1  
US-10-692-367-11  
; Sequence 11, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)....(774)  
US-10-692-367-11

Query Match 100.0%; Score 774; DB 19; Length 774;  
Best Local Similarity 100.0%; Pred. No. 1.1e-184;  
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGATGACAGAACTGCGGTGCGAGCAAACTATGCTGACGAAAGTTGGCTACTGCGGC 60  
DB 1 TCGATGACAGAACTGCGGTGCGAGCAAACTATGCTGACGAAAGTTGGCTACTGCGGC 60

QY 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGGGCGGCGGTGCGGCGGCGGT 120  
DB 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGGGCGGCGGTGCGGCGGCGGT 120

QY 121 GCG 180  
DB 121 GCG 180

QY 181 GTCAACGACGCGTCTTCAACCGGCATCAAGAACAGGCGCGGCGCGGTGCGAGGCGAAG 240  
DB 181 GTCAACGACGCGTCTTCAACCGGCATCAAGAACAGGCGCGGCGCGGTGCGAGGCGAAG 240

QY 241 AACTTTTACACCGGAGCGGTTCCTCGAGGCGATTCGAGGCGATTCGCGGCTTCGCGCAT 300  
DB 241 AACTTTTACACCGGAGCGGTTCCTCGAGGCGATTCGAGGCGATTCGCGGCTTCGCGCAT 300

QY 301 GCGGCTCCGAGGTGCGAGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGCGAC 360  
DB 301 GCGGCTCCGAGGTGCGAGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGCGAC 360

QY 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCCCTACTGCGACCCG 420  
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCCCTACTGCGACCCG 420

QY 421 ACCAAGAGGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
DB 421 ACCAAGAGGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
DB 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY 541 GACCCCGCAGGTTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
DB 541 GACCCCGCAGGTTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 601 ATGAACAACGTGCAACCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
DB 601 ATGAACAACGTGCAACCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 661 GCGCGCTCGAGTGCACCGGAGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
DB 661 GCGCGCTCGAGTGCACCGGAGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

QY 721 AGGCAGTACTGCG 774  
DB 721 AGGCAGTACTGCG 774

## RESULT 2

US-10-389-432B-11  
; Sequence 11, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: r2c2 nucleic acid  
US-10-389-432B-11

Query Match 99.6%; Score 771; DB 18; Length 771;  
Best Local Similarity 100.0%; Pred. No. 6.2e-184;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGATGACAGAACTGCGGTGCGAGCAAACTATGCTGACGAAAGTTGGCTACTGCGGC 60  
DB 1 TCGATGACAGAACTGCGGTGCGAGCAAACTATGCTGACGAAAGTTGGCTACTGCGGC 60

QY 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGGGCGGCGGTGCGGCGGCGGT 120  
DB 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGGGCGGCGGTGCGGCGGCGGT 120

QY 121 GCG 180  
DB 121 GCG 180

QY 181 GTCAACGACGCGTCTTCAACCGGCATCAAGAACAGGCGCGGCGCGGTGCGAGGCGAAG 240  
DB 181 GTCAACGACGCGTCTTCAACCGGCATCAAGAACAGGCGCGGCGCGGTGCGAGGCGAAG 240

QY 241 AACTTTTACACCGGAGCGGTTCCTCGAGGCGATTCGAGGCGATTCGCGGCTTCGCGCAT 300  
DB 241 AACTTTTACACCGGAGCGGTTCCTCGAGGCGATTCGAGGCGATTCGCGGCTTCGCGCAT 300

QY 301 GCGGCTCCGAGGTGCGAGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGCGAC 360  
DB 301 GCGGCTCCGAGGTGCGAGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGCGAC 360

QY 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCCCTACTGCGACCCG 420  
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCCCTACTGCGACCCG 420

QY 421 ACCAAGAGGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
DB 421 ACCAAGAGGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
DB 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY 541 GACCCCGCAGGTTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
DB 541 GACCCCGCAGGTTGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 601 ATGAACAACGTGCAACCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
DB 601 ATGAACAACGTGCAACCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 661 GCGCGCTCGAGTGCACCGGAGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
DB 661 GCGCGCTCGAGTGCACCGGAGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

QY 721 AGGCAGTACTGCG 771  
DB 721 AGGCAGTACTGCG 771

## RESULT 3

US-10-692-367-29  
; Sequence 29, Application US/10692367  
; Publication No. US20050050595A1



```
QY 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCACGCGCAC 360
DB 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCACGCGCAC 360
QY 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
DB 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
QY 421 ACCAAGAGCGAGTGGCGCTGCGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
DB 421 ACCAAGAGCGAGTGGCGCTGCGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
QY 481 ATCTCGTGGAACTACAATCAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGCGGCTCGGG 540
DB 481 ATCTCGTGGAACTACAATCAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGCGGCTCGGG 540
QY 541 GACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGGCTTCAAGGCGGGGCTCTGGTTCTGG 600
DB 541 GACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGGCTTCAAGGCGGGGCTCTGGTTCTGG 600
QY 601 ATGAACACGTCGACCGTGTGATGCGCGAGGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
DB 601 ATGAACACGTCGACCGTGTGATGCGCGAGGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
QY 661 GCGCGCTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720
DB 661 GCGCGCTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720
QY 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGGGCAACACCTCACCTGCTGA 774
DB 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGGGCAACACCTCACCTGCTGA 774
```

## RESULT 5

```
US-10-389-432B-29
; Sequence 29, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-29
```

Query Match 98.0%; Score 758.2; DB 18; Length 771;  
Best Local Similarity 99.0%; Pred. No. 1e-180; Mismatches 8; Indels 0; Gaps 0;  
Matches 763; Conservative 0;

```
QY 1 TCGATGTCAGAACTGCGGCTGCGCGCAACAGTATGTCGAGCAAGTTTGGCTACTGCGGC 60
DB 1 TCGATGTCAGAACTGCGGCTGCGCGCAACAGTATGTCGAGCAAGTTTGGCTACTGCGGC 60
QY 61 ACGACGCGAGTACTGCGCGCAACGCGGTGCGAGTGGGCGGCGGCTCGGCGCGCGGT 120
DB 61 ACGACGCGAGTACTGCGCGCAACGCGGTGCGAGTGGGCGGCGGCTCGGCGCGCGGT 120
```

```
QY 121 GCGCGCGCGCGCGCGAGCGCGCGAGCGCGCGGTCGCAACAGTGGCTAAATGTG 180
DB 121 GCGCGCGCGCGCGCGCGCGCGCGAGCGCGCGGTCGCAACAGTGGCTAAATGTG 180
QY 181 GTCAACCGACGCGTTCTTTCAACGCGCATCAAGAACACAGGCGCGGAGCGGTCGAGGGCAAG 240
DB 181 GTCAACCGACGCGTTCTTTCAACGCGCATCAAGAACACAGGCGCGGAGCGGTCGAGGGCAAG 240
QY 241 AACTTCTACACCGCGAGCGGTTCTTCGAGGCGCATCGCGGTCACCGGGCTTCGCGCAT 300
DB 241 AACTTCTACACCGCGAGCGGTTCTTCGAGGCGCATCGCGGTCACCGGGCTTCGCGCAT 300
QY 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCACGCGCAC 360
DB 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCACGCGCAC 360
QY 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
DB 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
QY 421 ACCAAGAGCGAGTGGCGCTGCGCGCGGCGAGAGTACTACGCGCGCGGGCTCGAG 480
DB 421 ACCAAGAGCGAGTGGCGCTGCGCGCGGCGAGAGTACTACGCGCGCGGGCTCGAG 480
QY 481 ATCTCGTGGAACTACAATCAGCGCGCGCGGAGGCGCATCGGCTTTCGACGCGGCTCGGG 540
DB 481 ATCTCGTGGAACTACAATCAGCGCGCGCGGAGGCGCATCGGCTTTCGACGCGGCTCGGG 540
QY 541 GACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGGCTTCAAGGCGGGGCTCTGGTTCTGG 600
DB 541 GACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGGCTTCAAGGCGGGGCTCTGGTTCTGG 600
QY 601 ATGAACACGTCGACCGTGTGATGCGCGAGGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
DB 601 ATGAACACGTCGACCGTGTGATGCGCGAGGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
QY 661 GCGCGCTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720
DB 661 GCGCGCTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720
QY 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGGGCAACACCTCACCTGCTGC 771
DB 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGGGCAACACCTCACCTGCTGC 771
```

## RESULT 6

```
US-10-389-432B-33
; Sequence 33, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-33
```

Query Match 97.8%; Score 756.6; DB 18; Length 771;



Best Local Similarity 98.8%; Pred. No. 2.6e-180;  
Matches 762; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTGGCGCTGCGAGCAAACTATCTGACGAAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGACAGAACTGGCGCTGCGAGCAAACTATCTGACGAAAGTTTGGCTACTGCGGC 60

Qy 61 ACACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGGCGCGCTGCGGCGCGGT 120  
Db 61 ACACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGGCGCGCTGCGGCGCGGT 120

Qy 121 GCG 180  
Db 121 GCG 180

Qy 181 GTACCCGACGCGTTCTTCAACCGGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 240  
Db 181 GTACCCGACGCGTTCTTCAACCGGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 240

Qy 241 AACTTCTACACCGAGCGGTTCCTGAGGCGATCGCGGCGATCGCGGCGGTTCGCGAT 300  
Db 241 AACTTCTACACCGAGCGGTTCCTGAGGCGATCGCGGCGATCGCGGCGGTTCGCGAT 300

Qy 301 GCGGCTCCGAGTTCGAGCGAAGCGCGAGATTGCGGCTTCTTCCGCGCGCGCGCGCG 360  
Db 301 GCGGCTCCGAGTTCGAGCGAAGCGCGAGATTGCGGCTTCTTCCGCGCGCGCGCGCG 360

Qy 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACCGCTACTGCGACCG 420  
Db 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACCGCTACTGCGACCG 420

Qy 421 ACCAAGAGCGAGTGGCG 480  
Db 421 ACCAAGAGCGAGTGGCG 480

Qy 481 ATCTGCTGAACTACAACTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db 481 ATCTGCTGAACTACAACTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

Qy 541 GACCCCGCGAGGTTGGCGCGGAGCGCGCGGTTCGAGGCGCGCTCTGCTGTTCTGG 600  
Db 541 GACCCCGCGAGGTTGGCGCGGAGCGCGCGGTTCGAGGCGCGCTCTGCTGTTCTGG 600

Qy 601 ATGAACAACGTGCAACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db 601 ATGAACAACGTGCAACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

Qy 661 GCGCGCTCGAGTGCACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Db 661 GCGCGCTCGAGTGCACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

RESULT 7

US-10-692-367-71  
; Sequence 71, Application US/10692367  
; Publication No. US200500595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086

PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; NAME/KEY: CDS  
; LOCATION: (1)...(774)  
US-10-692-367-71

Query Match 94.0%; Score 727.6; DB 19; Length 774;  
Best Local Similarity 96.3%; Pred. No. 4.8e-173;  
Matches 745; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTGGCGCTGCGAGCAAACTATCTGACGAAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGACAGAACTGGCGCTGCGAGCAAACTATCTGACGAAAGTTTGGCTACTGCGGC 60

Qy 61 ACACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGGCGCGCTGCGGCGCGGT 120  
Db 61 ACACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGGCGCGCTGCGGCGCGGT 120

Qy 121 GCG 180  
Db 121 GCG 180

Qy 181 GTACCCGACGCGTTCTTCAACCGGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 240  
Db 181 GTACCCGACGCGTTCTTCAACCGGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 240

Qy 241 AACTTCTACACCGAGCGGTTCCTGAGGCGATCGCGGCGATCGCGGCGGTTCGCGAT 300  
Db 241 AACTTCTACACCGAGCGGTTCCTGAGGCGATCGCGGCGATCGCGGCGGTTCGCGAT 300

Qy 301 GCGGCTCCGAGTTCGAGCGAAGCGCGAGATTGCGGCTTCTTCCGCGCGCGCGCGCG 360  
Db 301 GCGGCTCCGAGTTCGAGCGAAGCGCGAGATTGCGGCTTCTTCCGCGCGCGCGCGCG 360

Qy 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACCGCTACTGCGACCG 420  
Db 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACCGCTACTGCGACCG 420

Qy 421 ACCAAGAGCGAGTGGCG 480  
Db 421 ACCAAGAGCGAGTGGCG 480

Qy 481 ATCTGCTGAACTACAACTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db 481 ATCTGCTGAACTACAACTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

Qy 541 GACCCCGCGAGGTTGGCGCGGAGCGCGCGGTTCGAGGCGCGCTCTGCTGTTCTGG 600  
Db 541 GACCCCGCGAGGTTGGCGCGGAGCGCGCGGTTCGAGGCGCGCTCTGCTGTTCTGG 600

Qy 601 ATGAACAACGTGCAACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db 601 ATGAACAACGTGCAACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

Qy 661 GCGCGCTCGAGTGCACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Db 661 GCGCGCTCGAGTGCACCGGTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

Qy 721 AGCAGTACTGCG 774  
Db 721 AGCAGTACTGCG 774



```
Db 301 GCGGGTTCAGGTGAGGCAAGCGGAGATCGCGCTTCTTCGCGCAGCCACGCAC 360
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGGTCAACAAGAGCAACGCCCTACTTGCAGCCG 420
Db 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGATCAACAAGAGCAACGCCCTACTTGCAGCCG 420
Qy 421 ACCAAGAGCAGTGCCTGTCGCGCGGGGCGAAGATCTACGCGCGCGCGCGCGCTGAG 480
Db 421 ACCAAGAGCAGTGCCTGTCGCGCGGGGCGAAGATCTACGCGCGCGCGCGCGCTGAG 480
Qy 481 ATCTCGTGGAACTACAATACGCGCGCGCGGAGGCGCATCGGCTTCGAGCGGGCTCGGG 540
Db 481 ATCTCGTGGAACTACAATACGCGCGCGGGGAGGCGCATCGGCTTCGAGCGGGCTCGGG 540
Qy 541 GACCCCGCAGGTCGCGCGGCAACCGCGTGTGGGTTCAAGGCGCGCTCTGGTTCGG 600
Db 541 GACCCCAACAGGTCGCGCGGAGCGCGTGTGGGTTCAAGGCGCGCTCTGGTTCGG 600
Qy 601 ATGAACAAGTCGACCGTGTGATGTCGCGAGGCTTCGGGCGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACAAGTCGACCGGTCGCGCGAGGCTTCGGGCGCACCATCAGGGCCATCAAC 660
Qy 661 GCGCGCTTCGAGTCAACGGAACCAACCGCGCAGATGAACGCGCGGTTCGGCTACTAC 720
Db 661 GCGCGCTTCGAGTCAACGGAACCAACCGCGCAGATGAACGCGCGGTTCGGCTACTAC 720
Qy 721 AGGCAGTACTCGCGCAGCTCGCGTCGACCGGGCAACACCTCACCTGC 771
Db 721 AAGCAGTACTCGCGCAGCTCGCGTCGACCGGGCAACACCTCACCTGC 771
```

## RESULT 10

```
US-10-692-367-23
; Sequence 23, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-23
```

```
Query Match 91.9%; Score 711.6; DB 19; Length 774;
Best Local Similarity 95.0%; Pred. No. 5e-169;
Matches 735; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
Qy 1 TCGATGCAGAACTCGGGTTCGCGCAAGCAACCTATCTGCGAGCAAGTTTGGCTACTGCGGC 60
```

```
Db 1 TCGATGCAGAACTCGGGTTCGCGCAAGCAACCTATCTGCGAGCAAGTTTGGCTACTGCGGC 60
Qy 61 ACAGCCGACGAGTACTGCGGCGCAGCGGTGCGAGTTCGGGCGCGCTCTGCGGCGCGGT 120
Db 61 ACAGCCGACGAGTACTGCGGCGCAGCGGTGCGAGTTCGGGCGCGCTCTGCGGCGCGGC 120
Qy 121 GCGCGCGCGCGCGCGGAGGCGCGGAGGAGTTCGGGCGCGAGTTCGGGCGCGAGTTCGGCTAATGTG 180
Db 121 GCGAGCAGTGCCTGCGCGCGGAGGCGCGGAGGAGTTCGGGCGCGAGTTCGGCTAATGTG 180
Qy 181 GTCAACCGACGCGTTCCTCAACCGCATCAAGAAACAGAGCGCGGAGGCGGTTCGGAGGCAAG 240
Db 181 GTCAACCGACGCGTTCCTCAACCGCATCAAGAAACAGAGCGCGGAGGCGGTTCGGAGGCAAG 240
Qy 241 AACTTCTACACCCGAGCGCGTTCCTCGAGGCGCATCGCGCGTACCCGCGTTCGGCGCAT 300
Db 241 AACTTCTACACCCGAGCGCGTTCCTCGAGGCGCATCGCGCGTACCCGCGTTCGGCGCAT 300
Qy 301 GCGCGCTCCGAGTTCGAGCGCAAGCGGAGATTCGGCGCTTCCTTCGGCGCAGCGCAC 360
Db 301 GCGCGGTTCGAGGTTCGAGCGCAAGCGGAGATTCGGCGCTTCCTTCGGCGCATTCACGCGAC 360
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGGTCAACAAGAGCAACGCCCTACTTGCAGCCG 420
Db 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGGTCAACAAGAGCAACGCCCTACTTGCAGCCG 420
Qy 421 ACCAAGAGGCAAGTTCGCGCGCGCGCGGAGGAGTCTACGCGCGCGCGCGCGCTGCGAG 480
Db 421 ACCAAGAGGCAAGTTCGCGCGCGCGCGGAGGAGTCTACGCGCGCGCGCGCGCTGCGAG 480
Qy 481 ATCTCGTGGAACTACAATACGCGCGCGCGGAGGAGGAGTTCGGCTTCGAGCGGGCTCGGG 540
Db 481 ATCTCGTGGAACTACAATACGCGCGCGCGGAGGAGGAGTTCGGCTTCGAGCGGGCTCGGG 540
Qy 541 GACCCCGCAGGTCGCGCGGAGCGCGTGTGGGTTCAAGGCGCGCTCTGGTTCGG 600
Db 541 GACCCCGACAGACTGCGCGGAGCAACCGCGTGTGGTTCGAGTTCGAGTTCGGTTCGG 600
Qy 601 ATGAACAACGTCGACCGGTGATCCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACAACGTCGACCGGTGATCCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 660
Qy 661 GCGCGCTTCGAGTCAACGGAACCAACCGCGCAGATGAACGCGCGGTTCGGCTACTAC 720
Db 661 GCGCGCTTCGAGTCAACGGAACCAACCGCGCAGATGAACGCGCGGTTCGGCTACTAC 720
Qy 721 AGGCAGTACTCGCGCAGCTCGCGTCGAGCGCGGCAACACCTCACCTGCTGA 774
Db 721 AGGCAGTACTCGCGCAGCTCGCGTCGAGCGCGGCAACACCTCACCTGCTGA 774
```

## RESULT 11

```
US-10-692-367-59
; Sequence 59, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
```

```
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-10-692-367-59

Query Match      91.7%; Score 710; DB 19; Length 771;
Best Local Similarity 95.7%; Pred. No. 1.3e-168;
Matches 741; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy      61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGGTCCGGGCGCGGT 120
Db      61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGGTCCGGGCGCGGT 120

Qy      121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db      121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177

Qy      181 GTCACCGACGCGTTCTTCAACGGGATCAAGCAACAGGCGCGGAGCGGCGCGGAGCGCAAG 240
Db      178 GTCACCGACGCGTTCTTCAACGGGATCAAGCAACAGGCGCGGAGCGGCGCGGAGCGCAAG 237

Qy      241 AACTTCTACACCGGAGCGGTTCTTCTGAGGCGATTCGCGCGGTACCGCGGCTTCGCGCAT 300
Db      238 AACTTCTACACCGGAGCGGTTCTTCTGAGGCGCGTCAAGGCGGTACCCAGGCTTCGCCCAT 297

Qy      301 GCGCGCTCCGAGGTACGCGCAAGCGGAGATGCGCGCTTCTTCCGCGACCGCACGCGAC 360
Db      298 GCGCGGTACAGGTCAGCGGCAAGCGCGAGATTCGCGCTTCTTCCGCGATGTCAACGAC 357

Qy      361 GAGACCGGCGATTTCTGTATCATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
Db      358 GAGACCGGCGATTTCTGTATCATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCGG 417

Qy      421 ACCAAGAGCGAGTGCCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db      418 ACCAAGAGCGAGTGCCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477

Qy      481 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db      478 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537

Qy      541 GACCCCGCGAGGTCGCGCGGACCGCGTGTGCGGTTCAAGCGCGCGCTCTGGTTCTGG 600
Db      538 GACCCCGCGAGGTCGCGCGGACCGCGTGTGCGGTTCAAGCGCGCGCTCTGGTTCTGG 597

Qy      601 ATGAACAACTGTCACCGTGTGATGCGCGAGGCTTCGCGCGCGCACCATCAGGCGCATCAAC 660
Db      598 ATGAACAACTGTCACCGTGTGATGCGCGAGGCTTCGCGCGCGCACCATCAGGCGCATCAAC 657

Qy      661 GCGCGCTTCGAGTGAACCGGGAACAAACCGCGCGAGATGAACGCGCGGTTCGGCTACTAC 720
Db      658 GCGCGCTTCGAGTGAACCGGGAACAAACCGCGCGAGATGAACGCGCGGTTCGGCTACTAC 717

Qy      721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCACCTGCTGA 774
Db      718 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCACCTGCTGA 771
```

RESULT 12

US-10-692-367-37

; Sequence 37, Application US/10692367

```
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-37
```

```
Query Match      91.7%; Score 710; DB 19; Length 774;
Best Local Similarity 94.8%; Pred. No. 1.3e-168;
Matches 734; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy      61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGGTCCGGGCGCGGT 120
Db      61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGGTCCGGGCGCGGC 120

Qy      121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db      121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy      181 GTCACCGACGCGTTCTTCAACGGGATCAAGCAACAGGCGCGGAGCGGCGCGGAGCGCAAG 240
Db      181 GTCACCGACGCGTTCTTCAACGGGATCAAGCAACAGGCGCGGAGCGGCGCGGAGCGCAAG 240

Qy      241 AACTTCTACACCGGAGCGGTTCTTCTGAGGCGCATTCGCGCGGTACCGCGGCTTCGCGCAT 300
Db      241 AACTTCTACACCGGAGCGGTTCTTCTGAGGCGCGTCAAGGCGGTACCCAGGCTTCGCCCAT 300

Qy      301 GCGCGCTCCGAGGTCCGAGCGCAAGCGGAGATTCGCGCTTCTTCCGCGACCGCACGCGAC 360
Db      301 GCGCGGTCCGAGGTCCGAGCGCAAGCGGAGATTCGCGCTTCTTCCGCGACCGCACGCGAC 360

Qy      361 GAGACCGGCGATTTCTGTATCATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420
Db      361 GAGACCGGCGATTTCTGTATCATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCGG 420

Qy      421 ACCAAGAGCGAGTGCCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db      421 ACCAAGAGCGAGTGCCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

Qy      481 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db      481 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

Qy      541 GACCCCGCGAGGTCGCGCGGACCGCGTGTGCGGTTCAAGGCGCGCGCTCTGGTTCTGG 600
```

Db 541 GACCCAAACAGGTCGCGCAGAGCCCGTGTGGGCTTCAAGGGCGGCGCTCTGGTTCGG 600  
Qy 601 ATGAACAAACGTCGACCGTGTGATGCGCGCAGAGGCTTTCGGCGCACCATCAGGGCCATCAAC 660  
Db 601 ATGAACAAACGTCGACCGGTCGCGCAGAGGCTTTCGGCGCACCATCAGGGCCATCAAC 660  
Qy 661 GCGGCCCTCGAGTGTCAACAGGGAACAAACCCCGCCAGATGAACGCGCGTCTGGCTACTAC 720  
Db 661 GCGGCCCTCGAGTGTCAACAGGGAACAAACCCCGCCAGATGAACGCGCGTCTGGCTACTAC 720  
Qy 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGCAACACCTCACCTGTCTGA 774  
Db 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGCCAAACCTCACCTGTCTGA 774

## RESULT 13

US-10-389-432B-23  
; Sequence 23, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-389-432B-23

Query Match 91.6%; Score 708.6; DB 18; Length 771;  
Best Local Similarity 94.9%; Pred. No. 2.8e-168;  
Matches 732; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
Qy 1 TCGATGCAGAACTCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Qy 61 ACACCCGACGAGTACTGCGCGGACCGGTCGCCAGTCCGCGCCGTCGCGCGCGCGGT 120  
Db 61 ACACCCGACGAGTACTGCGCGGACCGGTCGCCAGTCCGCGCCGTCGCGCGCGCGGT 120  
Qy 121 GCG 180  
Db 121 GCG 180  
Qy 181 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 181 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Qy 241 AACTTCTACACCGGAGCGCGTTCCTCGAGGCGCATCGCGCGGTATCCCGGGCTTCGCGCAT 300  
Db 241 AACTTCTACACCGGAGCGCGTTCCTCGAGGCGCATCGCGCGGTATCCCGGGCTTCGCGCAT 300  
Qy 301 GCGCGCTCGAGGTTCAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCAACGCCACGCAAC 360  
Db 301 GCGCGCTCGAGGTTCAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCATGTCAACGCAAC 360  
Qy 361 GAGACCGGGCATTTCTGTACTACAGCGGTCAACAGAGCAACGCGCTACTGCGACCGCG 420

Db 361 GAGACCGGGCATTTGTGCTATCATCAACGAGGTCAACAGAGCAACGCTACTTCGACCCG 420  
Qy 421 ACCAAGAGGAGTGGCCGCTGCGCGCGCGGAGAGTACTACGCGCGCGCGCGCGCGCTGAG 480  
Db 421 ACCAAGAGGAGTGGCCGCTGCGCGCGCGGAGAGTACTACGCGCGCGCGCGCGCGCTGAG 480  
Qy 481 ATCTGTGGAACTCAACTACG 540  
Db 481 ATCTGTGGAACTCAACTACG 540  
Qy 541 GACCCCGCAGGTCG 600  
Db 541 GACCCCGCAGGTCG 600  
Qy 601 ATGAACAAACGTCGACCGCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db 601 ATGAACAAACGTCGACCGCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Qy 661 GCGCCCTCGAGTGCAGGGAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Db 661 GCGCCCTCGAGTGCAGGGAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Qy 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGCAACACCTCACCTGC 771  
Db 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGCAACACCTCACCTGC 771

## RESULT 14

US-10-389-432B-59  
; Sequence 59, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-389-432B-59

Query Match 91.3%; Score 707; DB 18; Length 768;  
Best Local Similarity 95.7%; Pred. No. 7.1e-168;  
Matches 738; Conservative 0; Mismatches 30; Indels 3; Gaps 1;  
Qy 1 TCGATGCAGAACTCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGGCTGCCAGCCAAACCTTCTGTCGACCAAGTTTGGCTACTGCGGC 60  
Qy 61 ACACCCGACGAGTACTGCGCGGACCGGTCGCCAGTCCGCGCCGTCGCGCGCGCGGT 120  
Db 61 ACACCCGACGAGTACTGCGCGGACCGGTCGCCAGTCCGCGCCGTCGCGCGCGCGGT 120  
Qy 121 GCG 180  
Db 121 GCGCGCGCGT---GCGCGCGAGGCGCGCGAGCGAGTGGCGGTGCGAACTGCTAAATGTG 177  
Qy 181 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 178 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCGCG 237

```
Qy 241 AACTTCTACACCCGGAGCGCGTTCTCTGAGGCCATCGCCGGGTTCGCGCAT 300
Db 238 AACTTCTACACCCGGAGCGCGTTCTCTGAGCGCGTCAAGGGGTACCCAGGCTTCGCCAT 297
Qy 301 GGCGGCTCCGAGGTCGAGCGCAAGCGGAGATTGCGGCTTCTTCGGCGACGCGCACGAC 360
Db 298 GGCGGCTCAAGGTGCGAGGCAAGCGCGAGATTGCGGCTTCTTCGGCGATGTACGGAC 357
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGGAGCCG 420
Db 358 GAGACCGGGCATTTCTGTCTACATCAGCGAGATCAACAGAGCAACGCGCTACTGGAGCCG 417
Qy 421 ACCAAGGCGAGTGGCCGTGCGCGCGGGGAGAGTACTAGGCGCGGGCCCGCTGCAG 480
Db 418 ACCAAGGCGAGTGGCCGTGCGCGCGGGGAGAGTACTAGGCGCGGGCCCGCTGCAG 477
Qy 481 ATCTCGTGGAACTACAACTACGCGGCCCGGGAGGCCATCGGCTTCGACGGGCTCGGG 540
Db 478 ATCTCGTGGAACTACAACTACGCGGCCCGGGAGGCCATCGGCTTCGACGGGCTCGGG 537
Qy 541 GACCCCGCAGGGTGGCGGAGCGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600
Db 538 GACCCCGCAGGGTGGCGGAGCGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 597
Qy 601 ATGAACAACGTGCACCGTGTGATGCCGCGAGGGCTTCGGCGGCACCATCAGGGCCATCAAC 660
Db 598 ATGAACAACGTGCACCGTGTGATGCCGCGAGGGCTTCGGCGGCACCATCAGGGCCATCAAC 657
Qy 661 GGCGGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGGCGCGGCTCGGCTACTAC 720
Db 658 GGCGGCTTCGAGTGGGAGCGGAAACAAACCCCGCCAGATGAACGGCGCGGCTCGGCTACTAC 717
Qy 721 AGGCAGTACTGCCGCGAGCTCGGCGTGCACCCGGGCAACACCTCACCTGC 771
Db 718 AGGCAGTACTGCCGCGAGCTCGGCGTGCACCCGGGCAACACCTCACCTGC 768
```

## RESULT 15

```
US-10-389-432B-37
; Sequence 37, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: rl AH9 nucleic acid
US-10-389-432B-37
```

```
Query Match 91.3%; Score 707; DB 18; Length 771;
Best Local Similarity 94.8%; Pred. No. 7,1e-168;
Matches 731; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
Qy 1 TCGATGCGAAGTGGCGGTGCGGCGAGCAAAAGTATGCTCGAGCAAGTTGGCTACTGCGGC 60
Db 1 TCGATGCGAAGTGGCGGTGCGGCGAGCAAAAGTATGCTCGAGCAAGTTGGCTACTGCGGC 60
```

```
Qy 61 ACAGCCGACGAGTACTGCGCGCAGCGGTGCGAGTCGCGGCCCGCTGCGCTCGGGCGCGGT 120
Db 61 ACAGCCGACGAGTACTGCGCGCAGCGGTGCGAGTCGCGGCCCGCTGCGCTCGGGCGCGGC 120
Qy 121 GGCGGCGCGCGCGCGCGCGCGAGGCGCGGAGTGTGCGGTGCGAAACGTGGCTTAATGTG 180
Db 121 GGCGGCGCGCGCGCGCGCGCGAGGCGCGGAGTGTGCGGTGCGAAACGTGGCTTAATGTG 180
Qy 181 GTCAACGACGGTCTTCAACGGCATCAAGAACAGAGCGCGGAGCGGTGCGAGGGCAAG 240
Db 181 GTCAACGACGGTCTTCAACGGCATCAAGAACAGAGCGCGGAGCGGTGCGAGGGCAAG 240
Qy 241 AACTTCTACACCCGGAGCGGTTCTCTGAGGCCATCGCCGGGTTCGCGCAT 300
Db 241 AACTTCTACACCCGGAGCGGTTCTCTGAGGCCATCGCCGGGTTCGCGCAT 300
Qy 301 GGCGGCTCCGAGTGTGAGCGCAAGCGCGAGATTGCGGCTTCTTCGGCGACGCGCAC 360
Db 301 GGCGGCTCGAGTGTGAGCGCAAGCGCGAGATTGCGGCTTCTTCGGCGACGCGCAC 360
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAGAGCAACGCGCTACTGCGACCCG 420
Db 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAGAGCAACGCGCTACTGCGACCCG 420
Qy 421 ACCAAGAGGCGAGTGGCGGTCGCGCGGGGAGAGTACTACGGGCGCGGCCCGCTGCAG 480
Db 421 ACCAAGAGGCGAGTGGCGGTCGCGCGGGGAGAGTACTACGGGCGCGGCCCGCTGCAG 480
Qy 481 ATCTCGTGGAACTACAACTACGCGGCCCGCGGAGGGCCATCGGCTTCGACGGGCTCGGC 540
Db 481 ATCTCGTGGAACTACAACTACGCGGCCCGCGGAGGGACATCGGCTTCAACGGGCTCGGC 540
Qy 541 GACCCCGCAGGGTGGCGCGGCGCGGTGCGGCTTCAGGCGCGGCTCTGGTTCTGG 600
Db 541 GACCCCGCAGGGTGGCGCGGCGCGGTGCGGCTTCAGGCGCGGCTCTGGTTCTGG 600
Qy 601 ATGAACAACGTGCACCGTGTGATGCCGCGAGGGCTTCGGCGGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACAACGTGCACCGGTTGGTCCGCGAGGGTTCGGCGGCACCATCAGGGCCATCAAC 660
Qy 661 GGCGGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGGCGCGGCTCGGCTACTAC 720
Db 661 GGCGGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGGCGCGGCTCGGCTACTAC 720
Qy 721 AGGCAGTACTGCCGCGAGCTCGGCGTGCACCCGGGCAACACCTCACCTGC 771
Db 721 AGGCAGTACTGCCGCGAGCTCGGCGTGCACCCGGGCAACACCTCACCTGC 771
```

Search completed: May 23, 2005, 17:32:09

Job time : 399.391 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:35:31 ; Search time 120.13 Seconds  
(without alignments)  
10542.593 Million cell updates/sec

Title: US-10-692-367-11

Perfect score: 774  
Sequence: 1 tcgatgcagaactcgsgtg.....gcaacaacctcaactgtgta 774

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647.8	83.7	1094	4	US-09-522-714-1
2	377	48.7	881	4	US-09-522-714-29
3	373.2	48.2	1048	4	US-09-522-714-21
4	296.8	38.3	1116	4	US-09-522-714-31
5	174.6	22.6	1079	1	US-08-181-271A-37
6	174.6	22.6	1079	1	US-08-449-315-37
7	174.6	22.6	1079	1	US-08-444-803-37
8	174.6	22.6	1079	1	US-08-449-043-37
9	174.6	22.6	1079	1	US-08-456-265A-37
10	174.6	22.6	1079	1	US-08-455-416-37
11	174.6	22.6	1079	1	US-08-455-244-37
12	174.6	22.6	1079	1	US-08-454-876-37
13	174.6	22.6	1079	2	US-08-457-364-37
14	174.6	22.6	1079	2	US-08-456-262-37
15	174.6	22.6	1079	2	US-08-456-240-37
16	174.6	22.6	1079	2	US-08-455-736-37
17	174.6	22.6	1079	2	US-08-971-217-37
18	174.6	22.6	1079	3	US-09-350-600-37
19	174.6	22.6	1079	4	US-09-906-234-37
20	165	21.3	1318	3	US-09-125-891-1
21	162.6	21.0	816	4	US-09-266-965-73
22	162.6	21.0	53500	4	US-09-266-965-73
23	161.8	20.9	1151	1	US-07-704-288C-2
24	161.8	20.9	1151	1	US-08-093-372-1
25	161.8	20.9	1151	1	US-08-379-259-2
26	156	20.2	1218	4	US-09-902-540-4667
27	156	20.2	29384	4	US-09-902-540-1229

28	153.8	19.9	960	4	US-09-534-229C-8	Sequence 8, Appli
29	135.4	17.5	1118	4	US-09-522-714-23	Sequence 23, Appli
30	128.4	16.6	972	4	US-09-534-229C-7	Sequence 7, Appli
31	125.2	16.2	1163	4	US-09-522-714-5	Sequence 5, Appli
32	124.8	16.1	1002	1	US-08-457-797A-9	Sequence 9, Appli
33	124.8	16.1	1002	1	US-08-812-025-9	Sequence 9, Appli
34	124.8	16.1	1002	3	US-09-138-873A-9	Sequence 9, Appli
35	121.2	15.7	1077	4	US-09-522-714-17	Sequence 17, Appli
36	110.8	14.3	583	4	US-09-522-714-25	Sequence 25, Appli
37	107.6	13.9	771	4	US-09-534-229C-6	Sequence 6, Appli
38	103.2	13.3	1013	4	US-09-522-714-19	Sequence 19, Appli
39	98.8	12.8	1619	4	US-09-522-714-11	Sequence 11, Appli
40	84.8	11.0	2636	3	US-09-125-891-3	Sequence 3, Appli
41	83.2	10.7	952	1	US-08-181-271A-38	Sequence 38, Appli
42	83.2	10.7	952	1	US-08-449-315-38	Sequence 38, Appli
43	83.2	10.7	952	1	US-08-444-803-38	Sequence 38, Appli
44	83.2	10.7	952	1	US-08-449-043-38	Sequence 38, Appli
45	83.2	10.7	952	1	US-08-456-265A-38	Sequence 38, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-522-714-1

; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)

US-09-522-714-1

Query Match	83.7%	Score	647.8	DB	4	Length	1094
Best Local Similarity	91.8%	Pred. No.	3.1e-112				
Matches	704	Conservative	0	Mismatches	42	Indels	21
Gaps	1						
Qy	6	GCAGAACTGCGGCTGCCAGCAACGATGTCGAGCAAGTTTGGCTACTCGCGGCAGC	65				
Db	149	GCAGAACTGCGGCTGCCAGCAACGATGTCGAGCAAGTTTGGCTACTCGCGGCAGC	208				
Qy	66	CGACGAGTACTGCGCGCAGCGGTGCCAGTCCGCGCGTGGCGCTCGCGCGCGTGGCGG	125				
Db	209	CGACGAGTACTGCGCGCAGCGGTGCCAGTCCGCGCGTGGCGCTCGCGCGCGTGGCGG	268				
Qy	126	CGCGCGCGCGCGCGGAGCGCGGCGGAGCGAGTGGCGGTGCGACGTGGCTAATGTGTCAC	185				
Db	269	CAGTGGCGGC-----GGTGGTGGCAACGTGGCTAGCTGCTGCAC	307				
Qy	186	CGACGCGTCTTCAACGGCATCAAGAACAGCGGCGGCGGTGCGAGGGCAAGACTT	245				
Db	308	CGGCTCTTCTTCAACGGCATCAAGAACAGCGGCGGCGGTGCGAGGGCAAGACTT	367				
Qy	246	CTACACCGGAGCGCGTTCCTCGAGGGCCATCGCGCGTACCCGGGCTTCGCGCATGGCGG	305				
Db	368	CTACACCGGAGCGCGTTCCTCGAGGGCCATCGCGCGTACCCGGGCTTCGCGCATGGCGG	427				
Qy	306	CTCGAGGTGAGCGCGAGCGCGGAGATTGCGCGCTTCTTCGCGCACGCCACGCGAGAC	365				

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Db 428 GTCCAGGTGCGAGGCGAGAGTCGCGCGCTTCTTCCGCGACGCCACGACGAGAC 487
Qy 366 CGGCAATTTCTGTACTACAGCGAGGTCAACAAGAGCAACGCTTACTGCGACCCGACAA 425
Db 488 CGGCAATTTCTGTACTACAGCGAGATCAACAAGAGCAACGCTTACTGCGACCCGACAA 547
Qy 426 GAGCAGTGGCGGTGCGCGCGGGGCGAGAGTACTACGGGCGCGCGCTGCGAGATCTC 485
Db 548 GAGCAGTGGCGGTGCGCGCGGGGCGAGAGTACTACGGGCGCGCGCTGCGAGATCTC 607
Qy 486 GTGGAATACAACTACGGGCGCGCGGAGGCGCATCGGCTTTCAGCGGCTCGGGGACCC 545
Db 608 GTGGAATACAACTACGGGCGCGCGGAGGCGCATCGGCTTTCAGCGGCTCGGGGACCC 667
Qy 546 CGGAGGGTGGCGCGGAGCGCGGTGGTGGCGTTCAAGCGGCGCGCTCTGGTTCTGGATGAA 605
Db 668 CGGAGGGTGGCGCGGAGCGCGGTGGTGGCGTTCAAGCGGCGCGCTCTGGTTCTGGATGAA 727
Qy 606 CAACGTGACCGTGTGATGCGCGAGGGCTTGGGCGCCACCATCAGGGCCATCAACGGGC 665
Db 728 CAGCGTGCACGGGTGGTGGCGAGGGGTTCGGGCGCCACCATCAGGGCCATCAACGGGC 787
Qy 666 CCTCGAGTGCAACGGGAACACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCA 725
Db 788 CCTCGAGTGCGGCGGGAACACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCA 847
Qy 726 GTACTGCGCGCAGCTCGCGGTGCGAGCCCGGGGCAACAACCTACCTGCT 772
Db 848 GTACTGCGCGCAGCTCGCGGTGCGAGCCCGGGGCAACAACCTACCTGCT 894
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## RESULT 2

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US-09-522-714-29
; Sequence 29, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(551)
US-09-522-714-29
```

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Query Match 48.7%; Score 377; DB 4; Length 881;
Best Local Similarity 80.7%; Pred. No. 9.4e-62;
Matches 453; Conservative 0; Mismatches 105; Indels 3; Gaps 1;
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```
Qy 215 AGGCGGGAGCGGTGCGAGGGCAAGACTTCTACCCGCGAGCGCTTCTCGAGGGCA 274
Db 1 ATCGCGGAGCTGGTGGCGAGGGCAAGCGCTTCTACCGGAAGCGCTTCTCGAGGGCA 60
Qy 275 TCGCGCGTACCCGGGCTTCGCGATGCGGCTCCGAGGTCGAGCGCAAGCGGAGATTG 334
Db 61 TCGCGCGTACCCGGGCTTCGCGATGCGGCTCCGAGGTCGAGCGCAAGCGGAGATTG 120
Qy 335 CCGCTTCTTCGCGCAACCGCACGAGACGGGCAATTTCTGTACTACAGGAGTCA 394
Db 121 CCGCTTCTTCGCGCATGTCACGACGAGACCGGGCAATTTGTGTACTACAGGAGTCA 180
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Qy 395 ACAAGAGCAACGCTTACTGCGACCCGACCAAGAGGCGAGTGGCGCGCGGGGCGAGA 454
Db 181 ACCTGGCGAAGTACTGGGACTGGAGCAGTGAGAAAGCAGTGGCCGCCACCCGAGGAGG 240
Qy 455 AGTACTACGGCGCGCGCGCTCGAGATCTCGTGGAACTTAACTACGGGCGCGCGGGGA 514
Db 241 GTTACTACGGCGCGCGCGCTCGAGCTGTCTGTGAACTACAACTACGGGCGCGGGGGA 300
Qy 515 GGGCCATCGGCTTCGAGCGGCTCGGGACCCCGGAGGCTGGCGGAGCGCGTGTGGTGG 574
Db 301 GAGGCTTCGGCTTCGAGCGGCTGGGAGACCCGACAGACTGGCGGAGGACCCCGTGTGT 360
Qy 575 CGTTCAAGCGCGCGCTCTGGTTCCTGGATGAACAACTGACCGCTGTGATGCGCGAGGGCT 634
Db 361 CGTTCAAGTTCGGCGCTCTGGTACTTGGATGGAGAACATGACACAGCTCATGCCCGAGGGT 420
Qy 635 TCGCGCGCACCATCAGGGCCATCAACGGCGCGCTTCGAGTG---CAACGGGAAACAACCCCG 691
Db 421 TCGCGCGCACCATCAGGGCCATCAACGGCTTCGACGAGTGTCAACGGCGGGGAAACAACGG 480
Qy 692 CCCAGATGAACGCGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTCGGGGTTCACC 751
Db 481 CCGAAATGAAGACCGGGTGGCTTCTACCTCGAGTACTGCCACCACTTCGGTGTTCACC 540
Qy 752 CGGCGCAACCACTCACCTGCT 772
Db 541 CCGGGCTCGACCTCAGTTGCT 561
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## RESULT 3

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US-09-522-714-21
; Sequence 21, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)...(854)
US-09-522-714-21
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Query Match 48.2%; Score 373.2; DB 4; Length 1048;
Best Local Similarity 71.3%; Pred. No. 4.9e-61;
Matches 555; Conservative 0; Mismatches 178; Indels 45; Gaps 3;
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Qy 6 GCAGAACTGCGGCTGCCAGGCCAAACGATATGTGAGCAAGTTTGGCTACTGCGGACGAC 65
Db 116 GCAGAACTGCGGCTGCCAGGCCCTGTGTGTCAGCCGGTTGCGGCTACTGCGGACGGG 175
Qy 66 CGAGGACTACTCGGCGCAGCGGTGCCAGTCCGGGCCGTGCGCTCGGGCGCGGTGGCGG 125
Db 176 CGAGGACTACTCGGCGCCCGGGTGCAGTCCGGGCCCTGCG----- 215
Qy 126 CGGCGCGGCGGCGGAGCGCGGAGGAGTGGCGGTGCGAACTGTGCTAATGTGGTCAAC 185
Db 216 -----GACGTGCCGAGAGCAACAAACGCGTCCGTGCGCAGCATCGTCAC 259
Qy 186 CGAGCGCTTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTTCGAGGGCAAGACTT 245
Db 260 GCGGCGCTTCTTTCGACGCGCTCTCTCGCGCAGGCGCGGCTTCGTGTCGAGGCAACGCGCTT 319
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Qy	246	CTACACCGGAGCGGTTCTCTCAGAGCCATCGCCGCGTACCGGGCTTCGCGCATGGCGG	305
Db	320	CTACACCGGAGCGGCTTCTCTCGCGCGCGGCTACTACCGCGGTTTCGGCGCGACCGG	379
Qy	306	CTCCGAGGTCCAGGCGCAAGCGCGAGATTGCCGCTTCTTCGCGCACGCGCACGACGAGAC	365
Db	380	CACCGTCGACGACTCCAAGCGCGAGATCGCCGCTTCTTCGGCAACGCCCAACCCAGAC	439
Qy	366	GGGGCATTTCTGTACATCATCGACGAGTGCTAAC- - -AAGAGGAAAGCGCTACTCTGGAGCCCGAC	422
Db	440	CATAAAGTTCCTGTACATCAACGAGATCGACGGGCGGACGAGAACTACTCGACACCGAA	499
Qy	423	CAAGAGCAGTGGCGGTGGCGCGGGGACAACTACTACGGGCGGCGGCCGCTGCAGAT	482
Db	500	CAACACGAGTGGCGGTGGCGAGGGGATCTACGGCGCGGCGCCGCTGCAGAT	559
Qy	483	CTCGTGAACTCAAACTACGGGCCCGGGGGAGGGCCATCGGCTTTCGACGGGCTCGGGGA	542
Db	560	CTCTGGAACCTTCAACTACGGGCCCGGGGCGAGAGCATCGCTTCGACGGGCTGGGCGA	619
Qy	543	CCCGGACGGGTGGCGGGGACGCCGTGTGTGGCTTCAAGCGGGGCGTCTGGTCTGTGAT	602
Db	620	CCCGGACGCGGTGGCGGGCAGCGCGCTGCTCGGCTTCGCGCTCTGGTACTGGAT	679
Qy	603	GAACACGTGCACCGTGTGAT- - - - -GCCGACGGGCTTCGGCGGCACCATCAGGGCCAT	656
Db	680	GAACACGTGCACGGGGCATCTGTCTCGGGCAGGGCTTTCGGCGGCACCATCCGGGCCAT	739
Qy	657	CAACGGCGCCCTCGAGTGCACACGGGAAACAAACCCGCGCCAGATGAACGCGCGCTCGGCTA	716
Db	740	CAACGGCGCGCTCGAGTGGACGCGCAAGAACCCCAACTCCCGTCAACACCGCGTCGCTA	799
Qy	717	CTACAGGCACTATCGCCGCCAGCTCGGGCTCGAACCCGGGCAACCAACTCACTGTGTA	774
Db	800	CTACAGCAGTCTTCGCAGGATTTTCGGCGTTCGACCCGGGCAACCAACTCACTGTGTA	857

## RESULT 4

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US-09-522-714-31
; Sequence 31, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: intron
; LOCATION: (445)...(512)
; NAME/KEY: CDS
; LOCATION: (42)...(444)
; NAME/KEY: CDS
; LOCATION: (513)...(922)
; US-09-522-714-31

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116	Db	GCAGAACTGCGGGTGC	CGCGT	CGGGCCCTGTGCTGCAGCGGGTT	CGGGTACTCGGGACGGG	176
66	Qy	CGACGAGTACTGCGGGACGGGTGCCAGATCGGGCCCGTGC	CGCGT	CGGGCGGGGCGGGTGC	CGGGTACTCGGGACGGG	125
176	Db	CGAGGACTACTGCGGGCGGGGTGCCAGATCGGGCCCGTGC	CGCGT	CGGGCGGGGCGGGTGC	CGGGTACTCGGGACGGG	215
126	Qy	CGGGCGGGCGGGAGCGCGGAGGAGGAGTGGCGGTGCGA	CGTGGT	CGAAGCGTGGCTTAATGTGTTGCAC	185	
216	Db	-----GACGTGCGGAGACCAACACGCGTCCGTGGCCAGCATCGTGCAC	259			
186	Qy	CGACGCGTTCTTCAACCGGCATCAAGAAACACGAGCCGGGAGCGGGTGC	CGAGGGCGAAGACTTT	245		
260	Db	GCGGGCTTCTTTCGACGCGCTCTCGCGACGCGCCGCGCTCGTGC	CGAGGGCGAAGACTTT	319		
246	Qy	CTACACCGGGAGCGCGTTCTTCGAGGCGCATCGCGCGGTAC	CGCGGGCTTTCGCGCATGCGGG	305		
320	Db	CTACACCGCGACCGCTTCTTCGCGCGCGCGGTACTAC	CGCGGGTTCGCGCGCACCGG	379		
306	Qy	CTCCGAGGTCCGAGCGCAAGCGCAGATGTCGCGCTTCTTTCGCGACGCGCACGACGAGAC	365			
380	Db	CACCGTCGACGCACTCCAAGCGCGAGATCGCGCGCTTCTTCGCGAAGCGCAACCGACGAGAC	439			
366	Qy	-----	365			
440	Db	CATAAGTACGTGCGAAACAACCGAAGCTCGTCCAAGCTCTAGCTGCTACTAATCAAGTTT	499			
366	Qy	-----CGGGCATTTCTGCTACATCAGCGAGGTCAC	414			
500	Db	CGACTGTTCGACAGTTCTGCTCATCAACAGAGATCGACGGGCGAGCAAGACTACTCTGC	559			
415	Qy	GACCCGACCAAGAGCGCAGTGCCTGGCGCGCGGGCAGAAAGTACTACGGGCGGGCCCG	474			
560	Db	GACCGGAACAACGCACTGGCGCTGCCAGCGCGGGAAGGGTACTACGGCGCGGCCCG	619			
475	Qy	CTGCAGATCTGTTGGAACTCAACTACGGGCGCGGGGAGGGCCATCGGCTTCGACGGG	534			
620	Db	CTGCAGATCTCTGGAACTTCAACTACGGGCGCGGGGCGAGAGCATCGGCTTCGACGGG	679			
535	Qy	CTCGGGGACCCCGCAGGTTGGCGGGGACGCGGTGGTGGCGTTCAAGGCGCGCTCTCGG	594			
680	Db	CTGGGCGACCCCGACGGTGGCGCGCAGCGCGCTGCTCGCGTTCGCGTCCGCGCTCTCGG	739			
595	Qy	TTCTGAGTGAACAACTGTCACCGTGTGAT-----GCCGACAGGGCTTCGGGCGCACCATC	648			
740	Db	TACTGGATGAACAACGTGTCACGGGGCCATCGTCTCCGCGCCAGGGCTTCGGCGCCACCATC	799			
649	Qy	AGGGCCATCAACGGGGCCCTCGAGTGCACAAGGGAACAACCCCGCCAGATGAACGGCGGC	708			
800	Db	CGGGCCATCAACGGCGCGCTCGAGTGGGACGGGCAAGAACCCCACTCCGTCACCAACCGC	859			
709	Qy	GTCCGCTACTACAGCGAGTACTGCGCGCAGCTCGGCGTTCGACCGGGCAACAACCTCACC	768			
860	Db	GTCCCTACTACAGCAGTCTCGCAGGATTTCCGCGTTCGACCGGGCAACAACCTCACC	919			
769	Qy	TGCTGA	774			
920	Db	TGCTGA	925			

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RESULT 5
US-08-181-271A-37
; Sequence 37, Application US/08181271A
; Patent No. 561395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harns, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice

```



GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESS: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,315  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-315-37  
Query Match 22.6%; Score 174.6; DB 1; Length 1079;  
Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;  
QY 7 CAGAACTGGGGCTGCCAGCAACAGTATGCTGCAGCAAGTTTGGCTACTTCGCGCAGCAGC 66  
DB 93 CAANAATGGGGTGGCTCCNAACCTCTGTTGAGTCAGTTCGGTTACTTGTGATCCGAC 152  
QY 67 GACAGTACTGCGGCGACCGGGTGCAGTGGGGCCCTGTCGGCTCGGGCGCGGTGGCGGC 126  
DB 153 GATGCATACTGCGGTGTGGATGCCATCAGTCTTGTGA----- 192  
QY 127 GCGGCGCGGGGCGGCGGAGCAGTGGGGGTGCGAAGCTGGCTATGTTGTCACC 186  
DB 193 -----GAGGTAGTGAACCCCGACCGGAGGGTTCGGTTCGTGATGTCAGCA 239  
QY 187 GACCGCTTCTTCAACCGGCATCAAGAACCCAGCGCGGAGCGGGTCCGAGGCAAGAACTTC 246  
DB 240 CAAAGTTTCTTTTAACTAATATCAACCAAGCTGTAATGTTGCGGGGGAAGATTC 299  
QY 247 TACACCGGAGCGCTTCTTCGAGGCCATGCGCGCTACCCCGGGCTTCGCGCATGCGCGC 306  
DB 300 TACACCGGTGACTCTTTTCGTTAAACGCGCTAATCTTCCCAACTTTGCCAATTTCTGTT 359  
QY 307 TCCGAGTTCGAGCGGCGAGCGAGATTGCGGCTTCTTCGCGCAGCGCCAGCGCAGAGC 366  
DB 360 AC-----CAGACGTGAATTTGCTACCATGTTGCTCATTTCACTACGAGAC 407  
QY 367 GGGCATTTCTGTACATCAGCGAGGTCAAC---AAGAGCAACCGCTACTTCGCAACCGCAGC 423  
DB 408 GGCATTTTGTGTACATAGAGATTAACGGAGCAACAGTAACTACTTCCAGAGCAGC 467  
QY 424 AAGAGCAGTGGCGGTGCGCGCGGCGAGAGTACTAGCGGCGCGCGCTTCGAGATC 483  
DB 468 AACACACAATACCCATGTGCACCGGGAAGAGGCTACTTCGGTGTGTCGATCCCACTA 527  
QY 484 TCGTGAAGTACAACTACCGGCGCGGAGGGCCATCGGCTTCGACGGGCTTCGGGAC 543  
DB 528 TCATGAAGTACAACTACCGAGCGTGTGTCGAGGCTTCAAGTCTTCGCTTACGCCAG 587  
QY 544 CCGGCGAGGGTGGCGGAGCGCGGTGGTGGGCTTCAAGCGCGCGCTCTGGTTCTGATG 603  
DB 588 CCGGAATTTGTGGGTAGCAACCACTGTAGCTTTTCAGGTTCGGTTTGTGTTTGGATG 647  
QY 604 AACACAGTGCAGCGTGTGATGCGGCGCGGCTTCGCGCGCACCACATCAGGGGCATCAACGGC 663  
DB 648 AATAGCGTAAGCGCGGTCTGAACCAAGGGTTTGGAGGCCACCATTAAGAGCTAATAATGG- 706  
QY 664 GGCCTCGAGTGCNAACGGGAACAAACCCCGCCAGATGAACGCGCGCGCTCGGCTACTACAG 723

Db 707 --AATGAATGTAAACGGTGGTAATTCGGTGCAGTCAACGCAAGGATGGATATAGA 764  
QY 724 CAGTACTGCCCGCAGCTCGCGTCGACCCCGGGCAACAACCTCACCTGCTGA 774  
Db 765 GACTATTGTGACAGCTTGGTGTGGACCCCTGGTCTTAACCTTAGTTGCTAA 815

## RESULT 7

US-08-444-803-37  
Sequence 37, Application US/08444803

Patent No. 5654414

GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Utnes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,803

FILING DATE: 19-MAY-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-444-803-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;

Best Local Similarity 56.5%; Pred. No. 5.2e-24;

Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY 7 CAGAACTGGCGTGCAGCAACAGTATGCTGAGCAAGTTTGGCTACTGCGGACGACC 66  
Db 93 CAAAACCTGGCGTGCCTCCAAACCTCTGTTGAGTCAGTTCGGTTACTTGGTACCGAC 152  
QY 67 GACGACTACTGGCGGACGCTGCCAGTGGGCGCCGCTCGCGCTCGGCGCGGTGGCGG 126  
Db 153 GATGCATACCTGCGGTGTTGATGCCGATCAGGTCCTTTGA----- 192  
QY 127 GCGCGCGCGCGGCGGAGCGGCGGAGGCGAGTGGCGGTGCGAACGTTGGTAAATGTTGCACC 186  
Db 193 -----GAGGTAGTGAACCCCGAGGCGGTGCGGTAGCATTTGTGACA 239  
QY 187 GACCGTTTCTTCAACGGCATCAAGAACCGAGCGGCGGAGCGGTTGCGAGGCGAAGACTTC 246  
Db 240 CAAGGTTTCTTTAAACAATATTATCAACCAAGTGGTAATGTTGCGCGGGGAAAGATTTC 299  
QY 247 TACACCGGAGCGCGTTCCTCGAGGCGCATCGCGCGGTACCCCGGCTTCGCGCATGGCGGC 306  
Db 300 TACACCGGAGCTCTTTTGGTTAAGCGCGCTAATCTTCCCAACTTGGCAATTCGTTT 359  
QY 307 TCGAGGTTCGAGCGCAAGCGCGAGATTGGCGCTTCTTTCGCGCACCGCACGAGAGACC 366  
Db 360 AC-----CAGACGTGAATTTGCTTACCATGTTTGTCTCATTTCACTCAGAGACC 407  
QY 367 GGGCATTTCTGCTACATCAGCAGGTTCAAC---AAGAGCAACGCTTACTTCGACCCGACC 423  
Db 408 GGACATTTCTGCTACATAGAGAGATTAAACGAGCAACACGTAACACTACTCCAGAGACG 467  
QY 424 AAGAGCGAGTGGCGGCGGCGGCGGAGAGTACTTACGCGCGCGCGCTCGCTGCGATC 483  
Db 468 AACACACATACCCATGTGACCGGGGAAAGGCTACTTGGTGTGTCGATCCCACTA 527  
QY 484 TCGTGGAACTACAACTACGCGCGCGCGGAGGGCCATCGGCTTCGACGCGGCTCGGGGAC 543

Db 528 TATGGAACACTCAACTAGGAGCGTGTGGTCAAAAGTCTCGGTGACCTTCTACGCCAG 587  
QY 544 CCCGCGAGGTGGCGGAGCCGCTGTGGGTTCAAGGCGGCGCTCTGTTCTGGATG 603  
Db 588 CCCGAACCTTGGGTAGCAACCCCACTAGCTTTCAGTCCGGTTTGTGGTTTGGATG 647  
QY 604 AACACGTGCACCGTGTGATCCGCGAGGGCTTCGCGCCACCATCAGGGCCATCAACGGC 663  
Db 648 AATAGCGTAAGCGCGTCTCGAACCAAGGTTTGGAGCCACCATTAGAGCTATTAATGG- 706  
QY 664 GCCCTCGAGTCAACGGGAACACCCCGCCAGATGAACGCGCGGCTCGGTACTACAGG 723  
Db 707 --AATGGAATGAACGGTGGTAAATTCGGTGCAGTCAACGCAAGGATTGGATATAGA 764  
QY 724 CAGTACTCCGCGAGTCCGGGTGAGCCCGGCGCAACACCTCACCTGCTGA 774  
Db 765 GACTATTGTGACAGCTTGGTGTGGACCTGCTGCTTAACCTTAGTTGCTAA 815

RESULT 8  
US-08-449-043-37  
; Sequence 37, Application US/08449043  
; Patent No. 5689044  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperrison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,043  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-449-043-37  
Query Match 22.6%; Score 174.6; DB 1; Length 1079;  
Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;  
QY 7 CAGAACTCGCGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTTGGCGCACGACC 66  
Db 93 CAAAACTCGCGTTGGCTCCAAAACCTCTGTTGCAGTCAGTTCCGTTACTTGTGTACCGAC 152  
QY 67 GACGAGTACTCGCGCAGCGGTGCAGTCGGGCCCGCTCCCGCTCGGGCGCGCGTGGCGGC 126  
Db 153 GATGCATACTCGCGTGTGGATGCCGATCAGGTCTCTTGA----- 192  
QY 127 GCGCGCGCGCGGAGCGCGGAGGAGTGGCGGAGTGGCGTAAATGTTGTCACC 186  
Db 193 -----GAGGTAGTGGAAACCCCGAGGGTTCGGTTCGTTAGCATTTGTGACA 239  
QY 187 GACGCGTTCTTCAACCGCATCAAGAACCAAGCCGCGGAGCGGTGCGAGGCGCAAGACTTC 246  
Db 240 CAAGTTTCTTTAACAATATTTATCAACCAAGCTGGTATGTTGCGCGGGAAGAAATTTC 299  
QY 247 TACACCGCGAGCGGTTCCTCGAGGCCATCCCGCGGTACCGGGGCTTCGCGCATGGCGGC 306  
Db 300 TACACCGGTGACTCTTTTCGTTAAACCGCGCTAATACTTCCCAACTTTGCGCAATTTCTGTT 359  
QY 307 TCCGAGGTGCGAGCGCGGAGGAGTTCGCGCCTTCTTCGCGCACGCCACGACGAGACC 366



360	AC-----CAGACGTGAATTCCTACCAATGTTGCTCATTTCTCTCAGAGACC	407
367	GGSCATTCTTCGTACTACATCAGCAGGTCAAC---AAGAGCAACGCGTACTCTCGACCCGACC	423
408	GGNCATTCTTCGTCTCANATAGAGAGATTAAACGGAGCAACGTAATACTACTCCGAGACGC	467
424	AGAGGCACTGCGCGGTGCGCCGCGGGCAGAAAGTACTACGGCGCGGCCCGCTGCGAGATC	483
468	AACACACAATACCCATGTGCACCGGGAAAAGGCTACTTTCGGTCTGTGTCGGATCCAACATA	527
484	TGCTGGAACTACAATAACGCGGCCCGCGGGAGGGCCATTCGGCTTCGACGGCGCTCGGGGAC	543
528	TCATGGAACATAACAATCAGCGAGCGTGTGGTCAAAAGTCTCTGGTCTTGACCTTCTTCA	587
544	CCCGGCAGGTCGCGCGGAGCGCCGTGTGTGGCGTTCAAGCGCGGCGCTCTGGTCTCGATG	603
588	CCCGAACTTGTGGTAGCAACCAACTGTAGCTTTCAGGTCCGGGTTGTGGTTTGGATG	647
604	AACAACGTGCACCGTGTGATGCCGACAGGCTTCGGCGCCACATCAGGGCCATCAACGGC	663
648	AATAGGCTAAGGCGGTTCTGAACCAAGGTTTGGAGCCCATTAGAGCTATTAAATGG-	706
664	GCCCTCGAGTGAACGGGAAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGG	723
707	--AATGGATGTAAACGGTGGTAAATTCCTGGTGCAGTCAACGCAAGGATGGATACTATAGA	764
724	CAGTATCGCCGCGAGCTGGCGGTGAGCCCGGGCAACAACCTCACCTGCTGA	774
765	GACTATTGTGGACAGCTTGGTGTGAGCCCTGGTCTTAACCTTAGTTCCTAA	815

## RESULT 10

US-08-455-416-37  
; Sequence 37, Application US/08455416

; Patent No. 5777200  
; GENERAL INFORMATION:

APPLICANT: Rvals. John A.

APPLICANT: Alexander, Dan

APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.

APPLICANT: Friedrich, Les

APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian

APPLICANT: Meins, Jr., Fr

APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-

APPLICANT: Payne, George B.

APPLICANT: Sperison, Christoph

APPLICANT: Stinson, Jeffrey

APPLICANT: Ukner, Scott J

APPLICANT: WILLIAMS, ERIC R.

APPLICANT: WILLIAMS, Shericca C.  
TITLE OR INVENTION. CHEMICALLY BENZOTATRIC AND ANTI-PATHOGENIC

;  
; TITLE OF INVENTION: CHEMICALLY REGULABLE AND ANI  
: TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

;; TITLE OF INVENTION: DNA S  
: NUMBER OF SEQUENCES: 106

; NUMBER OF SEQUENCES: 1  
: CORRESPONDENCE ADDRESS:CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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;
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31 MAY 2005

;; FILING DATE: 31-MAY-1995  
; CI ASSOCIATION: 800

; CLASSIFICATION: 800

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 08/181,271
3 FILING DATE: 13-JAN-94
4 APPLICATION NUMBER: US 08/093,301
5 FILING DATE: 16-JUL-1993
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 07/937,197
8 FILING DATE: 6-NOV-1992
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/678,378
11 FILING DATE: 1-APR-1991
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/305,566
14 FILING DATE: 6-FEB-1989
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/165,667
17 FILING DATE: 8-MAR-1988
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/042,847
20 FILING DATE: 6-APR-1993
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/632,441
23 FILING DATE: 21-DEC-1990
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/425,504
26 FILING DATE: 20-OCT-1989
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/848,506
29 FILING DATE: 6-MAR-1992
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/768,122
32 FILING DATE: 27-SEP-1991
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 07/580,431
35 FILING DATE: 7-SEP-1990
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/368,672
38 FILING DATE: 20-JUN-1989
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/329,018
41 FILING DATE: 24-MAR-1989
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 08/045,957
44 FILING DATE: 12-APR-1993
45 ATTORNEY/AGENT INFORMATION:
46 NAME: Elmer, James Scott
47 REGISTRATION NUMBER: 36,129
48 REFERENCE/DOCKET NUMBER: S-19825/
49 TELECOMMUNICATION INFORMATION:
50 TELEPHONE: (919)541-8614
51 TELEFAX: (919)541-8689
52 INFORMATION FOR SEQ ID NO: 37:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 1079 base pairs
55 TYPE: nucleic acid
56 STRANDEDNESS: single
57 TOPOLOGY: linear
58 MOLECULE TYPE: DNA
59
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	Query Match	22.6%	Score 174.6	DB 1	Length 1079
	Best Local Similarity	56.5%	Pred. No. 5.2e-24		
	Matches 436	Conservative	0	Mismatches 284	Indels 51
				Gaps	4
Qy	7	CAGAACTGCGGTCGCCAGCCAAACGATATGTCGAGCAAGTTTGGCTACTCGGCACGACC	66		
Db	93	CAAAACTGCGGTTGCGCTCCAAACCTCTGTTCAGTCAGTTTCGGTTACTGTGTGATCCGAC	152		
Qy	67	GACGAGTACTGCGGCGACGGGTGCCACTGCGGCCCGTGCCGCTCGGCGCGGGTGGCGGC	126		
Db	153	GATGCATACTGCGGTGTGGATGCCGATCAGGTCTTTGTA	192		
Qy	127	GGCGCGCGCGCGGAGCGCGCGGAGGCAGTGGCGGGTGCAGAACGTGCTGAATGTGGTCACC	186		

Db 193 -----GAGTAGTGGAAACCCCGACCGAGGTCGGTCGGTAGCATTTGTGACA 239  
Qy 187 GACCGGTTCTTCAACGGCATCAAGAACAGCGCCGGGAGCGGTCGAGGGCAAGATTC 246  
Db 240 CAAGGTTCTTTAAACAATATTATCAACCAAGCTGTAATGTTGCGGGGGAAGATTC 299  
Qy 247 TACACCGGAGCGGTTCTTCAAGCCCATCCCGGTTACCGGGCTTCGGCATGCGGGC 306  
Db 300 TACACCGGTGACTCTTTGTTTAAAGCGCGCTTAATCTTTCCCAACTTTTGCCTTCTGTT 359  
Qy 307 TCCGAGTCGAGCGCAAGCGGAGATTGCCCGCTTCTTCGCGCACGCGCACCGAGAGACC 366  
Db 360 AC-----CAGAGGTGAATTTGCTACCATGTTTGTCTATTTCACTCACGAGACC 407  
Qy 367 GGGGATTTCTGCTACATCAGCGAGGTCAAC---AAGAGCAAGCGCTACTGCGACCCGACC 423  
Db 408 GGACATTTCTGCTACATAGAGAGATTAAACGAGCAACACGTAACCTACTGCGCAGAGCAGC 467  
Qy 424 AAGAGGAGTGGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCTGCAGATC 483  
Db 468 AACACAAATACCCATGTGCAACCGGGAAGGCTACTTCGGTCTGTGTCGATCCAATA 527  
Qy 484 TCGTGGAACTACAACTACGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGGAC 543  
Db 528 TCATGGAACTACAACTACGGAGCGGTGTGTCAAGTCTCGGTCTTGACCTTCTACGCCAG 587  
Qy 544 CCGGCGAGGTGGCGCGGAGACCGCGTGTGCGGTTCAAGCGCGGCTCTGTTCTGATG 603  
Db 588 CCGGAACTGTGGGTAGCAACCCAACTGTAGCTTTCAAGTCCGGTGTGTTGTTGTTGATG 647  
Qy 604 AACACGTGACCGTGTGATCCGCGGCGTTCGCGCGCACCATCAGCGGCGCATCAACGGC 663  
Db 648 AATAGCGTAAGCGCGGTCTGAACCAAGGTTTGAGCCACATTAAGCTATTATAGG- 706  
Qy 664 GCCCTCGAGTGCAACGGGAACAACCCCGCCAGATGAACGCGCGCGTGGCTACTACAGG 723  
Db 707 --AATGAATGTAACGGTGGTAATTCGGTGCAGTCAACGCAAGATTGGATATAGATA 764  
Qy 724 CAGTACTCCCGCAGCTCGGCGTGCACCGCGGCAACACCTCAGCTGCTGTA 774  
Db 765 GACTATTGTGACAGCTTGTGTGAGACCCCTGCTTAACCTTAGTTGCTAA 815

RESULT 11  
US-08-455-244-37  
; Sequence 37, Application US/08455244  
; Patent No. 5789214  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr. Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne

; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,244  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-455-244-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;







; FILING DATE: 20-JUN-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/329,018  
 ; FILING DATE: 24-MAR-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/045,957  
 ; FILING DATE: 12-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Elmer, James Scott  
 ; REGISTRATION NUMBER: 36,129  
 ; REFERENCE/DOCKET NUMBER: S-19825/P1/CDC 1727  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8614  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1079 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-457-364-37

Query Match 22.6%; Score 174.6; DB 2; Length 1079;  
 Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
 Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY	7	CAGAACTGCGGCTGCAGCCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC	66
DB	93	CAAACTGCGGTTGGCTCCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC	152
QY	67	GACGAGTATCGCGGCGACGGGTGCCAGTTCGGGCGCGGTGCCGCTCGGGCGCGGTGGGGC	126
DB	153	GATGCATATCGCGTGTGGATGCCATCAGGTCTCTTGTGA	192
QY	127	GGCGGCGCGGAGGCGGCGGAGGCGAGTGGCGGTGCGAAGTGGCTAATGTGGTCACC	186
DB	193	-----GAGGTAGTGGAAACCCCGAGGGTTCGGTGGTGA	239
QY	187	GACGCGTTCTTCAACGGGCATCAAGAACAGGCGGAGCGGCTGCGAGGCGCAAGACTTC	246
DB	240	CAAGTTTCTTTAACAATATATCAACCAAGCTGTAATGTTGCGGGGGAAGAATTC	299
QY	247	TACACCGGAGCGGTTCTCGAGGCCATCCCGCGTACCCGGGCTTCGCGCATCGGCGC	306
DB	300	TACACCGTGACTCTTTGGTTAAACGCGCTAATCTTTCCCAACTTTGGCCAACTCTGTT	359
QY	307	TCCGAGTTCGAGCGCAAGCGGAGATTTGCGCGCTTCTTGGCGGACGCCACGCGACGAGCC	366
DB	360	AC-----CAGACGTGAATTTGCTACCATGTTTGTCTCATTTCTCACTCAGCAGACC	407
QY	367	GGGCATTTCTGTACATCAGCGAGGTCAAC---AAGACCAACGCTACTCGGACCCGACC	423
DB	408	GGACATTTCTGTACATAGAAGATTAACGGAGCAACACGTAACTACTGCGCAGAGCAGC	467
QY	424	AAGAGGCGAGTGGCGGTGCGCGCGGGGAGAAAGTACTACGGGCGCGGCCCTGCGATC	483
DB	468	AACACAAATACCATGTGCAACCGGAAAAGGCTACTTTCGGTCTGGTCCGATCCACTA	527
QY	484	TCGTGGAACATAACAATCAGGCGCCCGCGGGGAGGGCCATTCGGCTTCGACGGGCTCGGGGAC	543
DB	528	TCATGGAACATAACAATCAGGAGCGTGTGGTCAAAAGTCTTCGGTCTTGACCTTCTACGCCAG	587
QY	544	CCCGGCGGTTGGCGGACGCGGTGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATG	603
DB	588	CCCGAATTTGTGGGTAGCAACCCCAACTGTAGCTTTTCAGGTTCGGGTTGTGGTATG	647
QY	604	AACAACTGTCACCGTGTATGTCGCGCAGGGGCTTCGGCGCCACCATCAGGGCCCATCAACGGC	663
DB	648	AATAGCGTAAGGCGGTTCTGAAACCAAGGGTTTGGAGGCCACCATTAGAGCTATTATGG-	706
QY	664	GCCCTCGAGTCAACGGGAACAAACCCCGCCAGATGAACGCGCGGTTCGGCTACTACAGG	723





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:11:31 ; Search time 360.896 Seconds  
(without alignments)  
12695.850 Million cell updates/sec

Title: US-10-692-367-11

Perfect score: 774

Sequence: 1 tcgatgagaaactgcggctg.....gcaacaacctcaactgctga 774

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : N Geneseq\_l6Dec04.\*
- 1: geneseqn1980s.\*
  - 2: geneseqn1990s.\*
  - 3: geneseqn2000s.\*
  - 4: geneseqn2001as.\*
  - 5: geneseqn2001bs.\*
  - 6: geneseqn2002as.\*
  - 7: geneseqn2002bs.\*
  - 8: geneseqn2003as.\*
  - 9: geneseqn2003bs.\*
  - 10: geneseqn2003cs.\*
  - 11: geneseqn2003ds.\*
  - 12: geneseqn2004as.\*
  - 13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774	100.0	774	13	AdS92627 Chitinase
2	761.2	98.3	774	13	AdS92645 Chitinase
3	759.6	98.1	774	13	AdS92649 Chitinase
4	727.6	94.0	774	13	AdS92687 Chitinase
5	714.8	92.4	774	13	AdS92661 Chitinase
6	711.6	91.9	774	13	AdS92639 Chitinase
7	710.6	91.7	774	13	AdS92675 Chitinase
8	710	91.7	774	13	AdS92653 Chitinase
9	706.8	91.3	774	13	AdS92677 Chitinase
10	706.8	91.3	774	13	AdS92681 Chitinase
11	703.6	90.9	774	13	AdS92679 Chitinase
12	702	90.7	774	13	AdS92663 Chitinase
13	692.4	89.5	774	13	AdS92689 Chitinase
14	690.8	89.3	840	11	AdJ12126 Maize cDN
15	686.8	88.7	765	13	AdS92683 Chitinase
16	686	88.6	774	13	AdS92699 Chitinase
17	682.8	88.2	774	13	AdS92623 Chitinase
18	680.4	87.9	753	13	AdS92659 Chitinase
19	678	87.6	780	13	AdS92691 Chitinase
20	677.2	87.5	765	13	AdS92641 Chitinase

21	676.4	87.4	780	13	AdS92655	AdS92655 Chitinase
22	674.8	87.2	771	13	AdS92657	AdS92657 Chitinase
23	674.6	87.2	777	13	AdS92631	AdS92631 Chitinase
24	669.4	86.5	777	13	AdS92619	AdS92619 Chitinase
25	662.8	85.6	753	13	AdS92697	AdS92697 Chitinase
26	659.6	85.2	753	13	AdS92667	AdS92667 Chitinase
27	658	85.0	753	13	AdS92651	AdS92651 Chitinase
28	653.2	84.4	753	13	AdS92685	AdS92685 Chitinase
29	648.4	83.8	753	13	AdS92671	AdS92671 Chitinase
30	647.8	83.7	1094	3	AAA96222	AAA96222 cDNA enco
31	646.8	83.6	753	13	AdS92647	AdS92647 Chitinase
32	646.8	83.6	753	13	AdS92693	AdS92693 Chitinase
33	645.6	83.4	750	13	AdS92695	AdS92695 Chitinase
34	645.2	83.4	753	13	AdS92673	AdS92673 Chitinase
35	638.8	82.5	753	13	AdS92637	AdS92637 Chitinase
36	637.2	82.3	753	13	AdS92665	AdS92665 Chitinase
37	635.6	82.1	753	13	AdS92669	AdS92669 Chitinase
38	630.8	81.5	753	13	AdS92643	AdS92643 Chitinase
39	600.2	77.5	756	13	AdS92621	AdS92621 Chitinase
40	598.6	77.3	756	13	AdS92629	AdS92629 Chitinase
41	597	77.1	756	13	AdS92625	AdS92625 Chitinase
42	495.6	64.0	636	9	ADA49298	Ada49298 Maize gen
43	495.6	64.0	636	12	ADJ44871	AdJ44871 Plant cDN
44	465	60.1	843	8	ADA70140	Ada70140 Rice gene
45	465	60.1	843	11	ADJ11575	AdJ11575 Rice DNA

ALIGNMENTS

RESULT 1  
AdS92627  
ID AdS92627 standard; DNA; 774 BP.  
XX  
AC AdS92627;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DB Chitinase variant polynucleotide #5.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
FN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
DR WPI; 2004-365417/34.  
DR P-PSDB; AdS92628.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Disclosure; SEQ ID NO 11; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The

CC furig is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX Sequence 774 BP; 139 A; 251 C; 278 G; 106 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 13; Length 774;  
Best Local Similarity 100.0%; Pred. No. 1.1e-121;  
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGATGAGAACTGGCTGCGGCTGCAGCAAACTATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTGGCTGCGGCTGCAGCAAACTATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Qy 61 ACGACCGACGAGTACTGCGGCGAGCGGGTGCCAGTGGGCCCGCTCGGGCGGCGGT 120  
Db 61 ACGACCGACGAGTACTGCGGCGAGCGGGTGCCAGTGGGCCCGCTCGGGCGGCGGT 120  
Qy 121 GCGCGCGCGCGCGCGGAGGCGGCGGAGCGAGTGGCGGTGCGAACGTGGCTAATGTG 180  
Db 121 GCGCGCGCGCGCGGCGGAGGCGGCGGAGCGAGTGGCGGTGCGAACGTGGCTAATGTG 180  
Qy 181 GTCACCGACGAGTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTGCGAGGCAAG 240  
Db 181 GTCACCGACGAGTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTGCGAGGCAAG 240  
Qy 241 AACTTTACACCCGAGCGGCTTCTCGAGGCCATGCGCCGCTACCCGGGCTTCGCGCAT 300  
Db 241 AACTTTACACCCGAGCGGCTTCTCGAGGCCATGCGCCGCTACCCGGGCTTCGCGCAT 300  
Qy 301 GCGGCTCCGAGGTCGAGCGCAAGCGGAGAGTTCGCGCTTCTTCGCGCACGCCACGCAC 360  
Db 301 GCGGCTCCGAGGTCGAGCGCAAGCGGAGAGTTCGCGCTTCTTCGCGCACGCCACGCAC 360  
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCCG 420  
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCCG 420  
Qy 421 ACCAAGAGCGAGTGCCGTGCGCGCGGCGAGAGTACTACGGGCGGCGCGCGGTGCGAG 480  
Db 421 ACCAAGAGCGAGTGCCGTGCGCGCGGCGAGAGTACTACGGGCGGCGCGCGGTGCGAG 480  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540  
Db 481 ATCTCGTGAATCAACTACGCGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540  
Qy 541 GACCCCGCGAGGTCGCGGCGAGCGCCGCTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600  
Db 541 GACCCCGCGAGGTCGCGGCGAGCGCCGCTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600  
Qy 601 ATGAACAACGTCACCGTGTGATGCGGAGGCTTCGGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
Db 601 ATGAACAACGTCACCGTGTGATGCGGAGGCTTCGGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
Qy 661 GCGGCGCTCGAGTGCAACGCGGAAACCCCGCCAGATGAACGCGGCGGCTCGGCTACTAC 720  
Db 661 GCGGCGCTCGAGTGCAACGCGGAAACCCCGCCAGATGAACGCGGCGGCTCGGCTACTAC 720  
Qy 721 AGGCAAGTACTGCGGCGAGCTCGGCGTGCACCGGCGGCAACACCTCACTGCTGA 774  
Db 721 AGGCAAGTACTGCGGCGAGCTCGGCGTGCACCGGCGGCAACACCTCACTGCTGA 774

## RESULT 2

AD92645  
ID AD92645 standard; DNA; 774 BP.

XX AD92645;

AC AD92645;

XX 02-DEC-2004 (first entry)

DT Chitinase variant polynucleotide #12.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX Heterodera.  
XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PTON-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92646.

XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 29; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 137 A; 251 C; 279 G; 107 T; 0 U; 0 Other;

Query Match 98.3%; Score 761.2; DB 13; Length 774;  
Best Local Similarity 99.0%; Pred. No. 1.6e-119;  
Matches 766; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TCGATGAGAACTGGCTGCGGCTGCAGCAAACTATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTGGCTGCGGCTGCAGCAAACTATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Qy 61 ACGACCGACGAGTACTGCGGCGAGCGGGTGCCAGTGGGCCCGCTCGGGCGGCGGT 120  
Db 61 ACGACCGACGAGTACTGCGGCGAGCGGGTGCCAGTGGGCCCGCTCGGGCGGCGGT 120  
Qy 121 GCGCGCGCGCGCGGCGGAGGCGGCGGAGCGAGTGGCGGTGCGAACGTGGCTAATGTG 180  
Db 121 GCGCGCGCGCGCGGCGGAGGCGGCGGAGCGAGTGGCGGTGCGAACGTGGCTAATGTG 180  
Qy 181 GTACCCGACGAGTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTGCGAGGCAAG 240  
Db 181 GTACCCGACGAGTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTGCGAGGCAAG 240  
Qy 241 AACTTTACACCCGAGCGGCTTCTCGAGGCCATGCGCCGCTACCCGGGCTTCGCGCAT 300  
Db 241 AACTTTACACCCGAGCGGCTTCTCGAGGCCATGCGCCGCTACCCGGGCTTCGCGCAT 300  
Qy 301 GCGGCTCCGAGGTCGAGCGCAAGCGGAGAGTTCGCGCTTCTTCGCGCACGCCACGCAC 360  
Db 301 GCGGCTCCGAGGTCGAGCGCAAGCGGAGAGTTCGCGCTTCTTCGCGCACGCCACGCAC 360  
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCCG 420  
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCCG 420





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XX PN WO2004037194-A2.
XX PD 06-MAY-2004.
XX XX 22-OCT-2003; 2003WO-US033588.
XX PF 22-OCT-2002; 2002US-0420666P.
XX PR 06-NOV-2002; 2002US-00290086.
XX PR 14-MAR-2003; 2003US-00389432.
XX XX (VERD-) VERDIA INC.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX XX Muller ML, True T, Simmons CR, Yalpani N;
XX XX WPI; 2004-365417/34.
XX DR P-PSDB; ADS92668.
XX XX
XX XX New chitinase polynucleotides and polypeptides, useful in producing
XX PT plants with enhanced resistance against a fungus or a nematode.
XX PS Claim 4; SEQ ID NO 71; 197pp; English.
XX XX
XX CC The invention relates to chitinase polypeptides and the polynucleotides
XX CC encoding them. A method of enhancing plant resistance to a fungus or
XX CC nematode comprises introducing into a plant a recombinant expression
XX CC cassette comprising a promoter operably linked to a chitinase
XX CC polynucleotide of the invention. The plant is maize or soybean. The
XX CC fungus is from the genus Fusarium. The nematode is from the genus
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX CC plant resistance to a fungus or nematode. This sequence represents a
XX CC chitinase variant polynucleotide of the invention.
XX SQ Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;

Query Match 94.0%; Score 727.6; DB 13; Length 774;
Best Local Similarity 96.3%; Pred. No. 7.5e-114;
Matches 745; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 TCGATGCGAAGTCTGGCTGCGGAGCCAAACCTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
DB 1 TCGATGCGAAGTCTGGCTGCGGAGCCAAACCTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGGAGTCCAGTGGGCGCGTGGCGGCGGT 120
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGGAGTCCAGTGGGCGCGTGGCGGCGGT 120
QY 121 GCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGAGTGGCGGTGCGAGCGTGGCTAATGTG 180
DB 121 GCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGAGTGGCGGTGCGAGCGTGGCTAATGTG 180
QY 181 GTCACCGACGCGTTCTTCAACGGCATCAAGAACACAGCGCGGAGCGGTGCGAGGCAAG 240
DB 181 GTCACCGACGCGTTCTTCAACGGCATCAAGAACACAGCGCGGAGCGGTGCGAGGCAAG 240
QY 241 AACTTCTACCCCGAGCGCGTTCTCTCGAGGCCATTCGCGCGGTACCCGGGCTTCGCGCAT 300
DB 241 AACTTCTACCCCGAGCGCGTTCTCTCGAGGCCATTCGCGCGGTACCCGGGCTTCGCGCAT 300
QY 301 GCGCGTCCGAGGTCGAGCGCAAGCGGAGATTGCGGCTTCTTCGCGCAGCCACGCGAC 360
DB 301 GCGCGGTCACAGGTCGAGCGCAAGCGGAGATTGCGGCTTCTTCGCGCAGCCACGCGAC 360
QY 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAAGCGCTTCTGCGACCGG 420
DB 361 GAGACCGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAAGCGCTTCTGCGACCGG 420
QY 421 ACCAAGAGCGAGTGGCGCGCGCGGCGGAGGAGTACTACGCGCGCGCGCGGTGCGAG 480
DB 421 ACCAAGAGCGAGTGGCGCGCGCGCGGCGGAGGAGTACTACGCGCGCGCGCGGTGCGAG 480
QY 481 ATCTGCTGGAAGTACAACTACGCGGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540
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DB 481 ATCTGCTGGAAGTACAACTACGCGGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540
QY 541 GACCCCGCAGGCTGCGCGGAGCGCGTGGTGCGCTTCAAGCGCGGCTCTGGTTCTGG 600
DB 541 GACCCCGCAGGCTGCGCGGAGCGCGTGGTGCGCTTCAAGCGCGGCTCTGGTTCTGG 600
QY 601 ATGAACAACGTCGACCGTGTGATCCGCGAGGGTTTCGGCGCCACCATCAGGGCCATCAAC 660
DB 601 ATGAACAACGTCGACCGTGTGATCCGCGAGGGTTTCGGCGCCACCATCAGGGCCATCAAC 660
QY 661 GCGCGCTCTGAGTGAACGCGGAACACCCCGCCAGATGAACGCGCGCTGCGGCTACTAC 720
DB 661 GCGCGCTCTGAGTGAACGCGGAACACCCCGCCAGATGAACGCGCGCTGCGGCTACTAC 720
QY 721 AGGACGACTACTGCGCGCAGCTCGCGTGGCGGCAACAACTCCTGCTGA 774
DB 721 AGGACGACTACTGCGCGCAGCTCGCGTGGCGGCAACAACTCCTGCTGA 774
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RESULT 5  
ADS92661

ID ADS92661 standard; DNA; 774 BP.

XX AC ADS92661;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #20.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX KW Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX XX (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX XX Muller ML, True T, Simmons CR, Yalpani N;

XX XX WPI; 2004-365417/34.

XX DR P-PSDB; ADS92662.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 45; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
encoding them. A method of enhancing plant resistance to a fungus or  
nematode comprises introducing into a plant a recombinant expression  
cassette comprising a promoter operably linked to a chitinase  
polynucleotide of the invention. The plant is maize or soybean. The  
polynucleotide is from the genus Fusarium. The nematode is from the genus  
Heterodera. The polynucleotides and polypeptides are useful in enhancing  
plant resistance to a fungus or nematode. This sequence represents a  
chitinase variant polynucleotide of the invention.

XX SQ Sequence 774 BP; 139 A; 249 C; 282 G; 104 T; 0 U; 0 Other;

Query Match 92.4%; Score 714.8; DB 13; Length 774;

Best Local Similarity 95.2%; Pred. No. 1.1e-111;

Matches 737; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 1 TCGATGACAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCCGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 61 ACACCGACGAGTACTGCGGCGAGCGGTCGCCAGTCCAGTCCGCGCGCTGCGGCGCGGT 120  
Db |||||  
Qy 61 ACACCGACGAGTACTGCGGCGAGCGGTCGCCAGTCCAGTCCGCGCGCTGCGGCGCGGT 120  
Db |||||  
Qy 121 GCG 180  
Db |||||  
Qy 181 GTCACCGACGCGTCTTCAACGCGCATCAAGACCAAGCGCGCGCGCGCGCGCGCGCG 240  
Db |||||  
Qy 181 GTCACCGACGCGTCTTCAACGCGCATCAAGACCAAGCGCGCGCGCGCGCGCGCGCG 240  
Db |||||  
Qy 241 AACTTCTACACCG 300  
Db |||||  
Qy 241 AACTTCTACACCG 300  
Db |||||  
Qy 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
Db |||||  
Qy 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
Db |||||  
Qy 361 GAGACCGCGCATTTCTGCTACATCAGCGGATCAACAGAGCAACCGCTTCTGCGACCG 420  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCG 480  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db |||||  
Qy 541 GACCCCGACAGGTCG 600  
Db |||||  
Qy 601 ATGAACACGTCACCGGTGTCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db |||||  
Qy 601 ATGAACACGTCACCGGTGTCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db |||||  
Qy 661 GCGCGCTCGAGTGCACCGGAAACAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Db |||||  
Qy 721 AGGACGATCTCG 774  
Db |||||  
Qy 721 AAGCAGTACTGCG 774  
Db |||||

RESULT 6

AD92639  
ID AD92639 standard; DNA; 774 BP.

XX AC AD92639;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #9.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

22-OCT-2003; 2003WO-US033588.  
22-OCT-2002; 2002US-0420666P.  
06-NOV-2002; 2002US-00290086.  
14-MAR-2003; 2003US-00389432.  
(VERD-) VERDIA INC.  
(PION-) PIONEER HI-BRED INT INC.  
Muller ML, True T, Simmons CR, Yalpani N;  
WPI; 2004-365417/34.  
P-PSDB; ADS92640.  
New chitinase polynucleotides and polypeptides, useful in producing  
plants with enhanced resistance against a fungus or a nematode.  
Claim 4; SEQ ID NO 23; 197bp; English.  
The invention relates to chitinase polypeptides and the polynucleotides  
encoding them. A method of enhancing plant resistance to a fungus or  
nematode comprises introducing into a plant a recombinant expression  
cassette comprising a promoter operably linked to a chitinase  
polynucleotide of the invention. The plant is maize or soybean. The  
fungus is from the genus Fusarium. The nematode is from the genus  
Heterodera. The polynucleotides and polypeptides are useful in enhancing  
plant resistance to a fungus or nematode. This sequence represents a  
chitinase variant polynucleotide of the invention.  
Sequence 774 BP; 146 A; 246 C; 271 G; 111 T; 0 U; 0 Other;

Query Match 91.9%; Score 711.6; DB 13; Length 774;  
Best Local Similarity 95.0%; Pred. No. 3.7e-111;  
Matches 735; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 1 TCGATGACAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 61 ACACCGACGAGTACTGCGGCGAGCGGTCGCCAGTCCAGTCCGCGCGCTGCGGCGCGGT 120  
Db |||||  
Qy 61 ACACCGACGAGTACTGCGGCGAGCGGTCGCCAGTCCAGTCCGCGCGCTGCGGCGCGGT 120  
Db |||||  
Qy 121 GCG 180  
Db |||||  
Qy 121 GCG 180  
Db |||||  
Qy 181 GTACACGACGCGTCTTCAACGCGCATCAAGACCAAGCGCGCGCGCGCGCGCGCGCG 240  
Db |||||  
Qy 181 GTACACGACGCGTCTTCAACGCGCATCAAGACCAAGCGCGCGCGCGCGCGCGCGCG 240  
Db |||||  
Qy 241 AACTTCTACACCG 300  
Db |||||  
Qy 241 AACTTCTACACCG 300  
Db |||||  
Qy 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGAGATTTGCGCGCTTCTTTCGCGCGCGCGCG 360  
Db |||||  
Qy 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGAGATTTGCGCGCTTCTTTCGCGCGCGCGCG 360  
Db |||||  
Qy 361 GAGACCGCGCATTTCTGCTACATCAGCGGTCAGCGGTCAGCGGTCAGCGGTCAGCGG 420  
Db |||||  
Qy 361 GAGACCGCGCATTTCTGCTACATCAGCGGTCAGCGGTCAGCGGTCAGCGGTCAGCGG 420  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCG 480  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCG 480  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db |||||  
Qy 541 GACCCCGACAGGTCG 600  
Db |||||

Db 541 GACCCGACAGACTGGCGCAGACCCCGTGTGTCTGTTCAAGTCGGCGCTCTGTTCTGG 600  
Qy 601 ATGAACAACGTGCAACCGTGTGATGCCGACGGCTTCGGCCGCCACCATCATGAGGCCATCAAC 660  
Db 601 ATGAACAACGTGCAACCGTGTGATGCCGACGGCTTCGGCCGCCACCATCATGAGGCCATCAAC 660  
Qy 661 GGGCCCTTCAGTGTCAACGGGAACACCCGCCCCAGATGAACGGCGCGTGGCTACTAC 720  
Db 661 GGGCCCTTCAGTGTGCGCGGGAACACCCGCCCCAGATGAACGGCGCGTGGCTACTAC 720  
Qy 721 AGGCAGTACTGCCGCCAGCTCGGGCTCGACCCGGGCAACAACTCACTTGTCTGA 774  
Db 721 AGGCAGTACTGCCGCCAGCTCGGGCTCGACCCGGGCAACAACTCACTTGTCTGA 774

RESULT 7

ADS92675  
ID ADS92675 standard; DNA; 771 BP.  
XX  
AC ADS92675;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #27.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92676.

XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.

XX  
PS Claim 4; SEQ ID NO 59; 197pp; English.

XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX  
SQ Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;

Query Match 91.7%; Score 710; DB 13; Length 771;  
Best Local Similarity 95.7%; Pred. No. 6.9e-111;  
Matches 741; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 1 TCGATGCGAAGTCTGGCTGCCAGCAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGCGAAGTCTGGCTGCCAGCAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 61 AGCACCGACAGTACTGCGCGACGCGTCCAGTTCGGGGCCCGCTCGGCGCGGGT 120  
Db 61 AGCACCGACGCTACTGCGCGACGCGTCCAGTTCGGGGCCCGCTCGGCGCGGGT 120  
Qy 121 GCGCGCGCGCGCGCGCGAGAGCGCGGAGGCGAGTGGCGGTCGAAACGTTGGCTAATGTG 180  
Db 121 GCGCGCGGTG---GCGCGGAGCGCGGAGGCGAGTGGCGGTCGAAACGTTGGCTAATGTG 177  
Qy 181 GTCAACGACGCGTCTTCAACGCGCATCAAGAACGAGCGCGGAGCGGTCGAGGGCAAG 240  
Db 178 GTCAACGACGCGTCTTCAACGCGCATCAAGAACGAGCGCGGAGCGGTCGAGGGCAAG 237  
Qy 241 AACTTCTACACCGGAGCGGTTCTCTCGAGGCGCATCGCCGCGTACCGCGGCTTCGCGCAT 300  
Db 238 AACTTCTACACCGGAGCGGTTCTCTCGAGGCGCATCGCCGCGTCAAGCGGTACCGAGCTTCGCCCAT 297  
Qy 301 GCGCGCTTCGAGTTCGAGCGCAAGCGCGAGATTTCCGCGCTTCTTCGCGCAACGCGCAC 360  
Db 298 GCGCGGTTCACAGGTTCAGGGCAAGCGCGAGATTTCCGCGCTTCTTCGCGCATGTCACGCGAC 357  
Qy 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCTACTTCGACCCG 420  
Db 358 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCTACTTCGACCCG 417  
Qy 421 ACCAAGAGGAGTGGCGCGTTCGCGCGGCGCAGAACTACTACGCGCGCGCGCTCGAG 480  
Db 418 ACCAAGAGGAGTGGCGCGTTCGCGCGGCGCAGAACTACTACGCGCGCGCGCTCGAG 477  
Qy 481 ATCTCGTGGAACTACAACCTACGCGCGCGCGGAGGGCCATCGGCTTCGAGCGGCTCGGG 540  
Db 478 ATCTCGTGGAACTACAACCTACGCGCGCGCGGAGGGCCATCGGCTTCGAGCGGCTCGGG 537  
Qy 541 GACCCGCGAGGTTCGCGCGGAGCGCGTTCGCGCTTCAAGCGCGCGCTCTGGTCTCGG 600  
Db 538 GACCCGCGAGGTTCGCGCGGAGCGCGTTCGCGCTTCAAGCGCGCGCTCTGGTCTCGG 597  
Qy 601 ATGAACAACGTCGACCGTGTGATGCGCGCGCGCTTCGCGCGCACCATCATGAGGCCATCAAC 660  
Db 598 ATGAACAACGTCGACCGTGTGATGCGCGCGCGCTTCGCGCGCACCATCATGAGGCCATCAAC 657  
Qy 661 GGGCCCTTCAGTGTCAACGGGAACACCCGCCCCAGATGAACGGCGCGTGGCTACTAC 720  
Db 658 GGGCCCTTCAGTGTGCGAGCGGGAACACCCGCCCCAGATGAACGGCGCGTGGCTACTAC 717  
Qy 721 AGGCAGTACTGCCGCCAGCTCGGGCTCGACCCGGGCAACAACTCACTTGTCTGA 774  
Db 718 AGGCAGTACTGCCGCCAGCTCGGGCTCGACCCGGGCAACAACTCACTTGTCTGA 771

RESULT 8

ADS92653  
ID ADS92653 standard; DNA; 774 BP.

XX  
AC ADS92653;

XX  
DT 02-DEC-2004 (first entry)

XX  
DE Chitinase variant polynucleotide #16.

XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX  
OS Synthetic.

XX  
PN WO2004037194-A2.

XX  
PD 06-MAY-2004.

XX  
PF 22-OCT-2003; 2003WO-US033588.

XX  
PR 22-OCT-2002; 2002US-0420666P.

XX  
PR 06-NOV-2002; 2002US-00290086.

XX  
PR 14-MAR-2003; 2003US-00389432.



Db 118 GCGCGCGTGGCGCGCGAGCGCGGAGGAGTGGCGGTGCGAAGCTGGCTAGCGTC 177  
Qy 181 GTCAACGACGGTCTTCAACGGCATCAAGAACAGGCGCGGAGCGGGTGGAGGCAAG 240  
Db 178 GTCACCGGCTCTTCTTCAACGGCATCAAGAGCCAGGCGCGGAGCGGGTGGAGGCAAG 237  
Qy 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGGTACCGGGCTTCGCGCAT 300  
Db 238 AACTTCTACACCGGAGCGGCTTCTGAGCGCGGTCAAGGCGTACCCAGGCTTCGCCCAT 297  
Qy 301 GCGCGCTCCGAGGTCGAGCGCAAGCGGAGATTCCCGCTTCTTTCGCGCAGCCACGAC 360  
Db 298 GCGCGCTCCGAGGTCGAGCGCAAGCGGAGATTCCCGCTTCTTTCGCGCAGCCACGAC 357  
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAGAGCAACGCTACTTGCACCG 420  
Db 358 GAGACCGGGCATTTCTGTACATCAACGAGATCAACAGAGCAACGCTACTTGCACCG 417  
Qy 421 ACCAAGGCGAGTGGCGCGCGCGGGGCGAGTACTACGGGCGGGCGCGCTGCAG 480  
Db 418 ACCAAGGCGAGTGGCGCGCGCGGGGCGAGTACTACGGGCGGGCGCGCTGCAG 477  
Qy 481 ATCTGTGGAACTACAATACGCGCGCGCGGGGCGAGTACTACGGGCGGGCGCTGCAG 540  
Db 478 ATCTGTGGAACTACAATACGCGCGCGCGGGGCGAGTACTACGGGCGGGCGCTGCAG 537  
Qy 541 GACCCCGCAGGGTGGCGCGGAGCGCGGTGGTGGCGTTCGAGCGGGCTTCGTTCTGG 600  
Db 538 GACCCCGCAGGGTGGCGCGGAGCGCGGTGGTGGCGTTCGAGCGGGCTTCGTTCTGG 597  
Qy 601 ATGAACACGTCACCGGTGATCGCGCAGGGCTTCGGCGCCACCATCAGGCGCATCAAC 660  
Db 598 ATGAACACGTCACCGGTGATCGCGCAGGGCTTCGGCGCCACCATCAGGCGCATCAAC 657  
Qy 661 GCGCGCTTCGAGTCAACCGGAAACAAACCCCGCGAGATGAACCGCGCGCTTCGCTACTAC 720  
Db 658 GCGCGCTTCGAGTCAACCGGAAACAAACCCCGCGAGATGAACCGCGCGCTTCGCTACTAC 717  
Qy 721 AGGAGTACTCCCGCAGCTCGGCGTGAACCGGGCAACACCTCACTGTCTGA 774  
Db 718 AAGCAGTACTCCCGCAGCTCGGCGTGAACCGGGCAACACCTCACTGTCTGA 771

RESULT 10

AD92681  
ID ADS92681 standard; DNA; 774 BP.

XX AC ADS92681;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #30.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX KW Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-0029086.

XX PR 14-MAR-2003; 2003US-00389432.

XX XX (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92682.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 65; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX SQ Sequence 774 BP; 142 A; 250 C; 272 G; 110 T; 0 U; 0 Other;

Query Match 91.3%; Score 706.8; DB 13; Length 774;  
Best Local Similarity 94.6%; Pred. No. 2.4e-110;  
Matches 732; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Qy 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTCCAGTCCGCGCCCGTCCGCGGCGGT 120  
Db 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTCCAGTCCGCGCCCGTCCGCGGCGGT 120  
Qy 121 GCGCGCGCGCGCGCGCGCGAGCGCGGAGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180  
Db 121 GCGCGCGCGCGCGCGCGCGAGCGCGGAGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180  
Qy 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACAGGCGCGGAGCGGTGCGAGGCGCAAG 240  
Db 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACAGGCGCGGAGCGGTGCGAGGCGCAAG 240  
Qy 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTACCGCGGCTTCGCGCAT 300  
Db 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTACCGCGGCTTCGCGCAT 300  
Qy 301 GCGCGCTCCGAGTTCGAGCGCGAGCGGAGTTCGCGGCTTCTTCGCGCAACCGCAC 360  
Db 301 GCGCGGTCGAGGTGCGAGGCGAGCGGAGTTCGCGGCTTCTTCGCGCATGTCCGCGAC 360  
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAGAGCAACGCTACTTGCAGCCG 420  
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAGAGCAACGCTACTTGCAGCCG 420  
Qy 421 ACCAAGGCGAGTGGCGCGCGCGCGGAGGAGTACTACGGGCGGGCGCGCGCTGCAG 480  
Db 421 ACCAAGGCGAGTGGCGCGCGCGCGGAGGAGTACTACGGGCGGGCGCGCGCTGCAG 480  
Qy 481 ATCTCGTGGAACTACAACCTACGGGCGCGGAGGCGCATCGGCTTCGAGCGGCTCGGG 540  
Db 481 ATCTCGTGGAACTACAACCTACGGGCGCGGAGGCGCATCGGCTTCGAGCGGCTCGCC 540  
Qy 541 GACCCCGCAGGGTGGCGCAGCGCGGTGGTGGCGTTCGAGCGGCGCTCTGTGTTCTGG 600  
Db 541 GACCCCGCAGGGTGGCGCAGCGCGGTGGTGGCGTTCGAGCGGCGCTCTGTGTTCTGG 600  
Qy 601 ATGAACACGTCGACCGGTGATCGCGCAGGGCTTCGCGCGCAACCATCAGGCGCATCAAC 660  
Db 601 ATGAACACGTCGACCGGTGATCGCGCAGGGCTTCGCGCGCAACCATCAGGCGCATCAAC 660  
Qy 661 GCGCGCTTCGAGTCAACCGGAAACAAACCCCGCGAGATGAACCGCGCGCTTCGCTACTAC 720  
Db 661 GCGCGCTTCGAGTCAACCGGAAACAAACCCCGCGAGATGAACCGCGCGCTTCGCTACTAC 720

QY 721 AGGCACTACTGCGCGCTCGAGCCGCGGCAACACCTCACTGCTGA 774  
 Db |||||  
 721 AAGCAGTACTCCGCCAGCTCGCGTGCAGCCAGGGCCCAACCTCACTTGTGA 774  
 |||||

RESULT 11  
 ADS92679  
 ID ADS92679 standard; DNA; 774 BP.  
 XX  
 AC ADS92679;  
 XX  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polynucleotide #29.  
 XX  
 XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR P-PSDB; ADS92680.  
 XX

PT New chitinase polynucleotides and polypeptides, useful in producing  
 plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 4; SEQ ID NO 63; 197pp; English.  
 XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
 encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.  
 XX  
 SQ Sequence 774 BP; 144 A; 256 C; 269 G; 105 T; 0 U; 0 Other;

Query Match 90.9%; Score 703.6; DB 13; Length 774;  
 Best Local Similarity 94.3%; Pred. No. 8.3e-110;  
 Matches 730; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 TCGATGACAGAACTCGCGCTGCAGCCAAACCTATGCTGCAGCAAGTTTGGTACTGCGGC 60  
 |||||  
 Db 1 TCGATGACAGAACTCGCGCTGCAGCCAAACCTATGCTGCAGCAAGTTTGGTACTGCGGC 60  
 |||||

QY 61 ACACACGACAGTACTCGCGGACGGGTGCCAGTCCGGCCCGTCCCGCTCGGGCGCGGT 120  
 |||||  
 Db 61 ACACACGACAGTACTCGCGGACGGGTGCCAGTCCGGCCCGTCCCGCTCGGGCGCGGC 120  
 |||||

QY 121 GCGCGCGCGCGCGCGGCGGCGGAGGCGGAGGCGGAGTGGCGGTGCAACCTGTAATGTG 180  
 |||||  
 Db 121 GCGCGCGCGCGCGCGGCGGCGGAGGCGGAGGCGGAGTGGCGGTGCAACCTGTAATGTG 180  
 |||||

QY 181 GTCAACGACGCGTTCTTCAACGGCATCAAGAACCGAGCCGCGGAGCGGTGCGAGGCGCAAG 240  
 |||||

Db 181 GTCAACGACGCGTTCTTCAACGGCATCAAGAACCGAGCCGCGGAGCGGTGCGAGGCGCAAG 240  
 |||||

QY 241 AACTTTCTACACCCGAGCGGTTCTCTCGAGGCCATCGCCCGGTACCCCGGGCTTCGCGCAT 300  
 |||||

Db 241 AACTTTCTACACCCGAGCGGTTCTCTGAGCGCGGTCAAGGGGTACCCAGGCTTCGCCCAT 300  
 |||||

QY 301 GCGGGCTCCGAGGTGCGAGCGGAGAGTTGCGCGCTTCTTCGCGGACGCGCACGCGAC 360  
 |||||

Db 301 GCGGGTCAACAGGTGCGAGGCAAGCGCGAGATGCGCGCTTCTTCGCGGACGCGCACGCGAC 360  
 |||||

QY 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTACTTGGACCCG 420  
 |||||

Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGTCAACAGAGCAACGCTTACTTGGACCCG 420  
 |||||

QY 421 ACCAAGGAGCAGTGGCGCTGCGCGCGGGGAGAGTACTACGGGCGGCGCGCTGCGAG 480  
 |||||

Db 421 ACCAAGGAGCAGTGGCGCTGCGCGCGGGGAGAGTACTACGGGCGGCGCGCTGCGAG 480  
 |||||

QY 481 ATCTCGTGGAACTACAACTACGGGCGCGCGGGAGGCGCATCGGCTTCGAGCGGCTCGG 540  
 |||||

Db 481 CTGTGCTGGAACTACAACTACGGGCGCGCGGGAGGAGCATCGGCTTCAACGGGCTCGCC 540  
 |||||

QY 541 GACCCCGGAGGCTGCGCGCGGACCGCTGTGTGCGTTCAAGCGCGCGCTCTGTGTTCTGG 600  
 |||||

Db 541 GACCCCAACAGGCTGCGCGCGGACCGCTGTGTGCGTTCAAGCGCGCGCTCTGTGTTCTGG 600  
 |||||

QY 601 ATGAACAACTGTCACCGTGTGATGCGCGAGGCTTCGCGCGCACCATCAAGGCGCATCAAC 660  
 |||||

Db 601 ATGAACAACTGTCACCGTGTGATGCGCGAGGCTTCGCGCGCACCATCAAGGCGCATCAAC 660  
 |||||

QY 661 GCGCGCTCGAGTGCACGAGCAACCGCGCGCGCGGAGTGAACGCGCGGCTCGGCTACTAC 720  
 |||||

Db 661 GCGCGCTCGAGTGCACGAGCAACCGCGCGCGCGGAGTGAACGCGCGGCTCGGCTACTAC 720  
 |||||

QY 721 AGGCACTACTGCGCGCTCGAGCCGCGGCAACACCTCACTGCTGA 774  
 |||||

Db 721 AAGCAGTACTCCGCCAGCTCGCGTGCAGCCAGGGCCCAACCTCACTTGTGA 774  
 |||||

## RESULT 12

ADS92663

ID ADS92663 standard; DNA; 771 BP.

XX ADS92663;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #21.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92664.

XX New chitinase polynucleotides and polypeptides, useful in producing

PT

PT	plants with enhanced resistance against a fungus or a nematode.
XX	Claim 4; SEQ ID NO 47; 197pp; English.
XX	The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
XX	Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;
SQ	Query Match 90.7%; Score 702; DB 13; Length 771; Best Local Similarity 95.1%; Pred. No. 1.5e-109; Matches 736; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
Qy	1 TCGATGCAGAACTCGGCTGCGCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db	1 TCGATGCAGAACTCGGCTGCGCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy	61 ACGACCGACGAGTACTGCGGCGAGCGGTGCCAGTCCGGCCCGTCCGCGCGCGGT 120
Db	61 ACGACCGACGAGTACTGCGGCGAGCGGTGCCAGTCCGGCCCGTCCGCGCGCGGT 117
Qy	121 GGCGCGCGCGCGCGCGCGCGCGCGAGTGGCGGCGAGTGGCGTGCAGAGTGGCTTAATGTG 180
Db	118 GGCGCGCGTGGCGCGCGCGAGGCGCGAGGCGAGTGGCGTGCAGAGTGGCTTAGCGTC 177
Qy	181 GTCAACCGACGCGTTCTTCAACGCGCATCAAGAACCAAGCCGCGAGCGGTGCGAGGCGAAG 240
Db	178 GTCAACCGACTCTCTTCTTCAACGCGCATCAAGAGCCAGCGCGGAGCGGCGAAG 237
Qy	241 AACTTCTACACCGGAGCGGCTTCTCGAGGCCATCGCGCGTACCGCGGCTTCGCGCAT 300
Db	238 AACTTCTACACCGGAGCGGTTCTCGAGCGCGCTTCTCGAGGCCGTACCGAGGCTTCGCCCAT 297
Qy	301 GGCGGCTCCGAGGTCGAGCGCAAGCGCGAGATTCGCGCTTCTTTCGGGCGAGCCACGCGAC 360
Db	298 GGCGGTCACAGGTCGAGGCGAAGCGCGAGATTCGCGCTTCTTTCGGCGATGTCAAGCAC 357
Qy	361 GAGACCGGCAATTTCTGTATCATAGCGAGTCAACAGAGCAACGCTTACTGCGACCGC 420
Db	358 GAGACCGGGCATTTCCGCTACATCAGCGAGGTCAACAGAGCAACGCTTACTGCGACCGC 417
Qy	421 ACCAGAGGCGAGTGGCGGTGCGCGCGGCGAGGAGTACTACGGCGCGCGCGCGTGCAG 480
Db	418 ACCAAGAGGCGAGTGGCGGTGCGCGCGGCGAGAGTACTACGGCGCGCGCGCGTGCAG 477
Qy	481 ATCTGTCGAACTCAAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540
Db	478 ATCTGTCGAACTCAAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 537
Qy	541 GACCCCGGAGGGTGGCGGGAAGCGCTGTGTGGCGTTCAAGGGCGCGCTCTGTGTTCTGG 600
Db	538 GACCCCGGAGGGTGGCGGGAAGCGCTGTGTGGCGTTCAAGGGCGCGCTCTGTGTTCTGG 597
Qy	601 ATGACACAGTGCACCGGTGATGCGCGAGGCGTTCGGCGCCACCATCAGGCGCATCAAC 660
Db	598 ATGACACAGTGCACCGGTGATGCGCGAGGCTTCGGCGCCACCATCAGGCGCATCAAC 657
Qy	661 GGCGGCTTCGAGTGCAGCGGAACAAACCCCGCCAGATGAACGCGCGGTTCGGCTACTAC 720
Db	658 GGCGGCTTCGAGTGCAGCGGAACAAACCCCGCCAGATGAACGCGCGGTTCGGCTACTAC 717
Qy	721 AGGCAAGTACTCGCGCGAGTGGCGTGCACCGGCGCAACACCTTCTGTCTGA 774
Db	718 AGGCAAGTACTCGCGCGAGTGGCGTGCACCGGCGCGCAACCTTCTGTCTGA 771





Db675CAACGTGCACCGTGTGATGCGCGAGGCGCTTCGGCGCCACCATCAGGGCCATCAACGGCGC734

Qy666CCTCGAGTGCNAACGGGAACAACCCCGCCAGATGAACCGCGCGTCCGGCTACTACAGGCA725

Db735CCTCGAGTGCNAACGGGAACAACCCCGCCAGATGAACCGCGCGTCCGGCTACTACAGCA794

Qy726GTACTGCCGCGAGCTCGGCGTGCAGCCCGGGCAACAACCTCACTGCG771

Db795GTACTGCCGAGCTCGGCGTGCAGCCCGAGGGCCCAACCTCACTTGC840

RESULT 15

ADS92683

IDADS92683 standard; DNA; 765 BP.

XXACADS92683;

XX02-DEC-2004 (first entry)

XXChitinase variant polynucleotide #31.

XXChitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XXHeterodera.

XXSynthetic.

XXWO2004037194-A2.

XX06-MAY-2004.

XX22-OCT-2003; 2003MO-US033588.

XX22-OCT-2002; 2002US-0420666P.

XX06-NOV-2002; 2002US-00290086.

XX14-MAR-2003; 2003US-00389432.

XX(VERD-) VERDIA INC.

XX(PION-) PIONEER HI-BRED INT INC.

XXMuller ML, True T, Simmons CR, Yalpani N;

XXWPI; 2004-365417/34.

XXP-PSDB; ADS92684.

XXNew chitinase polynucleotides and polypeptides, useful in producing

XXplants with enhanced resistance against a fungus or a nematode.

XXClaim 4; SEQ ID NO 67; 197pp; English.

XXThe invention relates to chitinase polypeptides and the polynucleotides

XXencoding them. A method of enhancing plant resistance to a fungus or

XXnematode comprises introducing into a plant a recombinant expression

XXcassette comprising a promoter operably linked to a chitinase

XXpolynucleotide of the invention. The plant is maize or soybean. The

XXfungus is from the genus Fusarium. The nematode is from the genus

XXHeterodera. The polynucleotides and polypeptides are useful in enhancing

XXplant resistance to a fungus or nematode. This sequence represents a

XXchitinase variant polynucleotide of the invention.

XXSequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

Query Match

Best Local Similarity 88.7%; Score 686.8; DB 13; Length 765;

Matches 728; Conservative 0; Mismatches 37; Indels 9; Gaps 1;

Qy1TCGATGCAGAACTCGGCGTGCAGCCAAACGTATGCTCAGCAAGTTTGGCTACTGCGGC60

Db1TCGATGCAGAACTCGGCGTGCAGCCAAACGTATGCTCAGCAAGTTTGGCTACTGCGGC60

Qy61ACGACCGAGAGTACTCGGCGAGCGGTGCCAGTCGGGCCCGCTCGCGTGGCGGCGGT120

Db61ACAAACGAGAGTACTCGGCGAGCGGTGCCAGTCGGGCCCGCTCGCGTGGCGGCTCG-----111

Qy121GGCGCGCGCGCGCGCGCGCGAGGCGAGTGGCGGTGCGAACGTGGCTAATGTG180

Db112GGCGCGCGCGCGCGCGCGAGGCGCGGAGGCGAGTGGTGGTGGAACTGGGTCTAGCGTC171

Qy181GTCACCGAGCGCTTCTTCAACGGCATCAAGAACAGCCCGGAGCGGTGCGAGGGCAAG240

Db172GTACCGCGTCTTCTTCAACGGCATCAAGAACAGCCCGGAGCGGTGCGAGGGCAAG231

Qy241AACTTCTTACACCGGAGCGCTTCTTGGAGGCATTCGCCCGCTAACCGGGCTTCGCGCAT300

Db232AACTTCTTACACCGGAGCGCTTCTTGGAGCGCGTCAAGCGGTCAACCGAGCTTCGCCCAT291

Qy301GGCGGCTCCGAGGTGAGCGCGAGATTCGCGCTTCTTCCGGCGACGCCACGCAC360

Db292GGCGGCTCAAGGTGAGCGCGAGATTCGCGCTTCTTCCGGCGACGCCACGCAC351

Qy361GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAAGAGCAACGCTTCTGCGACCCG420

Db352GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAAGAGCAACGCTTCTGCGACCCG411

Qy421ACCAAGAGCGAGTGGCGGTGCGCGCGGGCGAGAGTACTACGGGCGCGCCGCTGCGAG480

Db412ACCAAGAGCGAGTGGCGGTGCGCGCGGGCGAGAGTACTACGGGCGCGCCGCTGCGAG471

Qy481ATCTGTGGAACTACAACCTACGGGCGCGGGGAGGSCCATCGCTTCGACGGCTCGGG540

Db472ATCTGTGGAACTACAACCTACGGGCGCGGGGAGGSCCATCGCTTCGACGGCTCGGG531

Qy541GACCCCGGAGGTGGCGCGGAGCGCGTGTGGCGTTCAAGGCGGCGCTCTGGTCTGG600

Db532GACCCCAACAGGTGGCGGAGGAGCGCGTGTGGCGTTCAAGGCGGCGCTCTGGTCTGG591

Qy601ATGAACAACGTGCACCGTGTGATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAAC660

Db592ATGAACAACGTGCACCGTGTGATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAAC651

Qy661GGCGCCCTCGAGTGCAGCGGGAACACCCCGCCAGATGAACGCGGCGCTCGGCTACTAC720

Db652GGCGCGCTCGAGTGCAGCGGGAACACCCCGCCAGATGAACGCGGCGCTCGGCTACTAC711

Qy721AGGCAGTACTGCGCGCCAGCTCGGCGTGCAGCCCGGGCAACACCTCACTTCTGTA774

Db712AGGCAGTACTGCGCGCCAGCTCGGCGTGCAGCCCGGGCCCAACCTCACTTCTGTA765

Search completed: May 23, 2005, 12:57:05

Job time : 363.896 secs

Result No.	Query #			DB	ID	Description
	Score	Match	Length			
1	687	88.8	843	6	MZECR162A	M84164 Zea mays ch
2	647.8	83.7	1094	8	AB32162A	AR321624 Sequence
3	637.8	82.4	810	8	MZECR17B	M84165 Zea mays ch
4	581.8	75.2	1094	8	AY532775	AY532775 Zea mays
5	562	72.6	1115	8	AY532768	AY532768 Zea mays
6	558.8	72.2	1101	8	AY532770	AY532770 Zea mays
7	554.4 <sup>4</sup>	71.6	1128	8	AY532740	AY532740 Zea diplo
8	552.4	71.4	1094	8	AY532778	AY532778 Zea mays
9	552.4	71.4	1094	8	AY532779	AY532779 Zea mays
10	550.8	71.2	1118	8	AY532773	AY532773 Zea mays
11	548.4	70.9	1107	8	AY532781	AY532781 Zea diplo
12	548.4	70.9	1110	8	AY532783	AY532783 Zea diplo
13	548.4	70.9	1110	8	AY532784	AY532784 Zea diplo
14	548.4	70.9	1110	8	AY532785	AY532785 Zea diplo
15	548.4	70.9	1110	8	AY532786	AY532786 Zea diplo
16	548.4	70.9	1110	8	AY532787	AY532787 Zea diplo
17	548.4	70.9	1110	8	AY532788	AY532788 Zea diplo
18	546.6	70.6	1132	8	AY532774	AY532774 Zea mays
19	541.2	69.9	1131	8	AY532780	AY532780 Zea mays

ALFWNNVHVHVPQGFATRAINGALECNPNPAQWNRVGYKYCOQLRVDPP  
NLIC"

ORIGIN  
Query Match 88.8%; Score 687; DB 8; Length 843;  
Best Local Similarity 93.5%; Pred. No. 1.1e-79;  
Matches 717; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 6 GCAGAACTGCGGCTGCCAGCAAAATGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 65  
Db 75 GCAGAACTGCGGCTGCCAGCAAAATGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 134  
Qy 66 CGACGAGTACTGCGGCGAGCGGTCGAGTCCGAGTCCGCGCCGTCGCGGCGGCGGTCGGG 125  
Db 135 CGACGCTTACTGCGGCGAGCGGTCGAGTCCGAGTCCGCGCCGTCGCGGCGGCGGCGGCGG 194  
Qy 126 CGGCGGCGGCGGCGAGCGGCGGAGCGAGTGGCGGTGCGAACTGCTTAATGTGGTTCAC 185  
Db 195 CGGCGGCGGCGGCGAGCGGCGGAGCGAGTGGCGGTGCGAACTGCTTAATGTGGTTCAC 254  
Qy 186 CGACGCGTTCTTCAACGCGATCAAGAACACGAGCGGAGCGGTCGAGGCGCAAGAACTT 245  
Db 255 CGACGCGTTCTTCAACGCGATCAAGAACACGAGCGGAGCGGTCGAGGCGCAAGAACTT 314  
Qy 246 CTACACCGGAGCGGTTCTTCGAGGCGCATCGCGCGTACCGCGGCTTGGCGATGGCGG 305  
Db 315 CTACACCGGAGCGGTTCTTCGAGGCGCATCGCGCGTACCGCGGCTTGGCGATGGCGG 374  
Qy 306 CTCGAGGTTCGAGCGCAAGCGCGAGTTCGCGCTTCTTCGCGACCGCACGACGAGAC 365  
Db 375 GACGAGGTTCGAGCGCAAGCGCGAGTTCGCGCTTCTTCGCGACCGCACGAGAC 434  
Qy 366 CGGCGATTTCTGCTACATCAGCGAGTCAACAAGAGCAACGCTTACTGCGACCGGACCA 425  
Db 435 CGGCAATTTCTGCTACATCAGCGAGTCAACAAGAGCAACGCTTACTGCGACCGGAGCA 494  
Qy 426 GAGCAGTGGCGGTGCGCGCGGCGGAGAGTACTACGCGCGCGCGCGCTGCGAGATCTC 485  
Db 495 CAGGCGAGTGGCGGTGCGCGCGGCGGAGAGTACTACGCGCGCGCGCGCTGCGAGATCTC 554  
Qy 486 GTGGAACTTCAACTACGCGCGCGGCGGAGGCGCATCGGCTTTCGACCGGCTTCGCGGACCC 545  
Db 555 GTGGAACTTCAACTACGCGCGCGGCGGAGGCGCATCGGCTTTCGACCGGCTTCGCGGACCC 614  
Qy 546 CGGCGAGGTGGCGGCGGAGCGCGGTGCGGTTCGAGCGCGCGCTTCTGGTTCTGATGAA 605  
Db 615 CAACAGGTGGCGGAGGAGCGCGGTGATCGCGTTCAGAGCGGCGCTTCTGGTTCTGATGAA 674  
Qy 606 CAACGTGCACCGTGTGATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCG 665  
Db 675 CAACGTGCACCGTGTGATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCG 734  
Qy 666 CTTGAGTGCACCGGAGCAAAACCGCGCGAGATGAACGCGCGCTTCGCTTACTACAGGCA 725  
Db 735 CTTGAGTGCACCGGAGCAAAACCGCGCGAGATGAACGCGCGCTTCGCTTACTACAGGCA 794  
Qy 726 GTACTGCGCGAGCTCCGCGTTCGAGCCGAGGCGCAACCTTCACTTCTGCT 772  
Db 795 GTACTGCGCGAGCTCCGCGTTCGAGCCGAGGCGCAACCTTCACTTCTGCT 841

RESULT 2  
LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6563020.  
ACCESSION AR321624  
VERSION AR321624.1 GI:33706864  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1094)  
AUTHORS Simmons, C.R. and Valpani, N.

TITLE Maize chitinases and their use in enhancing disease resistance in crop plants  
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;  
FEATURES Location/Qualifiers  
source 1.1094  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 83.7%; Score 647.8; DB 6; Length 1094;  
Best Local Similarity 91.8%; Pred. No. 1.2e-74;  
Matches 704; Conservative 0; Mismatches 42; Indels 21; Gaps 1;

Qy 6 GCAGAACTGCGGCTGCCAGCAAAATGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 65  
Db 149 GCAGAACTGCGGCTGCCAGCAAAATGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 208  
Qy 66 CGACGAGTACTGCGGCGAGCGGTCGAGTCCGAGTCCGCGCCGTCGCGGCGGCGGTCGGG 125  
Db 209 CGACGAGTACTGCGGCGAGCGGTCGAGTCCGAGTCCGCGCCGTCGCGGCGGCGGCGAG 268  
Qy 126 CGGCGGCGGCGGAGCGGCGGAGCGAGTGGCGGTGCGAACTGCTTAATGTGGTTCAC 185  
Db 269 CAGTGGCGGC-----GGTGGTGCAGAACGTGGCTTAGCGTCTGCTCAC 307  
Qy 186 CGACGCGTTCTTCAACGCGCATCAGAACACGAGCGCGGAGCGGTCGAGGCGCAAGAACTT 245  
Db 308 CGGCTCTTCTTCAACGCGCATCAGAACACGAGCGCGGAGCGGTCGAGGCGCAAGAACTT 367  
Qy 246 CTACACCGGAGCGGCTTCTTCGAGGCGCATCGCGCGTACCCGCGGCTTCGCGATGCGCG 305  
Db 368 CTACACCGGAGCGGCTTCTTCGAGGCGCATCGCGCGTACCCAGGCGTACCCCGATGCGCG 427  
Qy 306 CTCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGACCGCACGAGAC 365  
Db 428 GTGCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGACCGCACGAGAC 487  
Qy 366 CGGCGATTTCTGCTTACATCAGCGAGGTCAACAAGAGCAACGCTTACTGCGACCGGACCA 425  
Db 488 CGGCGATTTCTGCTTACATCAGCGAGATCAACAAGAGCAACGCTTACTGCGACCGGACCA 547  
Qy 426 GAGCAGTGGCGGTGCGCGCGGCGGAGAGTACTACGCGCGCGGCGCGCTTCGATGATCTC 485  
Db 548 GAGGCGATGGCGGTGCGCGCGGCGGAGAGTACTACGCGCGCGGCGCGCTTCGATGATCTC 607  
Qy 486 GTGGAACTTCAACTACGCGCGCGGCGGAGGCGCATCGGCTTCGACCGGCTTCGCGGACCC 545  
Db 608 GTGGAACTTCAACTACGCGCGCGGCGGAGGCGCATCGGCTTCGACCGGCTTCGCGGACCC 667  
Qy 546 CGGCGAGGTGGCGGAGCAACGCGGTGGGTGCGGTTCAAGCGCGCGCTTCGATGATGAA 605  
Db 668 CGGCGAGGTGGCGGAGCAACGCGGTGGGTGCGGTTCAAGCGCGCGCTTCGATGATGAA 727  
Qy 606 CAACGTGCACCGTGTGATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCG 665  
Db 728 CAGCGTGCACCGGCGGTGCGCGAGGCGTTCGCGCGCACCATCAGGCGCATCAACGCGCG 787  
Qy 666 CTTGAGTGCACCGGAGCAAAACCGCGCGAGATGAACGCGCGCTTCGCTTACTACAGGCA 725  
Db 788 CTTGAGTGCACCGGAGCAAAACCGCGCGAGATGAACGCGCGCTTCGCTTACTACAGGCA 847  
Qy 726 GTACTGCGCGAGCTCCGCGTTCGAGCCGAGGCGCAACCTTCACTTCTGCT 772  
Db 848 GTACTGCGCGAGCTCCGCGTTCGAGCCGAGGCGCAACCTTCACTTCTGCT 894

RESULT 3  
LOCUS MZCHITB 810 bp DNA linear PLN 27-APR-1993  
DEFINITION Zea mays chitinase B (seed chitinase) gene, 3' end.  
ACCESSION M84165  
VERSION M84165.1 GI:168442  
KEYWORDS chitinase B.



Query Match	75.2%; Score 581.8; DB 8; Length 1094;
Best Local Similarity	83.2%; Pred. No. 3.9e-56; Indels 92; Gaps 1;
Matches	715; Conservative 0; Mismatches 52;
QY	6 GCAGAACTCGCGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTGGCTACTCGCGCAGCAG 65
DB	98 GCAGAACTCGCGCTGCCAGCCCTAACTTCTGCTGCAGCAAGTTTGGCTACTCGCGCAGCAG 157
QY	66 CGACAGATCTCGCGGAGCGGTGCGCATCTCGGCGCCCTGCGCTCGCGCGCGGTGGCGG 125
DB	158 CGACGCCCTACTCGCGCGACCGGTGCGCATCTCGGCGCCCTGCGCTCGCGCGCGGTGGCGG 217
QY	126 CGCGCGCGCGCGCGAGCGCGGAGCGAGTGGCGGCTGCGAAGCTGGCTAATGTGGTTCAC 185
DB	218 CGCGCGCGCGCGCGAGCGCGGAGCGAGTGGCGGCTGCGAAGCTGGCTAATGTGGTTCAC 277
QY	186 CGACCGGTTCTTCAACCGGCATCAAGAACCGCGCGGAGCGCGGTGCGAGGCGCAAGAACTT 245
DB	278 CGACCGGTTCTTCAACCGGCATCAAGAACCGCGGAGCGCGGTGCGAGGCGCAAGAACTT 337
QY	246 CTACACCGCGAGCGGTTCTCGAGCGCCATCGCGCGTACCCTGGCTTCGGCGCATGGCG 305
DB	338 CTACACCGCGAGCGGTTCTCGAGCGCCCTGTAACCGGTACCGGGCTTCGCCCATGGCG 397
QY	306 CTTCGAGGTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCAAGCGCGCAAGCGAG 365
DB	398 GACGAGGTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCAAGCGCGCAAGCGAG 457
QY	366 CGGGC----- 370
DB	458 CGGACGTAAAGTTATTAAACACTTAACTAGCTAGCATGCGAGGACCTTTGATCTGACGCGACCG 517
QY	371 -----ATTTCTGCTCATCAGCGAGGTC 393
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QY	454 AAGTACTACGGCGCGCGCGCTGCGAGATCTCGTGGAACTCAACTACGCGCCCGCGCGGG 513
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QY	634 TTCCGGCGCCACCATCAGGGCCCATCAACCGCGCCCTCGAGTGCAACGGGAAACAACCCCGCC 693
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QY	754 GGCAACAACCTCACCTTGCT 772
DB	938 GGGCCCAACCTCACTTGCT 956
RESULT 5	AY532768 1115 bp DNA linear PLN 29-JUL-2004
LOCUS	Zea mays subsp. parviglumis isolate pi chitinase (chiA) gene,
DEFINITION	complete cds.
ACCESSION	AY532768
VERSION	AY532768.1 GI:48093317
KEYWORDS	

452	CGGAGTAAAGTTATTAACACCTAATTA	CTAGCTAGCATGCGAGGACCTTTGATCTGACCG	511
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393	CAACAAGAGCAACGCTACTGCGACCGACCAAGAGGCGAGTGGCTGGCGCGCGGGCA	452	
572	CAACAAGAGCAACGCTACTGCGACCGAGCAACAGGCAGTGGCTGGCGCGCGGGCA	631	
453	GAAGTACTACGCGGCGCGGCTCGCTGAGATCTCGTGGAACTACAACTACGGGCCCGCGGG	512	
632	GAAGTACTACGCGGCGCGGCTCGCTGAGATCTCGTGGAACTACAACTACGGGCCCGCGGG	691	
513	GAGGGCCATCGGCTTCGACGGGCTCGGGGACCCCGGCAGGGTGGCGCGGACGCCGTGGT	572	
692	GAGGACATCGGCTTCAGAGGGCTCGCGACCCCAACAGGGTGGCGAGGACGCCGTGAT	751	
573	GGCGTTCAAGCGGGCGGCTCTGGTCTTGTGATGAACAAACGTCGACCGTGTGATGCCGACGGG	632	
752	CGCGTTCAAGACGGCGCTCTGGTCTTGTGATGAACAAACGTCGACCGTGTGATGCCGACGGG	811	
633	CTTCGGGCGCCACCATCAGGGCCATCAA	CGGCGCCCTCGAGTGCACGGGAAACAACCCCGC	692
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693	CCAGATGAACCGCGCGTGGCTACTACAGGCAGTACTGCGCGCCAGCTCGGGCGTGCAGCC	752	
872	CCAGATGAACGGCGCGTGGCTACTACAAGCAGTACTGCGCAGAGCTCCGGGTGCAGCC	931	
753	GGGCAACAACCTCACTGCT	772	
932	AGGGCCCAACCTCACTTGTCT	951	

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RESULT_6
LOCUS      AY532770               linear   PLN 29-JUL-2004
DEFINITION Zea mays subsp. parviglumis isolate p3 chitinase (chia) gene, complete cds.
ACCESSION  AY532770
VERSION    AY532770.1 GI:48093321
KEYWORDS
SOURCE     Zea mays subsp. parviglumis
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REFERENCE  1 (bases 1 to 1101)
AUTHORS   Tiffin,P.
TITLE     Comparative evolutionary histories of chitinase genes in the genus zeo and family poaceae
JOURNAL   Genetics 167 (3), 1331-1340 (2004)
PUBMED    15280246
REFERENCE  2 (bases 1 to 1101)
AUTHORS   Tiffin,P.
TITLE     Direct Submission
JOURNAL   Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Query Match 71.4%; Score 552.4; DB 8; Length 1094;
Best Local Similarity 82.0%; Pred. No. 2.4e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 104; Gaps 2;

Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGTCGAGCAAGTTTGGCTACTGCGGCACGAC 65
Db 101 GCAGAACTGCGGCTGCCAGCTTAATCTGCTGAGCAAGTTTGGCTACTGCGGCACGAC 160
Qy 66 CGACAGTACTGCGGCAAGCGGTGCCAGTCCGAGTCGGGCGCGTTCGCGGCGCGGTGCGG 125
Db 161 CGACGACTACTGCGGCGACGGTCCAGTCCGCGCGCGTTCGCGGCGCGTTCGCGGCG 211
Qy 126 CGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 185
Db 212 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 271
Qy 186 CGACGCGTCTTCAACGGCATCAAGAACACGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 245
Db 272 CGACGCGTCTTCAACGGCATCAAGAACACGAGCGCGGCGGCGGCGGCGGCGGCGGCG 331
Qy 246 CTACACCGGAGCGGCTTCCTCGAGGCGCATGCGCGCGTACCGCGGCTTCGCGCATGCGG 305
Db 332 CTACACCGGAGCGGCTTCCTGAGCGCGTCAACAGTACCGCGGCTTCGCGCATGCGG 391
Qy 306 CTCCGAGTTCGAGCGGCAAGCGGCGGATGCGCGCTTCTTCGCGCACGCGCAGCGAGAC 365
Db 392 GACGAGGTGGAGGGCAAGCGGCGGATGCGCGCTTCTTCGCGCACGCTCAGCGCAGAC 451
Qy 366 CGGCG-----370
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Qy 751 CCGGGCAACACCTCACTGCT 772
Db 932 CCAGGGCCCAACCTCACTGCT 953

RESULT 9
AY532779
LOCUS 1094 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea mays subsp. parviglumis isolate p13b chitinase (chia) gene,
complete cds.
ACCESSION AY532779
VERSION AY532779.1 GI:48093339
KEYWORDS
SOURCE Zea mays subsp. parviglumis
ORGANISM Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1094)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1094)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA

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TC"

ORIGIN
Query Match 71.4%; Score 552.4; DB 8; Length 1094;
Best Local Similarity 82.0%; Pred. No. 2.4e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 104; Gaps 2;

Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGTCGAGCAAGTTTGGCTACTGCGGCACGAC 65
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Db	212	CGGCGGCGGCGGCGGAGCGGAGCGAGCAGTGGCGGTGCCAAGTGGCTAATGTGCTCAC	271
Qy	186	CGACGCGTCTTCAACCGCATCAAGAACACGAGCGCGGAGCGGCGTGGCGGCGGAGGCGCAAGAACTT	245
Db	272	CGACGCGTCTTCAACCGCATCAAGAACACGAGCGCGGAGCGGCGTGGCGGCGGAGGCGCAAGAACTT	331
Qy	246	CTACACCGGAGCGGCTTCTCGAGGCGATGCGCGGTACCGCGGCTTTCGGCGATGGCGG	305
Db	332	CTACACCGGAGCGGCTTCTCGAGGCGGTCAACAGTACCGCGGCTTTCGGCGATGGCGG	391
Qy	306	CTCCGAGGTGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCACGCCACGCGACGAGAC	365
Db	392	GACGAGGTGGAGGCGAAGCGGAGATGCGCGCTTCTTCGCGCACGCTCACGCGACGAGAC	451
Qy	366	CGGCG-----	370
Db	452	CGGAGCTAAGTTATTACACTTAACCTAACATACGGAAGTACGATGCGAGGACCTTTGATCTGAC	511
Qy	371	-----	371
Db	512	CGACCGATCATCGTCTGACCATGATTTTATCAGATTTCTGCTACATCAGCGAG	571
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LOCUS			
DEFINITION			
Zea mays subsp. parviglumis isolate p6 chitinase (chiA) gene, complete cds.			
ACCESSION			
AY532773			
VERSION			
AY532773.1 GI:48093327			
KEYWORDS			
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ORGANISM			
Zea mays subsp. parviglumis			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
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1 (bases 1 to 1118)			
Tiffin, P.			
Comparative evolutionary histories of chitinase genes in the genus			
Zea and family poaceae			
Genetics 167 (3), 1331-1340 (2004)			
15280246			
REFERENCE			
2 (bases 1 to 1118)			
Tiffin, P.			
Direct Submission			
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,			
1445 Gortner Ave., St. Paul, MN 55108-1095, USA			
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Query Match 71.2%; Score 550.8; DB 8; Length 1118;			
Best Local Similarity 81.9%; Pred. No. 3,9e-62;			
Matches 706; Conservative 0; Mismatches 52; Indels 104; Gaps 2;			
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Qy	66	CGACGAGTACTGCGGCGCAGCGGTCCAGTCCGGCCCGTGCCTGCGGCGCGGTGGCGG	125
Db	164	CGACGCTTACTGCGGCGCAGCGGTGCCAGTCCGGCCCGTGCCTGCGGCGCGGTGGCGG	214
Qy	126	CGGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	185
Db	215	CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	274
Qy	186	CGACGCGTCTTCAACGCGCATCAAGAACACGAGCGCGGAGCGGCGGCGGCGGCGG	245
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Qy	246	CTACACCGGAGCGGCTTCTCGAGGCGCATCCGCGGTACCGCGGCTTTCGCGCATGGCGG	305
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Qy	306	CTCCGAGGTCCAGGCGCAAGCGGAGATGCGCGCTTCTTCGCGCACGCCACGCGACGAC	365
Db	395	GACGAGGTGGAGGCGAAGCGGAGATGCGCGCTTCTTCGCGCACGCTCACGCGACGAC	454
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Db 935 CCAGGCGCCACCTCACTTGTCT 956

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LOCUS Zea diploperennis isolate d1 chitinase (chia) gene, complete cds.  
DEFINITION  
ACCESSION AY532781  
VERSION AY532781.1 GI:48093343  
KEYWORDS  
SOURCE Zea diploperennis  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1107)  
Tiffin, P.  
Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
Genetics 167 (3), 1331-1340 (2004)  
15280246  
2 (bases 1 to 1107)  
Tiffin, P.  
Direct Submission  
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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ORIGIN  
Query Match 70.9%; Score 548.4; DB 8; Length 1107;  
Best Local Similarity 81.6%; Pred. No. 7.9e-62;  
Matches 707; Conservative 0; Mismatches 51; Indels 108; Gaps 2;  
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Qy 126 CGGCGGCGGCGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 185  
Db 206 CGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 265  
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Qy 306 CTCGAGGTCGAGCGCAAGCGGAGATTGCGCGCTTCTTCGCGCAACCGCGCGAGCGAGAC 365  
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Qy 366 CGGCGC----- 370  
Db 446 CGGAGCTAAGTTATTAAACACCTAATTAAACACGGAACCTAGCATGCGAGGACCTTGTATC 505  
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Zea diploperennis isolate d3 chitinase (chiA) gene, complete cds.  
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 Tiffin, P.  
 Comparative evolutionary histories of chitinase genes in the genus  
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 Tiffin, P.  
 Direct Submission  
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 Tiffin, P.  
 Comparative evolutionary histories of chitinase genes in the genus  
 Zea and family poaceae  
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 PUBMED 15280246  
 REFERENCE 2 (bases 1 to 1110)  
 Tiffin, P.  
 Direct Submission  
 TITLE  
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ORIGIN
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Best Local Similarity 81.6%; Pred. No. 7.9e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 108; Gaps 2;

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clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
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JOURNAL Genetics 167 (3), 1331-1340 (2004)
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AUTHORS Tiffin,P.
TITLE Direct Submission
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Tiffin,P.			
Comparative evolutionary histories of chitinase genes in the genus			
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Tiffin,P.			
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Qy	371	-----ATTTCGTACATCAG	386
Db	506	TGACCGACCGATCATCGTCATGTCGACCATGTCATTTTCGATCAGATTTCTGCTACATCAG	565
Qy	387	CGAGGTCAACAAGAGCAACCGCTACTCGACCCCAAGAGGAGGAGTGGCGCGCGCGC	446
Db	566	CGAGATCAACAAGAGCAACCGCTACTCGACCGGCAACAGGCACTGGCGCGTGGCGGC	625
Qy	447	GGGCGAGAGTACTACGGGCGCGCGCGCTCGAGATCTCGTGAACCTACACTACGCGGC	506
Db	626	GGGCGAGAGTACTACGGGCGCGCGCGCTCGAGATCTCGTGAACCTACACTACGCGGC	685
Qy	507	CGCGGGAGGCGCATCGGCTTCGACGCGGCTCGGGGACCCCGCAGGCTGGCGCGGACGC	566
Db	686	CGCGGGAGGACATCGGCTTCAACGGGCTCGCGACCCCAACAGGGTGGCGAGGACGC	745
Qy	567	CGTGTGCGGTTCAAGGCGCGCTCTGTTCTGATGAACAAAGTGCACCGTGTGATGCC	626

Db	746	CGTGATCCGGTTCAGACGGCGCTCTGGTTCTGGATGAACAACGTGCACCCGTGTGATGCC	805
Qy	627	GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAACGGGAACAA	686
Db	806	GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGCAACGGGAACAA	865
Qy	687	CCCCGCCAGATGAACGGCGGCTCGGCTACTACAGGCAGTACTGCCGCCAGCTCGGGGT	746
Db	866	CCCCGCCAGATGAACGGCGGCTCGGCTACTACAGGCAGTACTGCCGCCAGCTCGGGGT	925
Qy	747	CGACCCGGGCAACACCTCAGCTGCT	772
Db	926	CGACCCGGGCAACCTCAGCTGCT	951

Search completed: May 23, 2005, 14:20:08  
Job time : 2526.67 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:19:13 ; Search time 129.26 Seconds  
(without alignments)

3253.303 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQCGQPNVCCSKFGVCG.....GYTRYCQLGVDPNNLTC 257

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO gpool/US10692367/runat 20052005 172255 20038/app query.fasta\_1.846  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297.5	89.4	1094	4	US-09-522-714-1
2	861.5	59.3	1048	4	US-09-522-714-21
3	825.5	56.9	1079	1	US-08-181-271A-37
4	825.5	56.9	1079	1	US-08-449-315-37
5	825.5	56.9	1079	1	US-08-444-803-37
6	825.5	56.9	1079	1	US-08-449-043-37
7	825.5	56.9	1079	1	US-08-456-265A-37
8	825.5	56.9	1079	1	US-08-455-416-37
9	825.5	56.9	1079	1	US-08-455-244-37
10	825.5	56.9	1079	1	US-08-454-876-37
11	825.5	56.9	1079	1	US-08-457-364-37
12	825.5	56.9	1079	2	US-08-456-262-37

13	825.5	56.9	1079	2	US-08-456-240-37	Sequence 37, Appl
14	825.5	56.9	1079	2	US-08-455-736-37	Sequence 37, Appl
15	825.5	56.9	1079	2	US-08-971-217-37	Sequence 37, Appl
16	825.5	56.9	1079	3	US-09-350-600-37	Sequence 37, Appl
17	825.5	56.9	1079	4	US-09-906-234-37	Sequence 37, Appl
18	825.5	56.9	1116	4	US-09-522-714-31	Sequence 31, Appl
19	727.5	50.1	881	4	US-09-522-714-29	Sequence 29, Appl
20	622.5	42.9	943	2	US-08-475-427-15	Sequence 15, Appl
21	622.5	42.9	943	2	US-07-842-165-15	Sequence 15, Appl
22	619.5	42.7	1152	1	US-08-047-413-10	Sequence 10, Appl
23	619.5	42.7	1152	3	US-08-229-050-10	Sequence 10, Appl
24	619.5	42.7	1152	3	US-08-801-563-10	Sequence 10, Appl
25	605	41.7	1225	1	US-08-286-020-1	Sequence 1, Appl
26	605	41.7	1225	1	US-08-603-919-1	Sequence 1, Appl
27	585.5	40.3	905	2	US-08-475-427-14	Sequence 14, Appl
28	585.5	40.3	905	2	US-07-842-165-14	Sequence 14, Appl
29	581.5	40.0	1151	1	US-07-704-288C-2	Sequence 2, Appl
30	581.5	40.0	1151	1	US-08-093-372-1	Sequence 2, Appl
31	581.5	40.0	1151	1	US-08-379-259-2	Sequence 4, Appl
32	579	39.9	1153	2	US-08-475-427-4	Sequence 4, Appl
33	579	39.9	1153	2	US-07-842-165-4	Sequence 4, Appl
34	579	39.9	1153	3	US-08-448-398-6	Sequence 6, Appl
35	579	39.9	1163	2	US-08-475-427-12	Sequence 12, Appl
36	579	39.9	1163	2	US-07-842-165-12	Sequence 12, Appl
37	579	39.9	1863	1	US-08-525-507-16	Sequence 16, Appl
38	579	39.9	1863	2	US-08-475-427-9	Sequence 9, Appl
39	579	39.9	1863	2	US-07-842-165-9	Sequence 9, Appl
40	578.5	39.8	960	4	US-09-534-229C-8	Sequence 8, Appl
41	573	39.5	972	4	US-09-534-229C-7	Sequence 7, Appl
42	543	37.4	1163	4	US-09-522-714-5	Sequence 5, Appl
43	538	37.1	3012	2	US-08-475-427-5	Sequence 5, Appl
44	538	37.1	3012	2	US-07-842-165-5	Sequence 5, Appl
45	532	36.6	1318	3	US-09-125-891-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-522-714-1  
; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-09-522-714-1

Alignment Scores:  
Pred. No.: 2.26e-121 Length: 1094  
Score: 1297.50 Matches: 229  
Percent Similarity: 93.33% Conservative: 9  
Best Local Similarity: 89.80% Mismatches: 10  
Query Match: 89.36% Indels: 7  
DB: 4 Gaps: 1

US-10-692-367-12 (1-257) x US-09-522-714-1 (1-1094)

QY 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22

Db 150 CAGAACTGCGCTGCCAGCAACGATGCTGACGAGATTGGTACTGCGGCACGACC 209  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 210 GACGAGTACTCGCGGACGCGGTGCGAGTCGCGGCGCGCTCGCGCGCGCGGCGCAGC 269  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 270 AGTGGCGGC-----GCTGTGCGAAGCGTGTAGCGTCTGCTACCC 308  
Qy 63 AspAlaPhePheAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 309 GGCTCTCTTCAACGGCATCAAGAGCCAGCGCGGAGCGGTGCGAGGGCAAGACTTC 368  
Qy 83 TyrThrArgSerAlaPheGluGluAlaAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 369 TACACCGGAGCGGTTCCTGAGCGCGCTCAAGCGCTACCCAGGCTTCGCGCATGGCGGG 428  
Qy 103 SerGluValGluArgLysArgGluAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 429 TCGCAGGTGCGGCAAGCGCGAGATCGCCGCTTCTTCGCGCAGCGCCACGACGAGACC 488  
Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrIys 142  
Db 489 GGGCATTTCCTACTACATCAGCGAGATCAACAGAGCAACGCTACTGCGACCCGACCAAG 548  
Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162  
Db 549 AGGCAGTGGCGGTGCGCGCGCGGCGAGAACTACTACGCGCGCGCGCTGCGAGTCTCG 608  
Qy 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182  
Db 609 TGGAACTCAACTACGCGCGCGCGGAGGCGCATCGCTTCGACGGCTTCGGGACCC 668  
Qy 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMetAsn 202  
Db 669 GGCAGGTGGCGCGGACGCGGTGTGCGCTTCAAGGCGCGCTCTGGTCTCGATGAAC 728  
Qy 203 AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 222  
Db 729 AGCGTGCAAGCGGTGTGTCGCGCGGCGGTTCGCGCGCACACCGCGGCGCATCAACGCGGCG 788  
Qy 223 LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln 242  
Db 789 CTCGAGTCCGCGGGAACACCCCGCCGAGATGAACGCGCGCGCTCGGCTACTACAGGAG 848  
Qy 243 TyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 849 TACTGCCCGCAGCTCGCGGTGCGACCCCGGCGCCCACTCACCTGC 893

## RESULT 2

US-09-522-714-21  
; Sequence 21, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21

; LENGTH: 1048  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (42)...(854)  
US-09-522-714-21

## Alignment Scores:

Pred. No.: 1,79e-77 Length: 1048  
Score: 861.50 Matches: 155  
Percent Similarity: 71.71% Conservative: 30  
Best Local Similarity: 60.08% Mismatches: 58  
Query Match: 59.33% Indels: 15  
DB: 4 Gaps: 3

US-10-692-367-12 (1-257) x US-09-522-714-21 (1-1048)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 117 CAGAACTGCGGTCGCGGTGCGGCTGCTGTCAGCGCGGTTCGGGTACTCGGAGCGGCG 176  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 177 GAGGACTACTGCGGCGCGGTGCGAGTTCGCGCGCTGC----- 215  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 216 -----GACGTGCGGAGACCAACACGCTCCGCGGCGAGCATCGTGACG 260  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 261 CCGGCTCTTCGAGCGGCTCTCGCGAGCGCGCGCTCGTGCGAGGCCCAACGCGCTTC 320  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 321 TACACCGCGAGCGCTCTCTCGCGCGCGGCTACTACCGCGGCTTCGCGCGCGCACCGGC 380  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 381 ACCGTGACGACTCAACAGCGGAGATCGCGCTTCTTCGCGCAACGCGCAACACGAGACC 440  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 441 ATAAAGTTCGTACTACATCAAGAGATCGAGCGGCGGAGCAAGACTACTGCGAGCGGAAC 500  
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 501 AACACGCGAGTGGCGGTGCGAGCGGGAAGGGGTACTACGCGCGCGCGCTCGAGATC 560  
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 561 TCCTGGAACTCAACTACGCGGCGCGGCGGAGCATCGGCTTCGAGCGGCTCGGCGAC 620  
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMet 201  
Db 621 CCGAGCGGTCGCGCGCGCGCGGTGCTCGGTTCCGCTTCGCGCTCGGTACTGGATG 680  
Qy 202 AsnAsnValHisArg-----ValMetProGlnGlyPheGlyAlaThrIleArgAlaIle 219  
Db 681 AACACGTCAGCGGCGCATGCTCTCGGCGCAGGCTTCGCGCGCACCATCCGCGGCGCATC 740  
Qy 220 AsnGlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 239  
Db 741 AACGCGCGCTCGAGTGCAGCGGCAAGACCCCAACTCCCGTCAACACCGCGTGCCTTAC 800  
Qy 240 TyrArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 801 TACAAGCAGTTCGCGAGGATTCGCGGTGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 854

## RESULT 3

US-08-181-271A-37  
; Sequence 37, Application US/08181271A  
; Patent No. 5614395  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.



Db 708 ---ATGAGTACGCTGTAATTCGGTGCAGTCAACGAGGATGGATATAGA 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 765 GACTATTGTGCACAGCTTGGTGTGGACCTGGTCTTAACCTTAGTTGC 812

## RESULT 4

US-08-449-315-37  
Sequence 37, Application US/08449315  
Patent No. 5650505  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr. Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESS: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,315  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/769,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-315-37

Alignment Scores:  
Pred. No.: 7,89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-449-315-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGlyThr 22  
Db 93 CAAAACTGCGGTGCGCTCCAAACCTCTGTTCAGTCAGTTCGTTACTGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42  
Db 153 GATGCATACCTGCGGTGTGGATGCCGATCAGTCTCTGTAGA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62  
Db 195 -----GGTAGTGGAAACCCGACCGCGGTGCGGTGCGTAGCATTTGTGACA 239  
Qy 63 AspalapheAsnGlylleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGGTTCTTTTAAACAATATTATCAACAAGCTGTAATGTTGCGCGGGAAGATTTC 299  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 300 TACACCGGTGACTCTTTTCGTTAACGCCGCTAATCTTCCCACTTTCGCAATCTCTGT 359  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122  
Db 360 ACC-----AGACGTGAAATTCCTACCATGTTTGTCTCATTTTCACCTCACGAGACC 407  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 408 GGACATTCTCTTACATAGAGAGATTAAACGAGCAACACGTAATACTACTACTGCCAGAGCAGC 467

Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 468 AACACAAATACCCATGTCACCGCGGAAAGAGCTACTTCGGTTCGGTCCGATCCAACTA 527  
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 528 TCATGGAACACTACAGGCGGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 587  
Qy 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201  
Db 588 CCCGAACCTGTGGTAGCAACCAACTGTAGCTTCAGTCGGGTTCGTTGGTATG 647  
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAGCGCGGTTCCTGAACAGGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTrpArg 241  
Db 708 ---ATGGAATGTAACTGGTGAATTCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 765 GACTATTGGACAGCTTGGTGTGGACCTGCTCCTAACCTTAGTTGC 812

## RESULT 5

US-08-444-803-37  
Sequence 37, Application US/08444803  
Patent No. 5654414

## GENERAL INFORMATION:

APPLICANT: Rvals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

## CORRESPONDENCE ADDRESS:

ADDRESS: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,803  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992

APPLICANT: Rvals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-444-803-37

Alignment Scores:  
Pred. No.: 7,89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-444-803-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGCGGTGCGCTCCAAACCTCTGTTGTCAGTCAGTTCGGTTCGTTACCGAC 152  
Qy 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 153 GATGCATACCTCGGTGTTGGATGCCGATCAGTCTCTTTGTAGA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 195 -----GGTAGTGAACCCCGACCGAGGGTCGGTCGTTGATTTGTGACA 239

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Qy 63 AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnSph 82
Db 240 CAAGGTTCTTTACAAATATTATCAACCAAGCTGGTAATGGTTCGGGGGAAAGATTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaLysProGlyPheAlaHisGlyGly 102
Db 300 TACACCGTGACTCTTTCGTTAACCGCGCTAATACTTCCCAACTTTGCCAATTCGT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaLysPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTTGCTACCAATGTTTGTCTATTTCACTCACGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTCTCTACATAGAGAGATTAAACGGACCAACGCTAATACTACTGCCAGAGACG 467
Qy 142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACAAATACCATGTCACCGCGGAAAGGCTACTTCGGTGTGGTTCGATCCAACTA 527
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACGACGCGTGTGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyrMet 201
Db 588 CCGAAGTGTGGTAGACCAACCACTGTACTTTCAGTCGGGTTGTGGTTTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGTTCTCAACCAAGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241
Db 708 ---ATGGAATGTAAACGGTGGTAATTCGGTCCAGCTCAACGCAAGGATTGGATCTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGACAGCTTGGTGTGAGACCTCGTCTCTAACCTTAGTTGC 812

RESULT 6
US-08-449-043-37
; Sequence 37, Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-449-043-37

Alignment Scores: 7.89e-74 Length: 1079
Pred. No.: 825.50 Matches: 146
Score: 69.92% Conservative: 33

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Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-449-043-37 (1-1079)

QY 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
DB 93 CAAAACTCGGTGGCTTCTGAACTCTGTTGAGTCAGTTCGGTTACTGGTACCGAC 152  
QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
DB 153 GATGCATACCTCGGTGGTGGATGCCATCAGTCTCTGTAGA----- 194  
QY 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
DB 195 -----GGTAGTGGAGACCCCGGAGGTCGGTGGTAGCATTTGTGACA 239  
QY 63 AspAlaPheAenGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
DB 240 CAAGGTTTCTTAAACATATTATCAACCAAGCTGGTATGTTGGCGGGGAAAGATTTC 299  
QY 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
DB 300 TACACCGGTGACTCTTGTAAACCGCTTAATCTTCCCAACTTGGCAATCTCTGTT 359  
QY 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122  
DB 360 ACC-----AGACGTGAAATGCTACCATGTTTGTCTCATTTCACTCAGGAGACC 407  
QY 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
DB 408 GGACATTTCTGCTACATAGAGATTAAACGGAGCAACACTACTCTGCGAGCAGC 467  
QY 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
DB 468 AACACACATACCATCTGTGACCCGGGAAAGGCTACTTGGTCTGTCGATCAACTA 527  
QY 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
DB 528 TCATGGAACTACAACACTACGAGCGGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 587  
QY 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201  
DB 588 CCCGAATTTGGGTAGACCAACCACTGTAGCTTTCAGTCCGCTGTTGTCGTTTGGATG 647  
QY 202 AsnAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
DB 648 AATAGCTTAGCCCGGTCTGCAACCAAGGGTTTGAGCCACCATTAGAGCTATTATGGA 707  
QY 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241  
DB 708 ---ATGGAATGTAACGGTGGTAATTCGGTGCAGTCAGTCAACGCAAGGATTGGATAC 764  
QY 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
DB 765 GACTATTGTGACAGCTTGGTGTGGACCCCTGCTCTCAACCTTAGTTGC 812

## RESULT 7

US-08-456-265A-37  
; Sequence 37, Application US/08456265A  
; Patent No. 5767369  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Ryals, John A.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Scinson, Jeffrey R.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,265A  
; FILING DATE: 31-MAY-95  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/181,271  
; FILING DATE: 13-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-456-265A-37

Alignment Scores:		
Pred. No.:	7,898-74	1079
Score:	825.50	146
Percent Similarity:	69.92%	Conservative: 30
Best Local Similarity:	57.03%	Mismatches: 63
Query Match:	56.85%	Indels: 17
DB:	16	Gaps: 4

US-10-692-367-12 (1-257) x US-08-456-265A-37 (1-1079)

Qy	3	GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr	22
Db	93	CAAAATCGCGTTGCGCTCCAAACCTCTGTGTGCAGTTCGGTTACTGTGTGTACCGAC	152
Qy	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly	42
Db	153	GATGCATCTCGGTGTGGATGCCGATCAGTCTCTTGAGA-----	194
Qy	43	GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr	62
Db	195	-----GGTAGTGGAAACCCCGACCGGAGGGTCGGTAGCATTTGTGACA	239
Qy	63	AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe	82
Db	240	CAAGGTTTCTTTAAACAATATTATCAACCAAGCTGGTAATGTTGCGCGGGAAAAAGATTTC	299
Qy	83	TyrThrArgSerAlaPheLeuGluAlaIleAlaIatYrProGlyPheAlaHisGlyGly	102
Db	300	TACACCGGTGACTCTTTCGTTAAACCGCGCTAATACTTTCGCCAACTTTGCCAAATTTCTGTT	359
Qy	103	SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr	122
Db	360	ACC-----AGACGTGAATTTGCTACCATGTTTGCTCATTTCACTCACGAGACC	407
Qy	123	GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr	141
Db	408	GGACATTTCTGCTACATAGAAGAGATTAAACGGAGCAACACAGTAACACTACTGCCAGAGCAGC	467
Qy	142	LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle	161
Db	468	AACACACAATACCCATGTGCACCGGAAAGAGCTACTTCGGTGTGGTCCGATCCAACTA	527
Qy	162	SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp	181
Db	528	TCATGGAACTACACTACGAGCGTGGTCAAAGTCTCGGTCTTGACCTTCTACGCCAG	587
Qy	182	ProGlyArgValAlaArgAspAlaValIleAlaPheLysAlaAlaLeuTrpPheTrpMet	201
Db	588	CCCGAACTTGTGGGTAGCAACCCAACTGTGTAGCTTTTCAGTCCGGGTTGTGGTTGGATG	647
Qy	202	AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly	221
Db	648	AATAGCGTAAGCCCGGTTCTGHAACCAAGGTTTGGAGCCACCATTAGACTATTATATGGA	707
Qy	222	AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg	241
Db	708	---ATGGAAATGTACGGTGGTAATTCGGTGCAGTCACACGCAAGGATTGGATACTATAGA	764
Qy	242	GlnTyrCysArgGlnLeuGlyValAspProGlyLysAsnAsnLeuThrCys	257
Db	765	GACTATTCTGGACAGCTGTGTGGACCCCTGCTCTTAACCTTAGTTATGTC	812

## RESULT 8

US-08-455-416-37  
; Sequence 37, Application US/08455416  
; Patent No. 5777200  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.



```

; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/POCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-416-37

Alignment Scores:
Pred. No.: 7,89e-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservative: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-455-416-37 (1-1079)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThr 22
Db 93 CAAAACTGGGTTGCGCTCCAAACTCTGTTGCGAGTCAGTTCGGTTACTGGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42
Db 153 GATCATACTCGCGTGTGGATCGGATCAGTCTCTGTGTA-----194
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 195 -----GGTAGTGGAAACCCCGACCGGCGGTCGTCGGTAGCATGTGACA 239
Qy 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 82
Db 240 CAAGTTTCTTAAATATTTATCAACCACTGATGTTGCGGGGGAAGATTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGly 102
Db 300 TACACCGGTGACTCTTTCGTTAAGCGCGCTAATCTTTCCCAACTTTGCCAATTCGTT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTTGCTACCATGTTTGTCTATTTCACTCAGGAGCC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAen--LysSerAenAlaTyrCysAenProThr 141
Db 408 GGACATTTCTGTACATAGAGATTTAAGGACCAACGTAACGTAACGTAACGTAACGTAACG 467
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCATCGTGCACCGGGAAGAGCTACTTCGGTCTGTCGATCAACTA 527
Qy 162 SerTrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACGGGCGGTGGTCAAAAGTCTCGGTCTTTCGCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 588 CCCGAATTGTTGGGTAGCAACCACTGTAGCTTTCAGTTCGGGTTTGTGTTTGTGATG 647
Qy 202 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGly 221
Db 648 AATAGCGTAGGCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGGA 707
Qy 222 AlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrArg 241

; Db 708 ---ATGGAATGTAACGGTGTAAATTCGGTGCAGTCAACGCAAGGATTTGGATCTATAGA 764
; Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
; Db 765 GACTATTGTGACAGCTTGTGTGGACCCCTGGTCTTAACCTTAGTTGC 812

RESULT 9
US-08-455-244-37
; Sequence 37, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
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;
; FILING DATE: 20-OCT-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-455-244-37

Alignment Scores:
Pred. No.: 7,89e-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservative: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-455-244-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGlyThr 22
Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTCAGTTCAGTTCGTTTACTGTGGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42
Db 153 GATGCATCTCGGTTCGTTGGATGCGATCAGTCTCTGTAGA----- 194
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyAlaAsnValAlaAsnValThr 62
Db 195 -----GGTAGTGGAAACCCGACCGAGGTCGTCGTCGATGTCGAC 239
Qy 63 AsplapheAsnGlyIleLysAsnGlnAlaGlySerGlyGlyLysAsnPhe 82
Db 240 CAAGGTTTCTTTTAAACAATATTATCAACCAAGCTGGTAAATGGTTCGCGGGGAAAGATTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCGTCTCTTCGTTTACCGCTTAATCTTCCCACTTTGCCAATCTCTGTT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAAATTTGCTACCATGTTTGTCTCACTTCACGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTTCTCTACATAGAGATTATACGGCAACAGTAACTACTACTGCGAGCAGC 467

142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCCTATGTCACCGGAAAGGCTACTTCGGTCTGTCGATCCAACTA 527
Qy 162 SerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACCACTACGGAGCGTGTGGTCAAAAGTCTCTGGTCTTGTACCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyrMet 201
Db 588 CCCGAATCTGTGGTAGCAACCACTGTAGCTTTAGTTCGGTTCGTTTGTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGGTTCTGAAACCAAGGTTTGGAGCCACCATTAGAGCTATTAAATGGA 707
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241
Db 708 ---ATGGAATGTAACGGTGGTAATTCGGTGTGCACTCAACGCAAGGATTTGGATATATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGCACAGCTTGTGTGGACCCCTGCTTAACCTTAGTTGC 812

RESULT 10
US-08-454-876-37
; Sequence 37, Application US/08454876
; Patent No. 5804693
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,876
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA: US 07/937,197
; APPLICATION NUMBER: 6-NOV-1992
```





APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,262  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-456-262-37  
Alignment Scores:  
Pred. No.: 7.89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 2 Gaps: 4  
US-10-692-367-12 (1-257) x US-08-456-262-37 (1-1079)  
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACCTGGCGTTCGGCTCCAAACCTCTGTTCAGTCAGTTCGGTTCGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 153 GATGCATACCTGGCGTGTGGATGCCGATCAGTCTCTTTGTA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 195 -----GGTAGTGGAAACCCCGACCGAGGGTCGGTCGGTAGCATTTGTGACA 239  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGGTTTCTTTAAACATATATTATCAACAGCTGCTGTAATGTTGCGGGGGAAGAATTC 299  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 300 TACACCGTGACTCTTTTCGTTAACCGCCTAATCTTTCCCACTTTGCCAATTTCTGT 359  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 360 ACC-----AGACGTGAAATTTGCTACCATGTTGTCTCATTTTCACTCACGAGACC 407  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 408 GGACATTTCTGTACATAGAGAGATTAAACGGACCAACCGTAACCTACTCTCCAGAGCAGC 467  
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 468 AACACACAATACCCATGTGCACCGGGAAGAGCTTTCGTCGTGGTCCGATCCAACTA 527  
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 528 TCATGGAACTACACTACCGGAGCGTGTGGTCAAAAGTCTCGGTCTTTCACCTTTCTAGCC 587  
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201  
Db 588 CCCGAACCTTGGGTAGCAACCCCACTGTAGCTTTCAGGTTCGGGTTTGTGGTTTGGATG 647  
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAAGCGCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArg 241  
Db 708 ---ATGGAATGTAACGGTGGTAAATTCGGTGCAGTCAACGACGAGGATGGATATAGATA 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257

Db 765 GACTATTGTGACAGCTTGGTGTGGACCCCTGGTCTTAACCTTAGTTGC 812

RESULT 13

US-08-456-240-37

Sequence 37, Application US/08456240

Patent No. 5856154

GENERAL INFORMATION:

APPLICANT: Ryals, John A.

APPLICANT: Alexander, Danny C.

APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.

APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian

APPLICANT: Meins, Jr., Frederick

APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc

APPLICANT: Payne, George B.

APPLICANT: Sperison, Christoph

APPLICANT: Stinson, Jeffrey R.

APPLICANT: Uknes, Scott J.

APPLICANT: Ward, Eric R.

APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,240

FILING DATE: 31-MAY-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/580,431

FILING DATE: 7-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1079 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-456-240-37

Alignment Scores:

Pred. No.: 7.89e-74 Length: 1079

Score: 825.50 Matches: 146

Percent Similarity: 69.92% Conservative: 33

Best Local Similarity: 57.03% Mismatches: 60

Query Match: 56.85% Indels: 17

DB: 2 Gaps: 4

US-10-692-367-12 (1-257) x US-08-456-240-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22

Db 93 CAAAACTGCGGTTGCGCTCCAAACCTCTGTTCAGTCAGTTGCGTTACTGTGGTACCGAC 152

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42

Db 153 GATGCATACGCGGTGTGGATCCGATCAGTCTCTGTAGA----- 194

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62

Db 195 -----GGTAGTGGAAACCCCGAGGCGTCCGTCGGTAGCATTTGTGACA 239

Qy 63 AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82

Db 240 CAAGGTTTCTTTAACAATATTATCAACCAAGCTGGTAATGTTGCGGGGAAAGATTC 299

Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIaIaIaIaIaIaIaIaIaIaIaIa 102

Db 300 TACACCGTGACTCTTTCGTTAACCGCGCTAATACTTTCCTCCCACTTTGCCAATTCGTT 359

Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122

Db 360 ACC-----AGACGTGAATTTGCTACCATGTTTGTCTCATTTCACTCAGGAGACC 407

Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaIaIaIaIaIaIaIa 141

Db 408 GGACATTTCTGTACATAGAGAGATTAAACGAGCAACACGAGCACTACTGCGAGAGCAGC 467

Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161

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Db 528 TCATGGAACTCAACTACGGAGCGTGGTCAAGTCTCGGTCTTGACCTTCTACGCCAG 587  
Qy 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201  
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Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAAGCCCGGTTCTGAACCAAGGTTTGGAGCCACCATTTAGAGCTATTAAATGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTrpArg 241  
Db 708 ---ATGGAAATGTAACGGTGGTAATTCGGTGCAGTCAACGAAGATTGGATCTATAGA 764  
Qy 242 GlnTrpCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 765 GACTATTGTGCAGACCTTGGTGTGGACCTCGTCTTAACCTTAGTTGC 812

## RESULT 14

US-08-455-736-37  
; Sequence 37, Application US/08455736  
; Patent No. 5880328  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,736  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-1994  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-455-736-37  
Alignment Scores:  
Pred. No.: 7.89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 2 Gaps: 4  
US-10-692-367-12 (1-257) x US-08-455-736-37 (1-1079)  
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGGGTTGGCTCCAAACCTCTGTTGCAGTCAGTTCCGTTACTGTGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 153 GATGCATACTCGCGTGTGGATGCCGATCAGTCCCTTTGTAGA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 195 -----GGTAGTGAACCCCGACCGAGGTCGTCGCTAGTAGATTGTGACA 239  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGGTTTCTTTTAAATAATTATCAACCAAGCTGTTAATGTTGCGCGGGAAGATTTC 299

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Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCGGTGACTCTTTCGTTAAACCGCTTAATCTTCCCAACTTTGCCAATCTGTT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTCGTACCATGTTTGTCTATTTCACTCACGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTTCTCTACATAGAGAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGC 467
Qy 142 LysArgGlnTyrProCysAlaAlaGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACATACCATGTCACCGGAAAGAGCTACTTCGGTCTGTCGATCCAACTA 527
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACGGAGCGTGTGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMet 201
Db 588 CCCGAACCTTGGGTGAGCAACCCCACTGTACCTTTCAGGTCGGTGTGTTGGTTTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAAGCGGTTCTGAACCAAGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707
Qy 222 AlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241
Db 708 --ATGGAATGTAACGGTGGTAATTCCTCGTGCAGTCAACGCAAGGATTGGATCTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGACAGCTTGTGTGAGCCCTGTCCTTACCTTAGTTGTC 812

RESULT 15
US-08-971-217-37
; Sequence 37, Application US/08971217
; Patent No. 5942662
; GENERAL INFORMATION:
; APPLICANT: Rvals, John A.
; APPLICANT: Rvals, Christian
; APPLICANT: Friedrich, Leslie
; APPLICANT: Beck, James
; APPLICANT: Uknes, Scott
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5942662artis Corporation
; STREET: 3054 Cornwallis Road, P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,217
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,364
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
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; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-971-217-37

Alignment Scores:
Pred. No.: 7,89e-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservatives: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 2 Gaps: 4

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Db 93 CAAAACTCGCGTTCGGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTACTGTGTGACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 153 GATGCATACCTCGCGTGTGGATGCCGATCAGGTCTCTGTGATA----- 194
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Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
Db 195 -----GGTAGTGGAAACCCCGAGGGTGGTGGTAGCATTTGTGACA 239
Qy 63 AspAlaPhePheAsnGlyIleIysAsnGlnAlaGlySerGlyCysGluGlyIysAsnPhe 82
Db 240 CAAGGTTTCTTAAACAATATTATCAACCAAGCTGTAATGGTTGCCGGGGAAAGATTTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCGGTACTCTTTCGTTAAGCCGCTAATACTTTCCCAACTTTGCCCAATTCTGTT 359
Qy 103 SerGluValGluArgIysArgGluIleAlaPhePheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTCCTACCATGTTTGCTCATTTTCACCTCAGGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn--LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTTCTGTACTAGTAGAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGC 467
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnIysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCCCATGTGCACCGGAAAAGGCTACTTCGGTGTGGTCCGATCCAACTA 527
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACACTACGGAGCGTGTGGTCAAAAGTCTCGGTCTTGACCTTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 588 CCGMACTTGTGGTAGCAACCCAACTGTAGCTTTCAGGTGGGTTTGTGGTTTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGTTCTGAAACCAAGSGTTTGGAGCCACCATTAGAGCTATTAAATGA 707
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241
Db 708 ---ATGGAATGTAACGGTGGTAATTCCGGTGCAGTCAACGCAAGGATTGGATACTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 765 GACTATTGTGACAGCTTGGGTGGACCCCTGGTCTTAACCTTAGTTGC 812
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Job time : 135.26 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: May 23, 2005, 19:25:43 ; Search time 414.647 Seconds  
(without alignments)  
3800.840 Million cell updates/sec

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Perfect score: 1452  
Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRQYRQLGVDENLTC 257

Scoring table:  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10692367 @CGN 1 1 456 @runat 20052005 172257 20130  
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-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgm2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgm2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgm2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq\*
- 4: /cgm2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgm2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgm2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq\*
- 7: /cgm2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgm2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgm2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgm2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq\*
- 11: /cgm2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgm2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgm2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq\*
- 14: /cgm2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq\*
- 15: /cgm2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq\*
- 16: /cgm2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq\*
- 17: /cgm2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq\*
- 18: /cgm2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq\*
- 19: /cgm2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq\*
- 20: /cgm2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq\*
- 21: /cgm2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq\*
- 22: /cgm2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1452	100.0	771	18	US-10-389-432B-11	Sequence 11, Appl
2	1452	100.0	774	19	US-10-692-367-11	Sequence 11, Appl
3	1435	98.8	771	18	US-10-389-432B-29	Sequence 29, Appl
4	1435	98.8	771	18	US-10-389-432B-33	Sequence 33, Appl
5	1435	98.8	774	19	US-10-692-367-29	Sequence 29, Appl
6	1435	98.8	774	19	US-10-692-367-33	Sequence 33, Appl
7	1405	96.8	774	19	US-10-692-367-71	Sequence 71, Appl
8	1382.5	95.2	768	18	US-10-389-432B-59	Sequence 59, Appl
9	1382.5	95.2	771	19	US-10-692-367-59	Sequence 59, Appl
10	1382	95.2	771	19	US-10-389-432B-45	Sequence 45, Appl
11	1382	95.2	774	19	US-10-692-367-45	Sequence 45, Appl
12	1377	94.8	771	18	US-10-389-432B-65	Sequence 65, Appl
13	1377	94.8	774	19	US-10-692-367-65	Sequence 65, Appl
14	1373.5	94.6	768	18	US-10-389-432B-61	Sequence 61, Appl
15	1373.5	94.6	771	19	US-10-692-367-61	Sequence 61, Appl
16	1366.5	94.1	768	18	US-10-389-432B-47	Sequence 47, Appl
17	1366.5	94.1	771	19	US-10-692-367-47	Sequence 47, Appl
18	1365.5	94.0	771	19	US-10-692-367-73	Sequence 73, Appl
19	1363	93.9	771	18	US-10-389-432B-63	Sequence 63, Appl
20	1363	93.9	774	19	US-10-692-367-63	Sequence 63, Appl
21	1361	93.7	771	18	US-10-389-432B-23	Sequence 23, Appl
22	1361	93.7	771	18	US-10-389-432B-37	Sequence 37, Appl
23	1361	93.7	774	19	US-10-692-367-23	Sequence 23, Appl
24	1361	93.7	774	19	US-10-692-367-37	Sequence 37, Appl
25	1356.5	93.4	765	19	US-10-692-367-67	Sequence 67, Appl
26	1353.5	93.2	750	18	US-10-389-432B-43	Sequence 43, Appl
27	1353.5	93.2	753	19	US-10-692-367-43	Sequence 43, Appl
28	1351.5	93.1	771	19	US-10-692-367-83	Sequence 83, Appl
29	1342	92.4	777	18	US-10-389-432B-39	Sequence 39, Appl
30	1342	92.4	780	19	US-10-692-367-39	Sequence 39, Appl
31	1339	92.2	780	19	US-10-692-367-75	Sequence 75, Appl
32	1338.5	92.2	753	19	US-10-692-367-81	Sequence 81, Appl
33	1333.5	91.8	762	18	US-10-389-432B-25	Sequence 25, Appl
34	1333.5	91.8	765	19	US-10-692-367-25	Sequence 25, Appl
35	1333	91.8	840	15	US-10-259-165-762	Sequence 762, App
36	1333	91.8	1138	17	US-10-425-114-30480	Sequence 30480, A
37	1333	91.8	1530	18	US-10-425-115-135817	Sequence 135817, A
38	1332	91.7	774	19	US-10-692-367-7	Sequence 7, Appl
39	1332	91.7	845	18	US-10-389-432B-7	Sequence 7, Appl
40	1323.5	91.2	750	18	US-10-389-432B-51	Sequence 51, Appl
41	1323.5	91.2	753	19	US-10-692-367-51	Sequence 51, Appl
42	1318.5	90.8	753	19	US-10-692-367-69	Sequence 69, Appl
43	1318.5	90.8	768	18	US-10-389-432B-41	Sequence 41, Appl
44	1318.5	90.8	771	19	US-10-692-367-41	Sequence 41, Appl
45	1315.5	90.6	750	18	US-10-389-432B-35	Sequence 35, Appl

#### ALIGNMENTS

RESULT 1  
US-10-389-432B-11  
; Sequence 11, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasseer  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; TITLE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 771

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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-11

Alignment Scores:
Pred. No.: 1.17e-166 Length: 771
Score: 1452.00 Matches: 257
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

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DB 1 TCGATGCAGAACTGCGGCTGCCAGCAACGATGCTCGGCGCCGCTCGCGCGCGGT 120
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTCGAGTGCAGCAAGTTTGGCTACTCGGC 60
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTTCTTCAACGGCATCAAGAACGAGCGGCGGAGCGGTGCGAGGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTATCCCGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCCGAGGTGCGCGCGAGCGCGAGATTGCGCGCTTCTCGCGACGCCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCGTGCAG 480
QY 161 IleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTGTGGAACACTACACTACGGGCGCGCGGAGGCGCATCGGCTTTCAGCGGCTCGGG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyr 200
DB 541 GACCCCGGCGAGGTGGCGGCGAGCGCGGTTTCAAGGCGCGCGCTCTGTTCTGG 600
QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
DB 601 ATGAACAACGTCACCGTGTGATGCGCGAGGCGTTCGCGCGCCACCATCAGGCGCCATCAAC 660
QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
DB 661 GCGCGCTCTCGAGTGCACCGGAGCAACCCCGCGCGAGATGAGCGCGCGGTGCGGTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
DB 721 AGGCGAGTACTGCGCGCAGCTCGCGCTCGACCGCGGCAACCAACCTCACCTGC 771

RESULT 2
US-10-692-367-11
; Sequence 11, Application US/10692367
; Publication No. US20050050595A1
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; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-11

Alignment Scores:
Pred. No.: 1.17e-166 Length: 774
Score: 1452.00 Matches: 257
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-10-692-367-12 (1-257) x US-10-692-367-11 (1-774)
QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGCGGCTGCCAGCAACGATGCTCGGCGCCGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTCGAGTGCAGCAAGTTTGGCTACTCGGC 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTTCTTCAACGGCATCAAGAACGAGCGGCGGAGCGGTGCGAGGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTATCCCGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCCGAGGTGCGCGCGAGCGCGAGATTGCGCGCTTCTCGCGACGCCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGGTGCAG 480
QY 161 IleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTGTGGAACACTACACTACGGGCGCGCGGAGGCGCATCGGCTTTCAGCGGCTCGGG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyr 200
DB 541 GACCCCGGCGAGGTGGCGGCGAGCGCGGTTTCAAGGCGCGCGCTCTGTTCTGG 600
QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
DB 601 ATGAACAACGTCACCGTGTGATGCGCGAGGCGTTCGCGCGCCACCATCAGGCGCCATCAAC 660
QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
DB 661 GCGCGCTCTCGAGTGCACCGGAGCAACCCCGCGCGAGATGAGCGCGCGGTGCGGTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
DB 721 AGGCGAGTACTGCGCGCAGCTCGCGCTCGACCGCGGCAACCAACCTCACCTGC 771
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Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
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Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCGGCGGGTGGCGGGGACCGCTGGTGGGCTTCAAGCGGCGCTCTGGTTCGG 600  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 601 ATGAACACGTCACCGTGTATCGCGCAGGCTTCGGCGCCACCATCAGGCGCCATCAAC 660  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 240  
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Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
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## RESULT 3

US-10-389-432B-29  
; Sequence 29, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: r1 Ad4 nucleic acid  
US-10-389-432B-29

## Alignment Scores:

Pred. No.: 1.37e-164 Length: 771  
Score: 1435.00 Matches: 254  
Percent Similarity: 99.22% Conservative: 1  
Best Local Similarity: 98.83% Mismatches: 2  
Query Match: 98.83% Indels: 0  
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-29 (1-771)

Qy 1 SerMetGlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAGAACTCGCGCTGCAGCAACGATGCTGCAGCAAGTTGGCTACTCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACGACCGACGAGTACTCGCGGCGACGGGTGCGAGTGGCGCGCTCGCGCGCGGCT 120  
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 121 GCG 180  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 181 GTCACCGACGCGCTCTTCAACGGCATCAAGAACCGGCGGAGCGGCTGCGAGGGCAAG 240

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleTyrProGlyPheAlaHis 100  
Db 241 AACTTTCATACACCGGAGCGGCTTCCTGAGGCCATCGCCGGGTACCCGGGCTTCGCGCAT 300  
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120  
Db 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGAGATTGCCGCTTCTTCGCGCACGCCACGCAC 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
Db 361 GAGACCGGGCATTTCTGCTATCATCAGCGAGGTCAACAAGAGCAACGCTACTCTGCGACCG 420  
Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGGAGTGGCGCTGCGCGCGCGGCGAGGACTACCGGCGCGCGCGCTGCGAG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACAACTACGGGCGCGCGGGAGGCCATCGGCTTCGACGGGCTCGG 540  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCGGCGAGTGGCGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 601 ATGAACACGTCACCGCTGTGATGCGCGCGGCTTCGCGCGCCACCATCAGGCGCCATCAAC 660  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
Db 661 GCGCGCTCGAGTGCAGCGGCGGGAACAACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCGCAGCTCGGCGTGCAGCCCGGCGGCGGCGGCGGCGGCGGCGG 771

## RESULT 4

US-10-389-432B-33  
; Sequence 33, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: r1 AG9 nucleic acid  
US-10-389-432B-33

## Alignment Scores:

Pred. No.: 1.37e-164 Length: 771  
Score: 1435.00 Matches: 254  
Percent Similarity: 99.22% Conservative: 1  
Best Local Similarity: 98.83% Mismatches: 2  
Query Match: 98.83% Indels: 0  
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-33 (1-771)

```
QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACTGGCGGTGTCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACAACCGACGAGTACTGCGCGCGACGGGTGTCAGTTCGGGCCCGTCCGCTCGGGGGCGGT 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCACCGACGGTTCCTTCAACGGCATCAAGCAACAGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
Db 241 AACTTCTACACCGGAGCGCGTTCCTCGAGGCCATCGCGCGGTACCCGGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 301 GCGCGCTCCGAGGTGCGACGCAAGCGCGAGATTGCCGCTTCTTCGCGCACGCCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCATCAAGCGCGGTACTGCGACCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGGCGCGGAGCGCGCGTGGTGGCGTTCAGGGCGCGCTCTGGTTCGCG 480
QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCGGCGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACACGTCACCGCGTGTGATCGCGAGGGCTTCGCGCGCACCATCAGGGCGCATCAAC 660
QY 221 GlyAlaLeuGluCysAenGlyAsnProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GCGCGCTTCGAGTGGCGCGGGAACAACCCCGCCAGATGAACGCGCGCGGTGCGGTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257
Db 721 AAGCAGTACTGCGCGCAGCTCGCGCTCGACCCAGGGCCCACTTCACTTGC 771
```

## RESULT 5

```
US-10-692-367-29
; Sequence 29, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
```

```
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-29
Alignment Scores:
Pred. No.: 1.37e-164 Length: 774
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
DB: 19 Gaps: 0
```

US-10-692-367-12 (1-257) x US-10-692-367-29 (1-774)

```
QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACTGGCGGTGTCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTGCGCGCGACGGGTGCGAGTTCGCGCGCGCGTCCGCTCGGGGGCGGT 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCACCGCGCGTTCCTTCAACGGCATCAAGCAACAGCGCGCGAGCGGTGCGAGGGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
Db 241 AACTTCTACACCGCGAGCGGTTCCTCGAGGCCATCGCGCGGTACCCGGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 301 GCGCGCTCCGAGGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCATCAAGCGCGGTACTGCGACCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGGCGCGGAGCGCGCGTGGTGGCGTTCAGGGCGCGCTCTGGTTCGCG 480
QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCGGCGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACACGTCACCGCGTGTGATCGCGAGGGCTTCGCGCGCACCATCAGGGCGCATCAAC 660
QY 221 GlyAlaLeuGluCysAenGlyAsnProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GCGCGCTTCGAGTGGCGCGGGAACAACCCCGCCAGATGAACGCGCGCGGTGCGGTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257
```

```

Db      721 AAGCAGTACTGCCGCGTGGCGTGCACCCAGGCGCCAAACCTCCTTGC 771
|||||
US-10-692-367-33
; Sequence 33, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-33
Alignment Scores:
Pred. No.: 1,376-164 Length: 774
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
Gaps: 19
DB:
US-10-692-367-12 (1-257) x US-10-692-367-33 (1-774)
Qy      1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysgly 20
Db      1 TCGATGCGAAGTTCGGCTGCCAGCCAAACGATATCTCGAGCAAGTTTGGCTACTGCGGC 60
|||||
Qy      21 ThrThrAspGluTyrcysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db      61 ACNACCGACGAGTACTGCGGCGACGGGTGCCAGTGGCGCCGCTCGCGCTCGGGCGCGGT 120
|||||
Qy      41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db      121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
|||||
Qy      61 ValThrAspAlaPhePheAsnGlyIleLysGlnAlaGlySerGlyCysGluGlyLys 80
Db      181 GTCACCGACGCGTCTTCAACGGCATCAAGAACCCAGCGCGGAGCGGTGGAGGGCAAG 240
|||||
Qy      81 AenPheTyThrArgSerAlaPheLeuGluAlaIleAlaTyProGlyPheAlaHis 100
Db      241 AACTTCTACACCGAGGCGGTCTCTCGAGCCATCGCGGTACCCGGGCTTCGGCGAT 300
|||||
Qy      101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120
Db      301 GCGCGCTCCGAGTCCAGCGAAGCGGAGATTGCGGCTTCTTCCGCGCAGCCAGCGAC 360
|||||
Qy      121 GluThrGlyHisPheCysTyTyIleSerGluValAenLysSerAsnAlaTyrcysaspPro 140
|||||
Db      361 GAGACCGGCGCATTTCTGCTACTATCAGCGAGGTCAACAGAGCAACGCCCTACTGCGACCCG 420
|||||
Qy      141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyTyTyGlyArgGlyProLeuGln 160
|||||
Db      421 ACCAAGAGGCGAGTGGCGTGGCGCGCGGAGAGTACTACGGGCGCGCGCGCTGCGAG 480
|||||
Qy      161 IleSerTrpAenTyArgTyGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
|||||
Db      481 ATCTCGTGGAACTACAACATACGGGCGCGCGGGAGGCCATCGGCTTCGACGGGCTCGGG 540
|||||
Qy      181 AspProGlyArgValAlaAtqAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
|||||
Db      541 GACCCCGCGAGGTGGCGGAGAGCCGCTGGTGGCTTCAAGCGCGCGCTCTGGTCTTGG 600
|||||
Qy      201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
|||||
Db      601 ATGAACAACGTCACCGTGTGATGCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660
|||||
Qy      221 GlyAlaLeuGluCysAenGlyAsnAenProAlaGlnMetAenAlaAatqValGlyTyTyTr 240
|||||
Db      661 GCGCGCTTCGAGTGGCGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720
|||||
Qy      241 ArgGlnTyrcysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
|||||
Db      721 AAGCAGTACTGCCGCGAGCTCGGCTGCACCGGCGCCAAACCTCCTTGC 771
|||||
RESULT 7
US-10-692-367-71
; Sequence 71, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-71
Alignment Scores:
Pred. No.: 6,156-161 Length: 774
Score: 1405.00 Matches: 245
Percent Similarity: 98.44% Conservative: 8
Best Local Similarity: 95.33% Mismatches: 4
Query Match: 96.76% Indels: 0
Gaps: 19
DB:
US-10-692-367-12 (1-257) x US-10-692-367-71 (1-774)
Qy      1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysgly 20

```

Db 1 TCGATGCAAGTCTGGGCTGCAGCCAACTATGCTGCAGCAAGTTTCGGCTACTCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACACCGACGAGTACTCGCGGACGGGTGCGAGTGCAGTCCGGCCCGCTCGCTCGCGGGCGGT 120  
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 121 GCG 180  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 181 GTCCACCGACGGTCTTCTCAACCGCATCAAGACCGCGCGCGCGCGCGCGCGCGCG 240  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100  
Db 241 AACTTCTACACCGCGCGCGTCTCTGAGCGCGCTCAAGCGCGTACCCAGGCTTCGCCCAT 300  
Qy 101 GlyGlySerGluValGluArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 301 GCGCGGTACAGGTGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaIleAlaIleAla 140  
Db 361 GAGACCGCGCATTTCTGTACATCAGCGAGATCAACAGACGCAACGCGCTACTCGCGCCG 420  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGCGAGTGGCG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACAACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCGCGAGGTGGCG 600  
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaIleAlaIleAlaHis 220  
Db 601 ATGAACAACGTCACCGTGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
Db 661 GCGCGCTCGAGTGCAGCGGGAACAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCGCAGCTCGCGCTCGACCCAGGCGCGCGCGCGCGCGCGCGCG 771

## RESULT 8

US-10-389-432B-59

; Sequence 59, Application US/10389432B

; Publication No. US20040250309A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias

; APPLICANT: Simmons, Carl

; APPLICANT: True, Thom

; APPLICANT: Yalpani, Nasser

; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE

; TITLE OF INVENTION: ACTIVITY

; FILE REFERENCE: 4894200300

; CURRENT APPLICATION NUMBER: US/10/389,432B

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/337,029

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 59

; LENGTH: 768

; TYPE: DNA

; ORGANISM: Unknown

## FEATURE:

; OTHER INFORMATION: Variant sequence produced by shuffling techniques

; OTHER INFORMATION: 4N1/33\_P4 nucleic acid

US-10-389-432B-59

## Alignment Scores:

Pred. No.: 3,33e-158 Length: 768  
Score: 1382.50 Matches: 244  
Percent Similarity: 96.89% Conservative: 5  
Best Local Similarity: 94.94% Mismatches: 7  
Query Match: 95.21% Indels: 1  
DB: 18 Gaps: 1

US-10-692-367-12 (1-257) x US-10-389-432B-59 (1-768)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAAGTCTGGGCTGCAGCCAACTATGCTGCAGCAAGTTTCGGCTACTCGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACACCGACGAGTACTCGCGGACGGGTGCGAGTGCAGTCCGGCCCGCTCGCTCGCGGG 117  
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 118 GGTGCGCGGTGCG 177  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 178 GTCAACCGACGGTCTTCTCAACCGCATCAAGACCGCGCGCGCGCGCGCGCGCGCG 237  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100  
Db 238 AACTTCTACACCGCGCGCGTCTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCAT 297  
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120  
Db 298 GCGCGGTACAGGTGCGAGGCAAGCGCGAGATTTCGCCGCTTCTTCGCCGCGCATGTCC 357  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaIleAlaIleAla 140  
Db 358 GAGACCGCGCATTTCTGTCTACATCAGCGAGATCAACAGAGCAACGCGCTACTCGCGC 417  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 418 ACCAAGAGCGAGTGGCG 477  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 478 ATCTCGTGGAACTACAACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 538 GACCCCGCGAGGTGGCG 597  
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaIleAlaIleAlaHis 220  
Db 598 ATGAACAACGTCACCGTGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 657  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
Db 658 GCGCGCTTCGAGTGCAGCGGGAACAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 717  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 718 AGCAGTACTGCGCGCAGCTCGCGCTCGACCCAGGCGCGCGCGCGCGCGCGCGCG 768

## RESULT 9

US-10-692-367-59

; Sequence 59, Application US/10692367

; Publication No. US2005005059A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias L.



```
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-10-692-367-59

Alignment Scores:
Pred. No.: 3,35e-158 Length: 771
Score: 1382.50 Matches: 244
Percent Similarity: 96.89% Conservative: 5
Best Local Similarity: 94.94% Mismatches: 7
Query Match: 95.21% Indels: 1
DB: 19 Gaps: 1

US-10-692-367-12 (1-257) x US-10-692-367-59 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGCTGCAGCAACAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGCTACTGCGCGCAGCGGTGCGAGTGCAGTCCGCGCGCTCG---GGCGGC 117
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 118 GGTGGCGCGGTGGCGCGCGAGCGCGCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 177
Qy 61 ValThrAspAlaPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 178 GTACCCGACGGTCTTCAACGGCATCAAGAACCAAGCGCGCGAGCGGTGCGAGGCGCAG 237
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaLeuAlaTyrProGlyPheAlaHis 100
Db 238 AACTTCTACACCGAGCGGTCTCTGAGCGCGTCAAGCGGTCAAGCGGTCAAGCGGTCAAG 297
Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaPheAlaHisAlaThrHis 120
Db 298 GCGCGGTTCACAGGTGCAGGCAAGCGCGAGATTGCCGCTTCTTCGCGCATGTCAAGCAC 357
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 358 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCTACTGCGACCCG 417
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGCGAGTGGCGGTGCGCGCGCGGAGGAGTACTACGCGCGCGCGCGCGCGCG 477
Qy 161 IleSerTyrAsnTyrGlyProAlaGlyArgAlaLeuGlyPheAspGlyLeuGly 180
Db 161 IleSerTyrAsnTyrGlyProAlaGlyArgAlaLeuGlyPheAspGlyLeuGly 180

Db 478 ATCTCGTGGAACTACAACTAGCGGCGCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 537
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyr 200
Db 538 GACCCCGCAGGCTGGCGCGGACGCGTGGTGGCGTTCAAGGCGCGCTCTGGTTCTGG 597
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 598 ATGAACAACGTCACCGCTGTGATGCCGAGCGCTTCGCGCGCACCATCAGGCGCATCAAC 657
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaAsnValGlyTyrTyr 240
Db 658 GCGCCCTCGAGTCCGAGCGGAGCAACCCGCCCGATGATGAACGCGCGCTCGGTACTAC 717
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 718 AGCGAGTACTGCGCGCAGCTCGGCGTGCAGCCAGGCGCCCAACCTCACTTGC 768

RESULT 10
US-10-389-432B-45
; Sequence 45, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/80_F8 nucleic acid
US-10-389-432B-45

Alignment Scores:
Pred. No.: 3,86e-158 Length: 771
Score: 1392.00 Matches: 241
Percent Similarity: 97.28% Conservative: 9
Best Local Similarity: 93.77% Mismatches: 7
Query Match: 95.18% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-45 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGCTGCAGCAACAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGCTACTGCGCGCAGCGGTGCGAGTGCAGTCCGCGCGCTCGCGCGCGGT 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ValThrAspAlaPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCCGACGCTTCTTCAACGGCATCAAGAACCAAGCGCGCGAGCGGTGCGAGGCGCAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaLeuAlaTyrProGlyPheAlaHis 100
Db 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaLeuAlaTyrProGlyPheAlaHis 100
```

```
Db 241 AACCTTACACCCGGAGCGGCTTCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCAT 300
Qy 101 GlySerGluValGluArgGlyArgGluLeuAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTGCGAGGTGCGAGGCAAGCGGAGATCGCGCTTCTTCGGCGCACGCCACGCAC 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAlaAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGGCGCGCGCGGCGGAGAGTACTACGGCGCGCGCGCGCTGCGAG 480
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGCGGCGCGCGGAGGCGCATCTGGCTTTGACGGGCTCGGG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCAACAGGTGGCGGGAAGCGCTGTGGCTTCAAGGGCGGCGCTCTGGTTCTGG 600
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAGCGTGCACGGGTGGTGGCGAGGCGGCTTCGGCGCGCACCCAGGCGCCATCAAC 660
Qy 221 GlyAlaLeuGlyCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGCGCTCGGTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTGCGCGCAGCTCGGCGTGCACCCAGGGCCCACTTGC 771
```

## RESULT 11

```
US-10-692-367-45
; Sequence 45, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-45
Alignment Scores: 3.87e-158 Length: 774
Pred. No.: 1382.00 Matches: 241
Score: 97.28% Conservative: 9
Percent Similarity:
```

```
Best Local Similarity: 93.77% Mismatches: 7
Query Match: 95.18% Indels: 0
DB: 19 Gaps: 0
US-10-692-367-12 (1-257) x US-10-692-367-45 (1-774)
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCATGTCAGAACTCGCGCTGCCAGCAAAAGTATGCTGCAGCGGTTTCGGCTACTCGCGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACCAGCCAGAGTACTCGCGCGAGCGGTCGCGCGCGCGCTGCCCGCTCGCGCGCGGT 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGT 180
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCACCGAGCGGTTCTTCAACGCGCATCAAGAACCCAGCGCGGAGCGGTCGAGGGCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCGCGAGCGGTTCTGAGCGCGCTCAAGCGCTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTGCGAGGTGCGAGGCAAGCGCGAGATCGCGCTTCTTCGCGCGCACGCCACGCAC 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGGCGCGTGGCGGCGGCGAGTACTACGGCGCGCGCGCTCGAG 480
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGCGGCGCGCGGAGGCGCATCGGCTTTGACGGGCTCGGG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCAACAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTGGTTCTGG 600
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAGCGTGCACGGGTGGTGGCGAGGCGGCTTCGGCGCGCGCGCGCTCAAC 660
Qy 221 GlyAlaLeuGlyCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGCGCTCGGTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTGCGCGCAGCTCGGCGTGCACCCAGGGCCCACTTGC 771
RESULT 12
US-10-389-432B-65
; Sequence 65, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
```

```
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/35_G5 nucleic acid
US-10-389-432B-65

Alignment Scores:
Pred. No.: 1.57e-157 Length: 771
Score: 1377.00 Matches: 240
Percent Similarity: 96.50% Conservative: 8
Best Local Similarity: 93.39% Mismatches: 9
Query Match: 94.83% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-65 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCAGCCAAACGTATGCTGCAGCAAGTTGGCTACTCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGCGGAGCGGTGCAGTCCGCGCGGTGCGCGCGGTGGCGGT 120

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCGACTCTCTTTCACGGCATCAGCAACCAAGCGCGCGGAGCGGTGCAGGGCAG 240

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
Db 241 AACTTCTACACCGCGAGCGGTCTCTGAGCGCGGTCAAGGCGGTACCCAGGCTTCGCCCAT 300

Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTGCGAGGTGCAGGCAAGCGCGCATCGCGCTTCTTCGCGCATGTCCAGCAC 360

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGACCAAGCATCTCGCACCG 420

Qy 141 ThrLysArgGlnTyrProCysAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGGCGAGTGGCGGTGCGCGCGGCGGAGGAGTACTACGCGCGGTGGCGCGGTG 480

Qy 161 IleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTGTGGAATACAACTACGCGCGCGCGGAGGCGCATCTCGCGTTCGAGCGGTGCGC 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyr 200
Db 541 GACCCCAACAGGTGGCGGAGGAGCGCGGTGTGGGTTCAGGCGCGGTCTGGTCTGG 600

Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACGTGCACCGGTGATCGCGCAGGGCTTCGCGCGCATCATCAGGGCCATCAAC 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProIleGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGGCGGGAACAACCCCGCCAGATGAACGCGCGGTGCGGTACTAC 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 721 AAGCAGTACTCGCGCAGCTCGCGGTGCAGCCAGGGGCCAACCTCACTTGC 771
```

```
RESULT 13
US-10-692-367-65
; Sequence 65, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-65

Alignment Scores:
Pred. No.: 1.57e-157 Length: 774
Score: 1377.00 Matches: 240
Percent Similarity: 96.50% Conservative: 8
Best Local Similarity: 93.39% Mismatches: 9
Query Match: 94.83% Indels: 0
DB: 19 Gaps: 0

US-10-692-367-12 (1-257) x US-10-692-367-65 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCAGCCAAACGTATGCTGCAGCAAGTTGGCTACTCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGCGGAGCGGTGCAGTCCGCGCGGTGCGCGCGGTGGCGGT 120

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCGACTCTCTTTCACGGCATCAGCAACCAAGCGCGCGGAGCGGTGCAGGGCAG 240

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
Db 241 AACTTCTACACCGAGCGGTCTCTGAGCGCGGTCAAGGCGGTACCCAGGCTTCGCCCAT 300

Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTGCGAGGTGCAGGCAAGCGCGCATCGCGCTTCTTCGCGCATGTCCAGCAC 360

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGACCAAGCATCTCGCACCG 420
```

```
Qy 141 ThrlyArgGlnTrrProCysAlaAlaGlyGlnlystYrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGCGAGTGGCGGTGGCGCGGGGAGAGTACTACGGGGCGTGGCCCTGGAG 480

Qy 161 IleSerTrpAsnTrpAsnTrpGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGAACACTACACTAGCGGCGCGGGAGGGCCATCGCTTCGAGGGCTCGCC 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaLeuTrpPheTrp 200
Db 541 GACCCCAACAGGTGGCGAGGAGCGCGCGGGGAGGGCCATCGCTTCGAGGGCTCGCC 600

Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaLeu 220
Db 601 ATGAACAACAGTGCACCGGTGATCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGGCCCTCGAGTGGCGGGGAGACACACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 721 AAGCAGTACTGCGCGAGTGGCGGTGCGAGCCGAGGGCCCACTTGC 771

RESULT 14
US-10-389-432B-61
; Sequence 61, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-61

Alignment Scores:
Pred. No.: 4.15e-157 Length: 768
Score: 1373.50 Matches: 242
Percent Similarity: 97.28% Conservative: 8
Best Local Similarity: 94.16% Mismatches: 6
Query Match: 94.59% Indels: 1
DB: 18 Gaps: 1

US-10-692-367-12 (1-257) x US-10-389-432B-61 (1-768)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCGAGAACTGCGGGTGGCGGAGCAACAGTATCTGAGCAAGTTCGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACGACCGACGAGTACTGCGGGCGAGCGGTGCGAGTCTGCGGCGCGCGCGCGCGCGCG 117

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 118 GCGCGCGGTGGCGGGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 177
```

```
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 178 GTACCGGCTCTCTTCTTCAACGCATCAAGAGCCAGCGCCGGGAGCGGTGGAGGGCAAG 237

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIle 100
Db 238 AACTTCTACACCGGAGCGGTCTCTGAGCGCGGTCAAGGCGTACCCAGGCTTCGCCCAT 297

Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaIleAlaPhePheAlaHisAlaThrHis 120
Db 298 GCGCGCTCCAGGTCGAGCGCAAGCGCGAGATTTCGCCCTTCTTCGCGCGCACGCCACGCAC 357

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 358 GAGACCGGGCATTTCTGCTACATCAACAGATCAACAGAGCAACGCGCTACTGCGACCCG 417

Qy 141 ThrLysArgGlnTrrProCysAlaAlaGlyGlnlystYrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGGCGAGTGGCGGTGGCGCGGGGAGGCGCATCGGCTTCGAGCGGCTCGAG 477

Qy 161 IleSerTrpAsnTrpAsnTrpGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 478 ATCTCGTGAACACTACACTAGCGGCGCGCGGGAGGGCCATCGGCTTCGAGCGGCTCGCC 537

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaLeuTrpPheTrp 200
Db 538 GACCCCGGAGGTGGCGGGGAGCGCGGTGGTGGCTTCAAGGGCGGCTCTGCTTCTGG 597

Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 598 ATGAACAACAGTGCACCGGTGATCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 657

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 658 GCGCGCTCGAGTGGCGGAGCAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 717

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 718 AAGCAGTACTGCGCGAGTGGCGGTGCGAGCCAGGGCCCACTTGC 768

RESULT 15
US-10-692-367-61
; Sequence 61, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
```

i LOCATION: (1)....(771)  
US-10-692-367-61

## Alignment Scores:

Pred. No.:	4.17e-157	Length:	771
Score:	1373.50	Matches:	242
Percent Similarity:	97.28%	Conservative:	8
Best Local Similarity:	94.16%	Mismatches:	6
Query Match:	94.59%	Indels:	1
DB:	19	Gaps:	1

US-10-692-367-12 (1-257) x US-10-692-367-61 (1-771)

Qy	1	SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly	20
Db	1	TCGATGCAGAACTGCGGTGCGAGCAACATATGCTGCAGCAAGTTGCGTACTGCGGC	60
Qy	21	ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly	40
Db	61	ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCCGTGCCGCCG---GGCGGC	117
Qy	41	Gly	60
Db	118	GGCGCGGTGCGCGCGCGCGAGCGCGCGGCGAGTGGCGGTGCGAACGTGGCTAGCGTC	177
Qy	61	ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys	80
Db	178	GTACCGCGCTCTCTTCAACGGCATCAAGAGCCAGCGCGGAGCGGTGCGAGGGCAAG	237
Qy	81	AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis	100
Db	238	AACCTTCTACACCGGAGCGCGTTCTGAGCCCGCTCAAGCGGTACCCAGGCTTCGCCAT	297
Qy	101	GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis	120
Db	298	GGCGGCTCCGAGGTTCGAGCGCAAGCGGAGATTGCGCGCTTCTTCGGCGCACGCCACGCAC	357
Qy	121	GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro	140
Db	358	GAGACCGGGCAATTCTGTCTACATCAACGAGATCAACAGAGCAACGCCCTACTGCGACCCG	417
Qy	141	ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln	160
Db	418	ACCAAGAGGCAAGTGGCGCTGCGCGCGGGGCGAAGTACTACGGGCGGCGCGCTGCGAG	477
Qy	161	IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly	180
Db	478	ATCTCGTGAACACTACAACCTACGGGCGCGCGGAGGCCATCGGCTTCGACGGGCTCGCC	537
Qy	181	AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyr	200
Db	538	GACCCCGGCGAGGTGGCGCGGAGCGCGGTGGTGGCTTCAAGGGCGGCGCTCTGGTTCTGG	597
Qy	201	MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn	220
Db	598	ATGAACACAGTGCACCGGTGATGATCCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC	657
Qy	221	GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr	240
Db	658	GGCGCGCTCGAGTGGAGCGGCAACACCCCGCCAGATGAACGCGCGCTCGGCTACTACTAC	717
Qy	241	ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys	257
Db	718	AAGCAGTACTGCCGCCAGCTCGCGGTGACCCAGGCGCCCAACCTCACTTGC	768

Search completed: May 23, 2005, 22:41:51  
Job time : 419.647 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:04:03 ; Search time 2300.33 Seconds  
(without alignments)  
4252.663 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQCGQPNVCKSKFYCG.....GYRQYRQLGVDPGNLTC 257

Scoring table:

	BLOSUM62	Ygapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Deiop 6.0			7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2 1/USPTO.spool/US10692367/runat 20052005 172255 20018/app query.fasta\_1.846  
-DB=EST -QMT=fastcap -SUPFIX=rest -MINMATCH=0.1 -LOECL=0 -LOEPT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10692367.CGN 1 1 3556 @runat 20052005 172255 20018 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

	1:	2:	3:	4:	5:	6:	7:	8:	9:
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gb_est2.*									
gb_hc.*									
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gb_est6.*									
gb_gsl1.*									
gb_gsl2.*									

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	1333	91.8	1179	3	AY103546	AY103546 Zea mays
2	1184	81.5	958	4	EG837479	EG837479 Zm10.10h0
3	1183.5	81.5	855	4	EG837663	EG837663 Zm10.0tel
4	1135.5	78.2	737	6	CD435649	CD435649 EL01N0364
5	1110.5	76.5	767	7	C0524416	C0524416 3530.1.16
6	1096	75.5	837	7	CN133023	CN133023 OX1.9.D11
7	1047	72.1	710	6	CD443492	CD443492 EL01N0427
8	1032	71.1	978	9	C0328450	C0328450 EG3CW08TV
9	1024	70.5	716	7	C0520138	C0520138 3530.1.13

10	1020.5	70.3	647	6	CA197556	CA197556 SCBPAD106
11	990	68.2	628	4	BM736454	BM736454 952051A06
12	989	68.1	625	5	BM895383	BM895383 952073H05
13	980.5	67.5	786	6	CA270202	CA270202 SQSLB205
14	977.5	67.3	801	7	CN151443	CN151443 WOUNDI.75
15	957.5	65.9	856	6	CB981065	CB981065 CAB70003
16	957.5	65.9	870	6	CB982079	CB982079 CAB70005
17	957.5	65.9	895	6	CB981562	CB981562 CAB70004
18	956.5	65.9	887	6	CB981996	CB981996 CAB70005
19	956.5	65.9	893	6	CB980773	CB980773 CAB70003
20	956.5	65.9	904	6	CB981568	CB981568 CAB70004
21	956.5	65.9	920	6	CB981043	CB981043 CAB70003
22	956	65.8	741	6	CD994869	CD994869 QBBI8d07
23	955.5	65.8	861	6	CB980332	CB980332 CAB70002
24	955.5	65.8	889	6	CB982059	CB982059 CAB70005
25	954.5	65.7	895	6	CB980998	CB980998 CAB70003
26	954	65.7	578	6	CD994156	CD994156 QBBI3f07
27	953.5	65.7	880	7	CF200723	CF200723 RR890915N
28	953	65.6	688	6	CA281399	CA281399 SCAGSD104
29	952	65.6	753	6	CD994885	CD994885 QBBI8e05
30	951.5	65.5	850	6	CB980173	CB980173 CAB70002
31	951.5	65.5	874	7	CF200575	CF200575 RR89015N0
32	951	65.5	820	6	CD995497	CD995497 QBBI25f07
33	950	65.4	812	7	CN132942	CN132942 OX1.9.D11
34	949.5	65.4	851	6	CB980181	CB980181 CAB70002
35	948	65.3	575	6	CD994132	CD994132 QBBI3e04
36	946	65.2	578	6	CD994454	CD994454 QBBI15f08
37	943.5	65.0	845	6	CB981100	CB981100 CAB70003
38	943.5	65.0	855	6	CB980750	CB980750 CAB70003
39	940.5	64.8	680	6	CA100718	CA100718 SCCCL700
40	935.5	64.4	873	7	CF202886	CF202886 RR890915N
41	933.5	64.3	818	7	CF201611	CF201611 RR890915N
42	933	64.3	618	2	BE918591	BE918591 OVI.8.G11
43	926	63.8	636	4	BG840312	BG840312 MEST9-A04
44	925	63.7	754	6	CD995176	CD995176 QBBI20h11
45	916.5	63.1	637	4	BI478959	BI478959 949071D05

#### ALIGNMENTS

RESULT 1	AY103546	Zea mays	PCOL55066	mrna	linear	HTC	16-OCT-2002
LOCUS	AY103546	Zea mays	PCOL55066	mrna	linear	HTC	16-OCT-2002
DEFINITION	Zea mays	PCOL55066	mrna	sequence.			
ACCESSION	AY103546						
VERSION	AY103546.1	GI:21206624					
KEYWORDS	HTC.						
SOURCE	Zea mays						
ORGANISM	Zea mays						

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1179)

HAINEY, C.P., DOLAN, M., MIAO, G.H., VOGEL, J.M., WHITSITT, M.S.,

ARTHUR, L.W., HANAFY, M., MORGANTE, M. and RINGEY, S.V. Design of

Maize Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 1179)

COE, E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST

searching at MSI, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

FEATURES Location/Qualifiers

source 1..1179 /organism="Zea mays"

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/mol_type="mrna"
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Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Alignment Scores:
Pred. No.: 4,22e-121 Length: 1179
Score: 1333.00 Matches: 232
Percent Similarity: 94.51% Conservativeness: 9
Best Local Similarity: 90.98% Mismatches: 14
Query Match: 91.80% Indels: 0
DB: 3 Gaps: 0

US-10-692-367-12 (1-257) x AY103546 (1-1179)
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Db 149 CAGAACTGCGGCTGCCAGCCAAACTTCTGCTGCAGCAAGTTTCGGTACTGCGGCAGCACC 208
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 209 GACGCTACTGCGGCGACGGTGCGAGTCGGGCGCGCTGCGCGCTGCGGCGGCGGCGGCG 268
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 269 GCGCGCGCGCGGAGGCGGCGGAGCGAGTGGCGTGCAGCAAGTTCGGTAAATGCTGCTACC 328
Qy 63 AspAlaPhePheAsnGlyVileLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 329 GACGCGTTCTTCAACGGCATCAAGAACACAGCGCGGAGCGGCTGCGAGGGCAAGAACTTC 388
Qy 83 TyrThrArgSerAlaPheLeuGluAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 102
Db 389 TACACCGCGAGCGGCTTCTGAGCGCGCTCAACCGCTACCGCGGCTTCCGCCATCGCGGG 448
Qy 103 SerGluValGluArgLysArgGluLeuAlaAlaPheAlaHisAlaThrHisGluThr 122
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Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142
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Qy 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db 629 TGGAACTAACAATACGGGCGCGCGGAGGAGCATCGGCTTCAACGGGCTCGCGACCCC 688
Qy 183 GlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202
Db 689 AACGGGTGGCGCAGGACCGGTGATCGCTTCAAGACGCGCTCTGCTTCTGGATGAAC 748
Qy 203 AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 222
Db 749 AACGTGACCGGTGTATCGCGAGGGCTTTCGGCGCGCACCATCAGGGCCATCAACGGCGCC 808
Qy 223 LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln 242
Db 809 CTCGAGTGCACGGGAACAAACCCCGCCAGATGAACGCGCGCGCTCGGCTACTACAGCAG 868
Qy 243 TyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257

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Db 869 TACTGCCAGCAGCTCCGCTGCGACCCAGGGCCCAACCTCTACTTGC 913

RESULT 2
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LOCUS Zm10_10h09_A Zm10_AAFRC_ECORC_Fusarium_graminearum_corn_silk Zea
DEFINITION mays cDNA Clone Zm10_10h09, mRNA sequence.
ACCESSION BG837479
VERSION BG837479.1 GI:14203802
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 958)
Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,U.A.,
Spott,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualifiers
1. 958
/organism="Zea mays"
/mol_type="mRNA"
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/clone="Zm10_10h09"
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/clone_lib="Zm10_AAFRC_ECORC_Fusarium_graminearum_corn_silk"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Field-grown corn was silk channel-inoculated
in the morning (~10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."

ORIGIN
Alignment Scores:
Pred. No.: 1,72e-106 Length: 958
Score: 1184.00 Matches: 218
Percent Similarity: 89.11% Conservativeness: 11
Best Local Similarity: 84.82% Mismatches: 23
Query Match: 81.54% Indels: 6
DB: 4 Gaps: 1

US-10-692-367-12 (1-257) x BG837479 (1-958)
Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrTh 22
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Qy 22 rAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 92 CGACGACTACTGCGCGCAGCGGTGCCAGTCCGCGCGCGCTCGCTCG-----GGCGG 142
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217 GCCAGATGACGGCGGTGGCTACTACTACAGGAGTACTGCCGCCAGCTCGGCGTGAC 158
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Qy 251 ProGlyAenAenLeuThrCys 257
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Db 157 CCGGGGCCAACCTCACCTGC 137

RESULT 4
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ACCESSION CD435649
VERSION CD435649.1 GI:31351292
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.P.,
Larkins, B., Beckraft, P. and Messing, J.
TITLE Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
JOURNAL Genome Res. 14 (10), 1932-1937 (2004)
COMMENT Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

FEATURES
source
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COS24416
3530..1161..E12.Y.1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
COS24416
ACCESSION COS24416
VERSION COS24416
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1 161.1 row: E column: 12.
Location/Qualifiers
1..767
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/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/note="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1, Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSPORT vector. This
is a Gateway compatible vector, permitting clone movement
```

to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unique clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,38e-99 Length: 767  
 Score: 1110.50 Matches: 196  
 Percent Similarity: 93.18% Conservative: 9  
 Best Local Similarity: 89.09% Mismatches: 8  
 Query Match: 76.48% Indels: 7  
 DB: 7 Gaps: 1

US-10-692-367-12' (1-257) x C0524416 (1-767)

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 Db 127 CAGAACTCGCGTGCAGCAAGCGTATGCTGCAGCAAGTTTGGCTACTCGCGCAGCACC 186  
 Qy 23 AspGluTyrcGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
 Db 187 GACGAGTACTCGCGGACGCGTGCAGTGCAGCGCGCTGCAGCGCGCGCGGCGAGC 246  
 Qy 43 GlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAenValAlaAenValValThr 62  
 Db 247 AGTGGCGC-----GGTGGTGGACGTTGGCTAGTGTCTCACC 285  
 Qy 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 82  
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 Qy 83 TyThrArgSerAlaPheLeuGluAlaIleAlaAlaPhePheAlaHisAlaThrHisGluThr 102  
 Db 346 TACACCGGAGCGGTCTCTGAGCGCGCTCAAGCGGTACCCAGCGTTCGCGCCATGCGCGG 405  
 Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
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 Db 466 GGGCATTTCTCTACATCAGCGAGATCAACAGAGCAAGCGCTACTCGACCCGACCAAG 525  
 Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrcGlyArgGlyProLeuGlnIleSer 162  
 Db 526 AGGCAAGTGGCGTTCGCGCGCGGCGAGAGTACTACGCGCGCGCGCTGCAGATCTCG 585  
 Qy 163 TrpAenTyrcAenTyrcGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182  
 Db 586 TGGAACTACAACTACGCGGCGCGGAGGAGGCCATCGGCTTCGACGGGCTCGGGAGACCC 645

Qy 183 GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAen 202  
 Db 646 GGCAGGGTGGCGCGAGCAGCGCTGCTGCGCTTCAAGCGCGCTCTGCTTCTGATGAAC 705  
 Qy 203 AenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAla 222  
 Db 706 AGCGTCACGCGGGTGGTGGCGAGGGGTTCGGCGCCACCACCGAGGCCATCAACGGCGCC 765

## RESULT 6

CN133023

LOCUS

DEFINITION

Ox1\_9\_D11.g1\_A002 Oxidatively-stressed leaves and roots Sorghum

bicolor cDNA clone Ox1\_9\_D11\_A002 5', mRNA sequence.

ACCESSION

CN133023

VERSION

CN133023.1

KEYWORDS

EST.

SOURCE

Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

1 (bases 1 to 837)

AUTHORS

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,

Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: oxidatively stressed leaves and roots

Unpublished (2003)

Other ESTs: Ox1\_9\_D11.b1\_A002

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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science; plant material and RNA prepared at Texas A &amp; M University;

sequencing done in the Laboratory for Genomics and Bioinformatics,

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGTCGCG).

Location/Qualifiers

1..837

/organism="Sorghum bicolor"

/mol type="mRNA"

/cultivar="BTx623"

/db xref="taxon:4558"

/clone="OX1\_9\_D11\_A002"

/lab host="DH10B-T1 phage-resistant E. coli"

/clone lib="Oxidatively-stressed leaves and roots"

/notes="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1:

XhoI; Site 2: XhoI; The library was prepared from polyA+

RNA from oxidatively stressed, hydroponically grown

sorghum seedlings. At 8 days of age, growth medium was

supplemented with hydrogen peroxide to 0.003% and leaves

were misted with 10 uM methyl viologen. Leaves and roots

were harvested at 3, 12 and 27 hr after treatment and all

tissue pooled. Double-stranded cDNA was cloned

unidirectionally into different DraIII sites of the

pME18S-FL3 vector (5-prime DraIII site is CACTGTGG,

3-prime DraIII site is CACCATGTG). XhoI excises the cDNA

insert."

## ORIGIN

Alignment Scores:

Pred. No.: 7.21e-98 Length: 837

Score: 1096.00 Matches: 199

Percent Similarity: 84.15% Conservative: 8

Best Local Similarity: 80.89% Mismatches: 27

Query Match: 75.48% Indels: 12

DB:	7	Gaps:	2
US-10-692-367-12 (1-257) x CN133023 (1-837)			
QY	3	GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr	22
Db	134	CAGAACTACGGCTGCCAGGCAAGTTACTGCTGCAGCAAGTTCCGTTACTCGGCACGACC	193
QY	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly	42
Db	194	GACGAGTACTCGCGCGACGGTGCCAGTCGCGGCCCGTGCCTCTCGCGCGGCGAGCAGT	253
QY	43	GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAlaAsnValAlaAsnValValThr	62
Db	254	GGAGGTGG-----AACGTGGCTGGCGTTGTTCACC	283
QY	63	AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGlyGlyLysAsnPhe	82
Db	284	GACGCATTCITCAACAGCATCAAGAACACAGCGCGGAACGGTGCGAGGGCAAGAACTTC	343
QY	83	TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly	102
Db	344	TACACCGCGAGCGGTTCCTGAGCGCGCCGACGCGTACAAAGGCTTC-----GGTGGC	397
QY	103	SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr	122
Db	398	AGTCTGGTGAGGCAAGCGGAGATCGCCGCTTCCTGCGCCACATCACGCACGACACC	457
QY	123	GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys	142
Db	458	GGACATTCCTGCTACATCAGCGAGATCAACAAGAACACAGCGCTACTCGCATCGACCAAC	517
QY	143	ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer	162
Db	518	AGGCAGTGGCGGTGTGCGCGGGCTCAGAAAGTACTACGCGCGCGCCGCTGCATAATCTCG	577
QY	163	TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro	182
Db	578	TGGAACTACACTACGGGCTTCGCGGAGGACATCGGCTTCGACGGGCTTCGGAACCGG	637
QY	183	GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn	202
Db	638	GACAGGTGGCGCAAGACCGCGTGTGCGCTTCAAGACGGCGCTCTGCTTCGACCAAC	697
QY	203	AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla	222
Db	698	AACGTGCACGGGTGATGTCGACGGGTTCGCGCGCCACCATCAGGGCCCATCAACGGCGCC	757
QY	223	LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln	242
Db	758	CTCGAGTGCAACGGCAAGATACTGCCAGATGAACGGCGGGTGGGCTACTACAGGCAG	817
QY	243	TyrCysArgGlnLeuGly	248
Db	818	TACTGCCAGACGCTCGGC	835
RESULT 7			
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LOCUS		EL01N0427B11.b	EndospERM_4 Zea mays cDNA, mRNA sequence.
DEFINITION		CD443492	
ACCESSION		CD443492.1	GI:31359135
VERSION		EST.	
KEYWORDS		Zea mays	
SOURCE		ORGANISM	
REFERENCE			
AUTHORS			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
TITLE			1 (bases 1 to 710); Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J. Characterization of the maize endospERM transcriptome and its comparison to the rice genome

## JOURNAL COMMENT

Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinsheng

Dr. Joachim Messing's lab

Waksman Institute, Rutgers University

190 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@waksman.rutgers.edu

Seq primer: T3

Location/Qualifiers

1. .710

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W22"

/db\_xref="taxon:4577"

/tissue\_type="EndospERM of 7-23DAP"

/clone\_lib="EndospERM\_4"

/notes="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:

XhoI"

## ORIGIN

Alignment Scores:

Pred. No.: 4,08e-93 Length: 710

Score: 1047.00 Matches: 183

Percent Similarity: 94.53% Conservative: 7

Best Local Similarity: 91.04% Mismatches: 5

Query Match: 72.11% Indels: 6

DB: 6 Gaps: 1

US-10-692-367-12 (1-257) x CD443492 (1-710)

QY 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22

Db 126 CAGAACTGCGGCTGCCAGCCAAACGCTGCTGCAGCAAGTTCCGTTACTCGGCACGACC 185

QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42

Db 186 GACGAGTACTGTGCGCAGCGGTGCCAGTCGCGGCCCGTGCCTCTCGCGCGGCGGCGGC 245

QY 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAlaAsnValAlaAsnValValThr 62

Db 246 GGCAGTGGTGGC-----GGTGGTGGCAACGTGGCTAGCTCGTCACC 287

QY 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGlyGlyLysAsnPhe 82

Db 288 AGTCTCTCTTCAACGGCATCAGAACACAGCGCGGAGCGGTGCGAGGGCAAGAACTTC 347

QY 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102

Db 348 TACACCGGAGCGGTTCTCTGAGCGCGCTCAAGGGCGTACCAGGCTTCGCCCATGGCGGG 407

QY 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122

Db 408 TCGCAGGTGACGGCAAGCGCGAGATCGCCGCTTCCTTCGCGCACGCCACGCCAGACC 467

QY 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys 142

Db 468 GGGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCCTACTCGGCCCGGACCAAG 527

QY 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162

Db 528 AGGCAGTGGCGGTGCGCGCGGCGGAGTACTACGCGCGCGGCGGCGGCTGCGAGTCTCG 587

QY 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182

Db 588 TGGAACTACAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGGACCCCC 647

QY 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202

Db 648 GGCAGGTGGCGCGGAGCGCGGTGTCGCGTTCAAGGGCGGCGCTCTGTTCTGATGAGC 707

QY 203 Asn 203

Db :::

[illegible]

is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20x to 80x reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unique clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,72e-91 Length: 716  
 Score: 1024.00 Matches: 180  
 Percent Similarity: 93.50% Conservative: 7  
 Best Local Similarity: 90.00% Mismatches: 13  
 Query Match: 70.52% Indels: 1  
 DB: 7 Gaps: 0

US-10-692-367-12 (1-257) x C0520138 (1-716)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerIysPheGlyTyrCysGlyThr 22  
 Db 117 CAGAACTCGCGTGCAGCAAACTTCTGTCGACGACGAGTTTCGGCTACTGCGGACGACC 176  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
 Db 177 GACGCTACTGCGGACGGGTGCAGTCGGGCCGCTGCTCCGCTCGCGGCGCGCGGCGG 236  
 Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValThr 62  
 Db 237 GCGCGCGCGCGGAGCGCGGAGGCGAGTGGCGTGGCAACGTGGCTTAATGTGTCAAC 296  
 Qy 63 AspAlaPheAenGlyIleIysAsnGlnAlaGlySerGlyCysGluGlyIysAsnPhe 82  
 Db 297 GACGGTTCCTTTCACGGCATCAAGAACAGCGCGGAGCGGTGCGAGGGCAAGAACTTC 356  
 Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
 Db 357 TACACCGCGAGCGGCTTCTGAGCGCGCTCAACGCGTACCCGGGCTTCGCCATCGCGGG 416  
 Qy 103 SerGluValGluArgGlyAlaAlaPheAlaHisAlaThrHisGluThr 122  
 Db 417 ACGGAGGTGGAGGCAAGCGGAGATCGCGCTCTTCTTCGCGCAGCTCACGACGAGACC 476  
 Qy 123 GlyHisPheCysTyrIleSerGluValAsnIysSerAsnAlaTyrCysAspProThrIys 142  
 Db 477 GGACATTTCTGCTACATCAGCGAGATCAACAGACCAACGCGCTACTGCGACGCGCAAC 536  
 Qy 143 ArgGlnTyrProCysAlaAlaGlyGlnIysTyrTyrGlyArgGlyProLeuGlnIleSer 162  
 Db 537 AGCGAGTGGCGGTGCGCGGCGGAGAGTACTACGCGGCGGCGCGCTCGCATCTCG 596  
 Qy 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182

Db 597 TGGAACTACAACTACGCGCGCC -GGAGGAGCATCGGCTTCAACGGGCTCGCGACCCC 655  
 Qy 183 GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202  
 Db 656 AACAGGGTGGCGAGGACGCGGTGATCGGTTCAAGACGCGCTCTGTGTTCTGGATGAC 715  
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 DEFINITION 5', mRNA sequence.  
 ACCESSION CA197556  
 VERSION CA197556.1 GI:35227930  
 KEYWORDS EST.  
 SOURCE Saccharum officinarum  
 ORGANISM Saccharum officinarum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.  
 REFERENCE 1 (bases 1 to 647)  
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
 TITLE The libraries that made SUCEST  
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br  
 Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bccccenter.fcav.unesp.br>  
 Plate: 067 row: A column: 11  
 Seq primer: T7 Promoter Primer.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:4547"  
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 /lab\_host="DH10B"  
 /clone\_lib="AD1"  
 /notes="Organ: seedlings inoculated with Gluconacetobacter diazotrophicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Gluconacetobacter diazotrophicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.51e-90 Length: 647  
 Score: 1020.50 Matches: 185  
 Percent Similarity: 88.29% Conservative: 11  
 Best Local Similarity: 83.33% Mismatches: 19  
 Query Match: 70.28% Indels: 7  
 DB: 6 Gaps: 2  
 US-10-692-367-12 (1-257) x CA197556 (1-647)  
 Qy 31 GlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 50  
 Db 3 CAGTCGGCGCGTCCGCTCGCGCGCGGTAGCCAGCGGTGGCAGCAGTGTGTGG 62  
 Qy 51 GlySerGlyGlyAlaAsnValAlaAsnValThrAspAlaPheAsnGlyIleIys 70

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Db 63 -----AACGTGGCTAGCGTTGTCTACCGACGCAATCTTCAACGGCATCAAG 107
Qy 71 AsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuGlu 90
Db 108 AACCAAGCGCGGAACGGTGGAGGCAAGAACTTCTACACCGAGTGGCTTCTTGAGC 167
Qy 91 AlaIleAlaAlaTyrProGlyPheAlaHisGlyCysSerGluValGluArgLysArgGlu 110
Db 168 GCCCGCGACTCTGTACAAGGGCTTC-----GGTGGCGGGTGGAGGGCAACGGCGAG 221
Qy 111 IleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGlu 130
Db 222 ATCCCGCGCTCTTCGGCAGCTCAGCAGACGAGACGACATTTCTGTACATCAGCGAA 281
Qy 131 ValAsnLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGly 150
Db 282 ATCAACAAGAACCAACGCTACTGCGACTCGAGCAACAGGCAAGTGGCGCGCGGA 341
Qy 151 GlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrPheTyrAsnTyrGlyProAla 170
Db 342 CAGAAGTACTACGGGCGCGCGCTCGAGATCTCGTGAACACTACAACACTACGGGCGCTGCC 401
Qy 171 GlyArgAlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaVal 190
Db 402 GGCAGGACATCGGCTTCAACGGGCTCGGGACCCCAACAGGGTGGCGAGACGCCGTG 461
Qy 191 ValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMetProGln 210
Db 462 ATCCGGTTCAAGACGGCGCTCTGCTTCTGGACGAAACAGCTGCACCGCGGTGATGTCGAG 521
Qy 211 GlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsnPro 230
Db 522 GGGTTCGGAGCACCATCAGGGCTATCAACGGAGCCCTCGAGTCAACGGAAACAACCCC 581
Qy 231 AlaGlnMetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyValAsp 250
Db 582 GCCCAGATGAACGGCGGGTGGGTACTTACAAAGCAGTACTGTGACGAGCTCGGCGTGCAC 641
Qy 251 ProGly 252
Db 642 CCGGGC 647

RESULT 11
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          mays cDNA, mRNA sequence.
ACCESSION BM736454
VERSION   BM736454.1 GI:19057787
KEYWORDS  EST.
SOURCE    Zea mays
          Zea mays
          Zea mays
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          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          Zea mays (bases 1 to 628)
          Walbot, V.
REFERENCE Zea mays from various cDNA libraries sequenced at Stanford
AUTHORS   University
          Unpublished (1999)
          Contact: Walbot V
JOURNAL   Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
COMMENT   Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 952051 row: A column: 06.
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FEATURES
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/lab_host="DH10B"
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rRNA)"
/notes="vector: pUC19, Site 1: EcoRI; Site 2: EcoRI; The
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis System
(Promega). cDNA was synthesized using both random and
oligo(dT) primers in separate reactions and equipped with
EcoRI adaptors. Library was size-fractionated on agarose
gels (for insert size >400bp) and non-directionally cloned
into EcoRI-digested pUC19 vector. Blue/white selection on
carbenicillin-containing plates was used to recover
positive clones."

ORIGIN
Alignment Scores: 1.5e-87 Length: 628
Pred. No.: 990.00 Matches: 180
Score: 92.68% Conservative: 10
Percent Similarity: 87.80% Mismatches: 15
Best Local Similarity: 68.18% Indels: 1
Query Match: 4 Gaps: 0
DB: 4

US-10-692-367-12 (1-257) x BM736454 (1-628)
Qy 53 GlyAlaAlaAlaValAlaAlaValValThrAspAlaPheAsnGlyIleLysAsnGln 72
Db 3 GGGCGGCGCAACGGTGAACGTGGC-AGCGACGCTTCTTCAACGGCATCAAGAACGAG 61
Qy 73 AlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuGluAlaIle 92
Db 62 GCCGGAGCGGTGGAGGCGCAAGAACTTCTACACCGAGCGGCTTCTTGAGCGCGTC 121
Qy 93 AlaAlaTyrProGlyPheAlaHisGlyGlySerGluValGluArgLysArgGluIleAla 112
Db 122 AACAAAGTACCGCGGCTTCGCCCATGCGGGACGAGGTGGAGGCAAGCGGAGATCGCC 181
Qy 113 AlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluValAsn 132
Db 182 GCCTTCTTCGGCAGCTGCAGCAGACCGGACATTTCTGTACATCAGCGAGATCAAC 241
Qy 133 LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGlyGlnLys 152
Db 242 AAGAGCAACGCTTACTCGGACGCAAGCAACAGGCAAGTGGCGCGGGCGGAGAG 301
Qy 153 TyrTyrGlyArgGlyProLeuGlnIleSerTyrPheTyrAsnTyrGlyProAlaGlyArg 172
Db 302 TACTTACGGCGCGCGCTGCGAGATCTCGTGGAACTTACAACTACGCGCGCGCGGAGG 361
Qy 173 AlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaValAla 192
Db 362 GACATCGGCTTCAACGGGCTCGCGGACCCCAACAGGGTGGCGGAGGACCGCTGCGG 421
Qy 193 PheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMetProGlnGlyPhe 212
Db 422 TTCAGACGGGCTCTGTGTTCTGGATGAACAACGTCGACCGTGTGATGCCCGGCTTC 481
Qy 213 GlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsnProAlaGln 232
Db 482 GGGCGCACCATCAGGGCCATCAACGGCGCTTCAGTGTCAACGGGAAACAACCCCGCCAG 541
Qy 233 MetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyValAspProGly 252
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Qy 253 AsnAsnLeuThrCys 257
Db 602 CCCAACCTCACTTGC 616
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RESULT 12
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ACCESSION BM895383
VERSION BM895383.1 GI:19350851
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 625)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952073 row: H column: 05.
FEATURES
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                rRNA)"
                /note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The
                library was prepared by George Rudenko using poly (A)
                selected RNA and Universal Riboclone cDNA Synthesis System
                (Promega). cDNA was synthesized using both random and
                oligo(dT) primers in separate reactions and equipped with
                EcoRI adaptors. Library was size-fractionated on agarose
                gels (for insert size >400bp) and non-directionally cloned
                into EcoRI-digested pUC19 vector. Blue/white selection on
                carbenicillin-containing plates was used to recover
                positive clones."
ORIGIN
Alignment Scores:
Pred. No.: 1.87e-87 Length: 625
Score: 989.00 Matches: 179
Percent Similarity: 93.60% Conservative: 11
Best Local Similarity: 88.18% Mismatches: 13
Query Match: 68.11% Indels: 1
DB: 5 Gaps: 0
US-10-692-367-12 (1-257) x BM895383 (1-625)
Qy 50 GlyGlySerGlyGlyAlaAsnValAlaAsnValThrAspAlaPheAsnGlyIle 69
Db 13 GGAGGCAGTGGCGGTGGAAGCTGGCTAACGG-GTCAGCGACGGCTTCTTCAACGGCATC 71
Qy 70 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 89
Db 72 AAGAACACAGGCCGCGAGCGGTGGAGGCGCAAGAACTTCTACCCGAGCGCGTCTCTG 131
Qy 90 GluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGlySerGluValGluArg 109
Db 132 AGCCCGGTGCAACAGTACCCGGCTTCGCCCATGGCGGACGGAGGTGGAGGCAAGCGC 191
Qy 110 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 129

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Db 192 GAGATCGCCGCTTCTTCGCGCACGTCACGACGAGACCGACATTTCTGTACATCAGC 251
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Db 252 GAGATCAACAAAGAGCAACGCTTACTGCGACGCAAGCAAGGAGTGGCGTGGCGGCG 311
Qy 150 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro 169
Db 312 GGGCAGAAGTACTACGGGGCGCGCGCTCGACATCTCGTGGAACTACAACTACGGGCCC 371
Qy 170 AlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAla 189
Db 372 GCGGGAGGAGACATCGGCTTCAACGGGCTCGCGACCCCAACAGGGTGGCGGAGACGCC 431
Qy 190 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMetPro 209
Db 432 GTGATCGGTTCAAGACGGCGCTCTGGTTCTGGATGAACACGTGCACTGCTGATGCCG 491
Qy 210 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsn 229
Db 492 CAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGGCGCTCGAGTCAACGGGAAACAAC 551
Qy 230 ProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyVal 249
Db 552 CCGGCCCAAGATGAACGGCGCGTCTGCTACTACAAGCAGTACTGCCACGAGCTCCGCGTC 611
Qy 250 AspProGly 252
Db 612 GACCCAGGG 620
RESULT 13
CA270202
LOCUS
DEFINITION CA270202.1 GI:35976513
5', mRNA sequence.
ACCESSION CA270202
VERSION CA270202.1
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 786)
AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 051 row: F column: 10
Seq primer: T7 Promoter Primer.
FEATURES
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        Location/Qualifiers
            1..786
                /organism="Saccharum officinarum"
                /mol_type="mRNA"
                /db_xref="taxon:4547"
                /clone="SCQSLB2051F10"
                /lab_host="DH10B"
                /clone_lib="LB2"
                /note="Organ: Lateral buds from plants adult plants
                growing in greenhouse; Vector: pSport1; Site 1: SalI;
                Site 2: NotI; An unidirectional cDNA library generated
                from [lateral buds from plants adult plants growing in

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greenhouse]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://auceut.lad.ic.unicamp.br/public>.

## ORIGIN

Alignment Scores:  
Pred. No.: 1.73e-86 Length: 786  
Score: 980.50 Matches: 183  
Percent Similarity: 84.48% Conservative: 13  
Best Local Similarity: 78.88% Mismatches: 25  
Query Match: 67.53% Indels: 11  
DB: 6 Gaps: 2

US-10-692-367-12 (1-257) x CA270202 (1-786)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThr 22  
Db 117 CAAACTCGCGCTGCCAGCAAACTACTGCTGCAGCAAGTTCTGGGTACTCGGCAGCACC 176

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 177 GACGACTACTGTGGGACGGGTGCCAGTTCGGGCCGCTGCCGCTGGGGGGGGCAGCCCA 236

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 237 GCGCGTGGCAGCAGTGGTGGTGGG-----AACGTGGGTAGCGTGTGTCAAC 281

Qy 63 AspaIaPheAenGlyIleGlyAenGlnAlaGlySerGlyCysGlyGlyGlyAenPhe 82  
Db 282 GACGATTCITCAACGGGATCAAAACACGCGCGGAAACGGGTGCGAGGGCAAGATTC 341

Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 342 TACACCGGAGTGGTCTCTGAGCGCGCCGACCTGCTACAAAGTTTC-----GGTGGC 395

Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122  
Db 396 GGGTCGGTGGAGGCAAGCGGAGATCGCCCTTCTTCGGCGCAGCTCAGCAGCAGCAGC 455

Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAenAlaTyrCysAspProThrLys 142  
Db 456 GGACATTTCTCTACATCAGCGGAAATCAACAGAACACCGCTACTCGACTCGAGCAAC 515

Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162  
Db 516 AGGAGTGGCGTGGCGCGGACAGAGTACTACGGCGCGCGCGCGCGCGCGCGCGCGCG 575

Qy 163 TrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAenGlyLeuGlyAspPro 182  
Db 576 TGGAACTACAACTACGGCGCTCGCGGAGGAGACATCGCTTCAACGGGCTCGGCAACCC 635

Qy 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAen 202  
Db 636 GACAGTGGCGCGGACGCGCGTTCGAGACGGCGCTCGGTCTTCTTATGAAC 695

Qy 203 AsnValHisArgVal-MetProGlnGlyPheGlyAlaThr-IleArgAlaIle-AsnGly 221  
Db 696 AACTTGACCGGGTGAATGTCNAGGGGTTTCGGACCCACCCATTCAGGCTATTAAACGA 755

Qy 222 Ala-LeuGluCysAenGlyAenAenPro 230  
Db 756 ACCCTCGAGTCAAGAGAAACCAACCC 783

## RESULT 14

CN151443  
LOCUS  
DEFINITION WOUND1\_75\_B02.g1 A002 Wounded leaves Sorghum bicolor cDNA clone  
WOUND1\_75\_B02\_A002 5', mRNA sequence.  
CN151443  
ACCESSION

## VERSION

CN151443.1 GI:45994576

## KEYWORDS

Sorghum bicolor (sorghum)

## SOURCE

Sorghum bicolor

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

## REFERENCE

## AUTHORS

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Anfuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.

## TITLE

A Sorghum EST database: mechanically damaged and methyl

## JOURNAL

jasmonate-treated leaves

## COMMENT

Unpublished (2003)

Other ESTs: WOUND1\_75\_B02.b1\_A002

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTCGG).

## FEATURES

## source

Location/Qualifiers

1..801

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/clones="WOUND1\_75\_B02\_A002"

/lab\_host="DH10B-Ti phage-resistant E. coli"

/clone\_lib="Wounded leaves"

/note="Organ: Leaf; Vector: pME188-FL3; Site 1: XhoI;

Site 2: XhoI. The library was prepared from polyA+ RNA

harvested from 8-day-old hydroponically grown, BTx623 sorghum seedlings. For some plants, one-half of the second leaf was crushed without damaging the midvein. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 uM. Leaves were harvested 3 and 27 hr after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME188-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.5e-86 Length: 801  
Score: 977.50 Matches: 176  
Percent Similarity: 83.70% Conservative: 14  
Best Local Similarity: 77.53% Mismatches: 29  
Query Match: 67.32% Indels: 8  
DB: 7 Gaps: 2

US-10-692-367-12 (1-257) x CN151443 (1-801)

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Db 138 CAGAACTCGCGCTGCCAGCAAACTACTGCTGCAGCAAGTTCTGGGTACTCGGCAGCACC 197

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42

Db 198 AGCGAGTACTGTGCACCGCGGTGCGGTGCGGCGCCCTGCACA-----GGG 242

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:14:26 ; Search time 2450.33 Seconds  
(without alignments)  
14890.544 Million cell updates/sec

Title: US-10-692-367-69  
Perfect score: 753  
Sequence: 1 tcgatgcagactcgcgctg.....ggcccaacctacttgcga 753

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	715.6	95.0	1094	6 AR321624	AR321624 Sequence
2	688.2	91.4	810	8 MZECHITB	M84165 Zea mays ch
3	638.2	84.8	843	8 MZECHITA	M84164 Zea mays ch
4	582.6	77.4	1121	8 AY532735	AY532735 Zea mays
5	578.6	76.8	1127	8 AY532723	AY532723 Zea mays
6	574.8	76.3	1080	8 AY532739	AY532739 Zea diplo
7	573.8	76.2	1081	8 AY532737	AY532737 Zea diplo
8	573.8	76.2	1081	8 AY532738	AY532738 Zea diplo
9	573.8	76.2	1081	8 AY532742	AY532742 Zea diplo
10	572.4	76.0	1114	8 AY532725	AY532725 Zea mays
11	570.4	75.8	1134	8 AY532734	AY532734 Zea mays
12	570.2	75.7	1123	8 AY532729	AY532729 Zea mays
13	568.2	75.5	1127	8 AY532733	AY532733 Zea mays
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15	562.6	74.7	1122	8 AY532736	AY532736 Zea diplo
16	561.8	74.6	1133	8 AY532727	AY532727 Zea mays
17	561.2	74.5	789	8 AY047607	AY047607 Sorghum b
18	561.2	74.5	819	8 AY047608	AY047608 Sorghum b
19	560.2	74.4	1123	8 AY532726	AY532726 Zea mays

20	559.6	74.3	1127	8 AY532730	AY532730 Zea mays
21	558.2	74.1	1130	8 AY532722	AY532722 Zea mays
22	555.6	73.8	1126	8 AY532732	AY532732 Zea mays
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26	548.8	72.9	1140	8 AY532731	AY532731 Zea mays
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39	538.8	71.6	1138	8 AY532728	AY532728 Zea mays
40	535.8	71.2	985	8 AY532721	AY532721 Tripsacum
41	535.2	71.1	1120	8 AY532769	AY532769 Zea mays
42	533	70.8	1094	8 AY532775	AY532775 Zea mays
43	532.6	70.7	1131	8 AY532780	AY532780 Zea mays
44	532.4	70.7	1122	8 AY532771	AY532771 Zea mays
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ALIGNMENTS

RESULT 1  
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LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6563020.  
ACCESSION AR321624  
VERSION AR321624.1 GI:33706864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1094)  
AUTHORS Simmons,C.R. and Yalpani,N.  
TITLE Maize chitinases and their use in enhancing disease resistance in crop plants  
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;  
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Db	329 CAAGAGCCAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTTACACCCGAGCGGTTTCTT 388
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LOCUS Zea mays chitinase B (seed chitinase) gene, 3' end. 810 bp DNA linear PLN 27-APR-1993
DEFINITION M84165
ACCESSION M84165.1 GI:168442
VERSION chitinase B.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Huyth, Q.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R.
and Shah, D.M.
Antifungal proteins from plants. Purification, molecular cloning,
and antifungal properties of chitinases from maize seed
J. Biol. Chem. 267 (10), 6635-6640 (1992)
PUBMED 1551872
COMMENT Original source text: Zea mays (library: Lamda GT 10 corn seed
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Best Local Similarity 95.9%; Pred. No. 1.1e-82;
Matches 718; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
Qy 6 GCAGAACTGCGGCTGCAGCCAAACGATATCTGCAGCAAGTTTCGGCTACTGCGGCAAC 65
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Qy 123 CAGCAGTGGCGGCTGCTGCAACGTTAGGCTCGTCAACCGGCTCTCTTCTTCAACGG 182
Db 180 CGGCGAGTGGTGGCGGCTGGTGGCAACGTTAGGCTCGTCAACGCTCTCTTCTTCAACGG 239
Qy 183 CATCAAGAACCCAGCCCGGAGCGGTCGAGGGCAAGAACTTTTACACCGGAGCGGCTT 242
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Db 780 CGTCGAGCCAGGGCCCAACCTCACTTGTCT 808
RESULT 3
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LOCUS Zea mays chitinase A (seed chitinase) gene, complete cds. 843 bp DNA linear PLN 27-APR-1993
DEFINITION M84164
ACCESSION M84164.1 GI:168440
VERSION chitinase A.
KEYWORDS Zea mays
SOURCE
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Db 586 ACATCAGCGAGATCAACAGAGCAACGCTACTTGGACCCGACCAAGAGGCGAGTGGCGGT 645
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Qy 599 TGATGCGCGAGGGCTTTCGGCGCCACCATCAGGGGCCATCAAGCGGCGCTCGAGTGGCGACG 658
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RESULT 6
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LOCUS Zea diploperennis isolate d5 chitinase (chIB) gene, complete cds.
DEFINITION AY532739
ACCESSION AY532739
VERSION AY532739.1 GI:48093259
KEYWORDS
SOURCE Zea diploperennis
ORGANISM Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1080)
Tiffin, P.
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
15280246
2 (bases 1 to 1080)
Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Query Match 76.3%; Score 574.8; DB 8; Length 1080;
Best Local Similarity 84.2%; Pred. No. 1.4e-67;
Matches 721; Conservative 0; Mismatches 22; Indels 113; Gaps 2;
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RESULT 7
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LOCUS      1081 bp      DNA      linear      PLN 29-JUL-2004
DEFINITION Zea diploperennis isolate d2 chitinase (chiB) gene, complete cds.
ACCESSION  AY532737
VERSION     AY532737.1  GI:48093255
KEYWORDS
SOURCE      Zea diploperennis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1081)
AUTHORS     Tiffin, P.
TITLE       Comparative evolutionary histories of chitinase genes in the genus
            ze and family poaceae
JOURNAL     Genetics 167 (3), 1331-1340 (2004)
PUBMED      15280246
REFERENCE   2 (bases 1 to 1081)
AUTHORS     Tiffin, P.
TITLE       Direct Submission
JOURNAL     Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
            1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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gene
mRNA
CDS
ORIGIN
Query Match      76.2%; Score 573.8; DB 8; Length 1081;
Best Local Similarity 84.1%; Pred. No. 1.9e-67;
Matches 721; Conservative 0; Mismatches 22; Indels 114; Gaps 2;

QY      6  CGAGAACTCGCGTCCAGCAAGATGCTGTCGAGCAAGTTCGCGTACTCGGCAAC 65
Db      106 CGAGAACTCGCGTCCAGCAAGATGCTGTCGAGCAAGTTCGCGTACTCGGCAAC 165
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QY      126 CAGTGGCGCGGTGTCGGAAGTGGCTAGCGTCTGTCACCGGCTCTCTTCAACGGCAT 185
Db      223 CAGTGGCGCGGTGTCGGAAGTGGCTAGCGTCTGTCACCGGCTCTCTTCAACGGCAT 282
QY      186 CAAGAACAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGCGAGCGGTCTCT 245
Db      283 CAAGAACAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGCGAGCGGTCTCT 342
QY      246 GAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCATGCGCGGTTCACAGGTGCGAGGCGAAGCG 305

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675  GATGAACGCGCGCATCGGCTACTTACAAGAGAGTACTCGCGCGAGTTCGCGGCTCGAGCCAGG 734
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735  GCCCAACCTCACCTGCT 751
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RESULT 8
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LOCUS      1081 bp      DNA      linear      PLN 29-JUL-2004
DEFINITION Zea diploperennis isolate d4 chitinase (chiB) gene, complete cds.
ACCESSION  AY532738
VERSION     AY532738.1  GI:48093257
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SOURCE      Zea diploperennis
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1081)
AUTHORS     Tiffin, P.
TITLE       Comparative evolutionary histories of chitinase genes in the genus
            ze and family poaceae
JOURNAL     Genetics 167 (3), 1331-1340 (2004)
PUBMED      15280246
REFERENCE   2 (bases 1 to 1081)
AUTHORS     Tiffin, P.
TITLE       Direct Submission
JOURNAL     Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
            1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Query Match      76.2%; Score 573.8; DB 8; Length 1081;
Best Local Similarity 84.1%; Pred. No. 1.9e-67;
Matches 721; Conservative 0; Mismatches 22; Indels 114; Gaps 2;

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LOCUS   AY532742 1081 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea diploperennis isolate d8 chitinase (chiB) gene, complete cds.
ACCESSION AY532742
VERSION  AY532742.1 GI:48093265
KEYWORDS
SOURCE  Zea diploperennis
ORGANISM Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1081)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1081)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Query Match      76.2%; Score 573.8; DB 8; Length 1081;
Best Local Similarity 84.1%; Pred. No. 1.9e-67;
Matches 721; Conservative 0; Mismatches 22; Indels 114; Gaps 2;

Qy      6 GCAGAACTGCGGCTGCCAGCCAAAGTATGCTGCAGCAAGTTCGGCTACTCGGCACAAC 65
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AUTHORS	Tiffin, P.
DIRECT SUBMISSION	Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
JOURNAL	Location/Qualifiers
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ORIGIN	Query Match 76.0%; Score 572.4; DB 8; Length 1114; Best Local Similarity 83.7%; Pred. No. 2.9e-67; Matches 725; Conservative 0; Mismatches 21; Indels 120; Gaps 2; QY 6 GCAGAACTCGCGTGCAGCCAAACGTAATGCTCAGCAAGTTCCGGTACTGCGGCAAC 65 Db 106 GCAGAACTCGCGTGCAGCCAAACGTAATGCTCAGCAAGTTCCGGTACTGCGGCAAC 165 QY 66 CGACGAGTACTCGCGGACGGGTGCAGTCCGCGCGCGTCCGCTCG---GGCGCGCGCG 122 Db 166 CGACGAGTACTCGCGGACGGGTGCAGTCCGCGCGCGTCCGCTCGCGCGCGCGCG 225 QY 123 CAGCAGTGGCGCGGTGGTGCAGAACTGCTAGCGTCTCAGCGGCTCTCTTTCAACGG 182 Db 226 CAGCAGTGGCGCGGTGGTGCAGAACTGCTAGCGTCTCAGCGGCTCTCTTTCAACGG 285 QY 183 CATCAAGAACACGCGCGGAGCGGTCGAGGCGCAGAACTTCTACACCGGAGCGGCTT 242 Db 286 CATCAAGAACACGCGCGGAGCGGTCGAGGCGCAGAACTTCTACACCGGAGCGGCTT 345 QY 243 CCTGAGCGCGTCAAGCGCTACCCAGGCTTTCGCCCATGGCGGGTTCACAGGTGCAGGGCAA 302 Db 346 CCTGAGCGCGTCAAGCGCTACCCAGGCTTTCGCCCATGGCGGGTTCGCGGTGCAGGGCAA 405 QY 303 GCGCGAGATCGCGCTCTTTCGCGCACGCCACGACGACGACCGGGC----- 349 Db 406 GCGCGAGATCGCGCTCTTTCGCGCACGCCACGACGACGACCGGGCTAAGTTGGGCTCG 465 QY 350 ----- 349 Db 466 GTCTTCGCGCGCGCAGGTTCTTTGATTTTGTACCATCATGCTGATCAATTTCTTTT 525 QY 350 -----ATTTCTGTATCATCAG 365 Db 526 TTTTGTGGAAAAATTCGCTGCTGTGTCTGTGTGCGAGCGGCGAGATTTCTGCTACATCAG 585 QY 366 CGAGATCAGCAAGAGCAACGCTTACTTCGACCCGACCAAGAGGAGTGGCGGCGCGCG 425 Db 586 CGAGATCAACAGAGCAACGCTTACTTCGACCCCGAGCAAGAGGAGTGGCGGCGCGCG 645 QY 426 GGGCGAGAGTACTACGGGCGGCGCGCTCGAGATCTCTGTGGAACACTACAACTAGGGCC 485

Db 646 GGGGAGAGTACTACGGGGCGGGCGCTGCAGATCTCGTGGAATCAACTACGGGCC 705  
Qy 486 CGCGGGAGGAGCATCGGCTTCGACGGGCTCGGGACCCCGGCGAGGTGGCGCGGACGC 545  
Db 706 CGCGGGAGGAGCATCGGCTTCGACGGGCTCGGGACCCCGGCGAGGTGGCGCGGACGC 765  
Qy 546 CGTGTGGCGTTCAAGGGCGGCTCTGGTTCTGGATGAACAACGTGACACGTTGATGCC 605  
Db 766 CGTGTGGCGTTCAAGGGCGGCTCTGGTTCTGGATGAACAACGTGACACGTTGATGCC 825  
Qy 606 CGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCGGAACA 665  
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Db 886 CCCGCCCGAGATGAACGGCGCGCTCGGCTACTACAGGCGAGTACTCGCGCCAGCTCGGCGT 945  
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## RESULT 11

LOCUS AY532734 1134 bp DNA linear PLN 29-JUL-2004  
DEFINITION Zea mays subsp. parviglumis isolate p13 chitinase (chiB) gene,  
complete cds.  
ACCESSION AY532734  
VERSION AY532734.1 GI:48093249

## KEYWORDS

SOURCE Zea mays subsp. parviglumis

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

Tiffin,P.  
Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
REFERENCE 2 (bases 1 to 1134)  
Tiffin,P.  
Direct Submission  
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA

## FEATURES

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## gene

## mRNA

## CDS

## ORIGIN

Query Match 75.8%; Score 570.4; DB 8; Length 1134;  
Best Local Similarity 83.5%; Pred. No. 5.3e-67;  
Matches 725; Conservative 0; Mismatches 21; Indels 122; Gaps 2;  
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Db 178 CGACAGTACTGCGGGCGACCGGGTGCAGTCCAGTCCGGGCCCGTGCCTCGCGCGCGCGCGG 237  
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Qy 303 GCGGAGATCGCGGCTTCTTCGGGCAAGCGCAAGCAGAGACCGGGC----- 349  
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Qy 350 ----- 349  
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Qy 724 GTGACCCAGGGCCCAACCTCACTTGTCT 751  
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## RESULT 12

AY532729  
LOCUS AY532729 1123 bp DNA linear PLN 29-JUL-2004  
DEFINITION Zea mays subsp. parviglumis isolate p6 chitinase (chiB) gene,  
complete cds.  
ACCESSION AY532729  
VERSION AY532729.1 GI:48093239

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KEYWORDS
SOURCE
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1123)
AUTHORS
Tiffin,P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1123)
AUTHORS
Tiffin,P.
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Best Local Similarity 83.4%; Pred. No. 5.7e-67;
Matches 728; Conservative 0; Mismatches 18; Indels 127; Gaps 2;
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Qy 123 CAGCAGTGGCGGCGGTGTCGACGCTGAGTGGTCTGCTACCGGCTCTTCTTCAACGG 182
Db 229 CAGCAGTGGCGGCGGTGTCGACGCTGAGTGGTCTGCTACCGGCTCTTCTTCAACGG 288
Qy 183 CATCAAGAACGAGCGCGGCGGTGCGAGGGCAAGAACTTCTACACCGCGAGCGGCTT 242
Db 289 CATCAAGAACGAGCGCGGCGGTGCGAGGGCAAGAACTTCTACACCGCGAGCGGCTT 348
Qy 243 CCTAGCGCGCTCAAGGGCTACCGAGGCTTCGCCCATGCGCGGCTCACAGGTGCAAGGCAA 302
Db 349 CCTAGCGCGCTCAAGGGCTACCGAGGCTTCGCCCATGCGCGGCTCGCAGGTGCGAGGCAA 408
Qy 303 GCGCGAGATCGCGCTTCTTTCGCGCAGCGCACGACGACGAGACCGGGC----- 349
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ORIGIN
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Qy      183 CATCAAGAACCAAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCCGGAGCGGTT 242
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Qy      243 CTTGAGCCCGCTCAAGGCGTACCAGGCTTCGCCCATGCGCGGTGCACAGGTGCGAGGGCAA 302
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Qy      303 GCGGAGATCGCGCTCTTTTCGCGACCGCACCGCACGACGAGACCGGCGC----- 349
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Qy      417 GTGCGCGCGGGGCGAGTACTAGCGGCGGCGCGCTGTCAGATCTCTGTGGAATCAAA 476
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DEFINITION
ACCESSION  AY532741
VERSION     AY532741.1
KEYWORDS    Zea diploperennis
SOURCE      Zea diploperennis
ORGANISM    Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1111)
AUTHORS    Tiffin, P.
TITLE      Comparative evolutionary histories of chitinase genes in the genus
            Zea and family poaceae
            Genetics 167 (3), 1331-1340 (2004)
PUBMED     15280246
REFERENCE   2 (bases 1 to 1111)
AUTHORS    Tiffin, P.
TITLE      Direct Submission
JOURNAL    Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
            1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
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Db      106 GCAGAACTGCGGCTGCCAGCCAAAGTCTGTCGACGAAGTTCCGCTACTCGGCACAAAC 165

Qy      66  CGACGAGTACTGCGCGACGCGGTGCCAGTCCGGCCCGTCCGCTCG---GGCGGCGGCG 125
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Qy      126 CAGTGGCGCGGTGGTGCAGAACGTTAGCGTCTGTCACCGGCTCTTTCTTCAACGGCAT 185
Db      223 CAGTGGCGCGGTGGTGCAGAACGTTAGCGTCTGTCACCGGCTCTTTCTTCAACGGCAT 282

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Db 283 CAAGAACAGCGCCGGGAGCGGTGCGAGGGCAAGAACTTCTACACCCGCGCGGTTCCT 342
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Db 343 GAGCGCGTCAAGCGGTACCCAGCGTTCGCCCATGCGGGTTCGAGGTGCAGGCGCAAGCG 402
Qy 306 CGAGATCGCCCGCTTCTTCGCGCACCGCACCGACGAGACCGGGC----- 349
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Qy 350 ----- 349
Db 463 TTCGCGCGCGCAGGTTCTTTGATTTTAAATTTGACCCATCATCTCATCAAAATTTTT 522
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Qy 724 GTCGACCCAGGCGCGCAACTCACTTGTCT 751
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LOCUS Zea diploperennis isolate d1 chitinase (chiB) gene, complete cds.
DEFINITION
ACCESSION AY532736
VERSION AY532736.1 GI:48093253
KEYWORDS
SOURCE
ORGANISM
Zea diploperennis
Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1122)
Tiffin,P.
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
15280246
REFERENCE 2 (bases 1 to 1122)
Tiffin,P.
Direct Submission
AUTHORS
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
LOCATION/Qualifiers
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source
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mRNA
CDS

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ORIGIN
Query Match 74.7%; Score 562.6; DB 8; Length 1122;
Best Local Similarity 82.9%; Pred. No. 5.9e-66;
Matches 724; Conservative 0; Mismatches 19; Indels 130; Gaps 2;
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Db 106 GCAGAACTCGCGCTGCAGCGCAACGATATCTGCAGCAAGTTCGGCTACTCGGCAACAAC 165
Qy 66 CGACAGTACTCGCGCGCGCGCGCTGCAGTGCAGCGCGCGCGCGCGCGCGCGCGAG 125
Db 166 CGACAGTACTCGCGCGCGCGCGCTGCAGTGCAGCGCGCGCGCGCGCGCGCGCGAG 222
Qy 126 CAGTGGCGCGGTGGTGCAGAAAGTGGTACGCTGCTCAGCGGCTCTTCTTCAACGGCAT 185
Db 223 CAGTGGCGCGGTGGTGCAGAAAGTGGTACGCTGCTCAGCGGCTCTTCTTCAACGGCAT 282
Qy 186 CAGAACACCGCGCGCGCGCGCTGCAGCGCGCAAGAACTTCTACACCGCGCGCGGTTCCT 245
Db 283 CAGAGCAGCGCGCGCGCGCGCTGCAGCGCGCAAGAACTTCTACACCGCGCGCGGTTCCT 342
Qy 246 GAGCGCGCTCAAGCGGTACCCAGCGTTCGCCCATGCGGGTTCACAGTGCAGGCGCAAGCG 305
Db 343 GAGCGCGCTCAAGCGGTACCCAGCGTTCGCCCATGCGGGTTCGAGGTGCAGGCGCAAGCG 402
Qy 306 CGAGATCGCGCGCTTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349
Db 403 CGAGATCGCGCGCTTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 462
Qy 350 ----- 349
Db 463 TATTAACCTCGCTTTCAGCGCGCGCGCGCGGTTCCTTGAATTTTGAACCATCATCTGATC 522
Qy 350 -----ATTTCGTGT 358
Db 523 AATTTTITTTTGGAAAATTTTTCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 582
Qy 359 ACATCAGCGAGATCAGCAAGAGCAAGCGCTTCTGCAGCGCGCGCGCGCGCGCGCGCGGT 418
Db 583 ACATCAGCGAGATCAGCAAGAGCAAGCGCTTCTGCAGCGCGCGCGCGCGCGCGCGCGGT 642
Qy 419 GCGCGCGCGCGCGAGAACTACTACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478
Db 643 GCGCGCGCGCGCGAGAACTACTACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 702
Qy 479 ACGGCGCGCGCGCGAGGAGCATCTCGGCTTCGACGCGGCTCGGGGACCCCGCGAGGGTGGCG 538
Db 703 ACGGCGCGCGCGCGAGGAGCATCTCGGCTTCGACGCGGCTCGGGGACCCCGCGAGGGTGGCG 762
Qy 539 GGGACGCGGTGGTGGCGGTTCAGCGCGCGCGCTCTGGTTCTGGATGAACCAACGTCGACCGTG 598
```



Db	763	GGGACGCGTGGTGGCGTTCAAGGGGGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGG	822
Qy	599	TGATGCGCGCAGGGCTTCGGCGCCACCATCAGGGGCCATCAACGGCGCGCTCGAGTGCACG	658
Db	823	TGGTGGCGCAGGGGTTCGGCGCCACCATCAGGGGCCATCAACGGCGCGCTCGAGTGCACG	882
Qy	659	GGAAACAACCCCGCCAGATGAACGGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGC	718
Db	883	GGAAACAACCCCGCCAGATGAACGGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGC	942
Qy	719	TCGGCGTCGACCCAGGGCCCAACCTCACTTGT	751
Db	943	TCGGCGTCGACCCCGGGCCCAACCTCACTTGT	975

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Job time : 2457.33 sec

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:11:31 ; Search time 351.104 Seconds  
(without alignments)  
12695.850 Million cell updates/sec

Title: US-10-692-367-69  
Perfect score: 753  
Sequence: 1 tcgatgcagactcgcgctg.....ggcccaacctcacttgctga 753

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001as.\*

5: Geneseq2001bs.\*

6: Geneseq2002as.\*

7: Geneseq2002bs.\*

8: Geneseq2003as.\*

9: Geneseq2003bs.\*

10: Geneseq2003cs.\*

11: Geneseq2003ds.\*

12: Geneseq2004as.\*

13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	753	100.0	753	13	AdS92685 Chitinase
2	732.2	97.2	753	13	AdS92667 Chitinase
3	725.8	96.4	753	13	AdS92671 Chitinase
4	722.6	96.0	753	13	AdS92693 Chitinase
5	719.4	95.5	753	13	AdS92697 Chitinase
6	717.8	95.3	753	13	AdS92651 Chitinase
7	716.2	95.1	753	13	AdS92659 Chitinase
8	715.6	95.0	1094	3	Aaa96222 cDNA enco
9	714.6	94.9	753	13	AdS92637 Chitinase
10	711.8	94.5	753	13	AdS92683 Chitinase
11	711.4	94.5	753	13	AdS92669 Chitinase
12	711.4	94.5	753	13	AdS92665 Chitinase
13	708.2	94.1	750	13	AdS92695 Chitinase
14	701.8	93.2	753	13	AdS92673 Chitinase
15	701.8	93.2	753	13	AdS92647 Chitinase
16	697.8	92.7	771	13	AdS92663 Chitinase
17	696.4	92.5	774	13	AdS92687 Chitinase
18	693	92.0	771	13	AdS92689 Chitinase
19	689.8	91.6	771	13	AdS92677 Chitinase
20	689	91.5	753	13	AdS92643 Chitinase

21	686.6	91.2	771	13	AdS92699	Chitinase
22	685	91.0	771	13	AdS92675	Chitinase
23	683.6	90.8	774	13	AdS92681	Chitinase
24	675.6	89.7	774	13	AdS92679	Chitinase
25	672.4	89.3	774	13	AdS92661	Chitinase
26	671.2	89.1	780	13	AdS92655	Chitinase
27	671.2	89.1	780	13	AdS92691	Chitinase
28	667.6	88.7	774	13	AdS92653	Chitinase
29	664.4	88.2	774	13	AdS92649	Chitinase
30	662.8	88.0	774	13	AdS92645	Chitinase
31	659.6	87.6	774	13	AdS92639	Chitinase
32	659.4	87.6	771	13	AdS92657	Chitinase
33	653.2	86.7	774	13	AdS92627	Chitinase
34	650.4	86.4	756	13	AdS92621	Chitinase
35	648.8	86.2	756	13	AdS92629	Chitinase
36	647.2	85.9	756	13	AdS92625	Chitinase
37	642	85.3	840	11	AdJ12126	Maize cDN
38	640.4	85.0	774	13	AdS92623	Chitinase
39	631.8	83.9	777	13	AdS92619	Chitinase
40	628.6	83.5	765	13	AdS92641	Chitinase
41	625.8	83.1	777	13	AdS92631	Chitinase
42	442	58.7	636	12	AdJ44871	Plant cDN
43	442	58.7	636	12	AdJ44871	Plant cDN
44	418.2	55.5	843	8	AdA70140	Rice gene
45	418.2	55.5	843	11	AdJ11575	Rice DNA

## ALIGNMENTS

### RESULT 1

AdS92685  
ID AdS92685 standard; DNA; 753 BP.

XX AC AdS92685;

XX DT 02-DEC-2004 (first entry)

XX DB Chitinase variant polynucleotide #32.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX DR P-PSDB; AdS92686.

XX New chitinase polynucleotides and polypeptides, useful in producing  
plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 69; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
encoding them. A method of enhancing plant resistance to a fungus or  
nematode comprises introducing into a plant a recombinant expression  
cassette comprising a promoter operably linked to a chitinase  
polynucleotide of the invention. The plant is maize or soybean. The





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XX WO2004037194-A2.
XX
XX PD 06-MAY-2004.
XX
XX PF 22-OCT-2003; 2003WO-US033588.
XX
XX PR 22-OCT-2002; 2002US-0420666P.
XX
XX PR 06-NOV-2002; 2002US-00290086.
XX
XX PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX DR P-PSDB; ADS92694.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 77; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
XX encoding them. A method of enhancing plant resistance to a fungus or
XX nematode comprises introducing into a plant a recombinant expression
XX cassette comprising a promoter operably linked to a chitinase
XX polynucleotide of the invention. The plant is maize or soybean. The
XX fungus is from the genus Fusarium. The nematode is from the genus
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX plant resistance to a fungus or nematode. This sequence represents a
XX chitinase variant polynucleotide of the invention.
XX
XX Sequence 753 BP; 142 A; 244 C; 262 G; 105 T; 0 U; 0 Other;

Query Match          96.0%; Score 722.6; DB 13; Length 753;
Best Local Similarity 97.5%; Pred. No. 9.7e-127;
Matches 734; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TCGATGCGAAGTGGCGGTGCGAGCCAAAGTATGCTGCAGCAAGTTCTGGCTACTGCGGC 60
DB 1 TCGATGCGAAGTGGCGGTGCGAGCCAAAGTATGCTGCAGCAAGTTCTGGCTACTGCGGC 60
QY 61 ACAACCGACGAGTACTGCGGCGACGGGTGCCAGTGGCGGCCGCTGCGGCGCGCGC 120
DB 61 AGCAGCGAGAGTACTGCGGCGACGGGTGCCAGTGGCGGCCGCTGCGGCGCGCGC 120
QY 121 GGCAGCAGTGGCGCGGTGGTGCAGAACGTGGCTAGCGTCCGTACCGGCTCCTTTCTCAAC 180
DB 121 GGCAGCAGTGGCGCGGTGGTGGAACTGGCCAGCATCGTGACCGGCTCCTTTCTCAAC 180
QY 181 GGCATCAGAACCGCGCGGAGCGGTGCGAGGGCAGAACTTACACCGGAGCGCG 240
DB 181 GGCATCAGAACCGCGCGGAGCGGTGCGAGGGCAGAACTTCTACACCGGAGCGCG 240
QY 241 TTCTGTAGCGCGTCAAGCGGTACCGAGCTTTCGCCCATGGCGGTACAGGTGCGAGGC 300
DB 241 TTCTGTAGCGCGCTCAGAGCGTACCAGCGTTCGCCCATGGCGGACGAGGTGAGAGGC 300
QY 301 AAGCGCGAGATGCGCGCTTTCTTCGCGCACGCCACGACGAGACCGGCAATTTCTGTTC 360
DB 301 AAGCGCGAGATGCGCGCTTTCTTCGCGCACGCCACGACGAGACCGGCAATTTCTGTTC 360
QY 361 ATCAGCGAGATCAGAGAGCAACCGCTTCTGCGACCGCGACCGAGAGCAATGCGCGTCC 420
DB 361 ATCAGCGAGATCAGAGAGCAACCGCTTCTGCGACCGCGACCGAGAGCAATGCGCGTCC 420
QY 421 GCGCGCGGCGCAGAGTACTACGGGCGCGCGCGCTGCGAGATCTCGTGGAACTACAACTAC 480
DB 421 GCGCGCGGCGCAGAGTACTACGGAGCGCGCGCGCTGCGAGATCTCGTGGAACTACAACTAC 480
QY 481 GGGCCCCGGGGAGGAGACATCGGCTTTCGACGCGGCTTCGGGGACCCCGCGAGGGTGGCGCG 540
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Db 481 GGGCCCGCGGGAGGGCCATCGGCTTCAGCGGCTCGGGGACCCCAACAGGGTGGCGGG 540
QY 541 GACGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTTGGATGAACAACGTCGACCGGTG 600
DB 541 GACGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTTGGATGAACAACGTCGACCGGTG 600
QY 601 ATGCGCGAGGGCTTCGGCGGCCACCATCAGGGCCCATCAACGGCGCGCTCGAGTGCAGCGG 660
DB 601 ATGCGCGAGGGCTTCGGCGGCCACCATCAGGGCCCATCAACGGCGCGCTCGAGTGCAGCGG 660
QY 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTTACTACAAGCAAGTACTGCGCGCAGTTC 720
DB 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTTACTACAAGCAAGTACTGCGCGCAGTTC 720
QY 721 GGGGTGCGACCGGGGCCCAACCTCACTTGCTGA 753
DB 721 GGGGTGCGACCGGGGCCCAACCTCACTTGCTGA 753
```

## RESULT 5

ADS92697  
ID ADS92697 standard; DNA; 753 BP.XX AC  
XX ADS92697;

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #38.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92698.

XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 81; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.

XX Sequence 753 BP; 140 A; 240 C; 263 G; 110 T; 0 U; 0 Other;

Query Match 95.5%; Score 719.4; DB 13; Length 753;

Best Local Similarity 97.2%; Pred. No. 3.9e-126;

Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;



```
Db 541 GACCCGCTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAACAAGTGCACCGGTG 600
Qy 601 ATGCCGAGGGCTTTCGGCGCCACCATCAAGGCCATCAACGGCGCGCTCGAGTGCACGGG 660
Db 601 ATGCCGAGGGCTTTCGGCGCCACCATCAAGGCCATCAACGGCGCGCTCGAGTGCACGGG 660
Qy 661 AACAAACCCGCCAGATGNAAGCGCGCATCGGCTACTACAGAGCAGTACTGCGCGCAGCTC 720
Db 661 AACAAACCCGCCAGATGNAAGCGCGCATCGGCTACTACAGAGCAGTACTGCGCGCAGCTC 720
Qy 721 GCGCTGACCCAGGCGCCCAACCTCACTTGTGA 753
Db 721 GCGCTGACCCAGGCGCCCAACCTCACTTGTGA 753

RESULT 7
AD92659
ID ADS92659 standard; DNA; 753 BP.
XX
AC ADS92659;
XX
XX 02-DEC-2004 (first entry)
XX
XX Chitinase variant polynucleotide #19.
XX
XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX Heterodera.
XX
XX Synthetic.
XX
XX WO2004037194-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
XX 22-OCT-2002; 2002US-0420666P.
XX
XX 06-NOV-2002; 2002US-00290086.
XX
XX 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX P-PSDB; ADS92660.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 43; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
XX encoding them. A method of enhancing plant resistance to a fungus or
XX nematode comprises introducing into a plant a recombinant expression
XX cassette comprising a promoter operably linked to a chitinase
XX polynucleotide of the invention. The plant is maize or soybean. The
XX fungus is from the genus Fusarium. The nematode is from the genus
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX plant resistance to a fungus or nematode. This sequence represents a
XX chitinase variant polynucleotide of the invention.
XX
XX Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;
XX
XX Query Match 95.1%; Score 716.2; DB 13; Length 753;
XX Best Local Similarity 96.9%; Pred. No. 1.5e-125;
XX Matches 730; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
XX
Qy 1 TCGATGCAGAACTGGCGTGCAGCCAAACGATATGCTCGAGCAAGTTTCGGCTACTGCGGC 60
Db 1 TCGATGCAGAACTGGCGTGCAGCCAAACGATATGCTCGAGCAAGTTTGGCTACTGCGGC 60
```

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Qy 61 ACAACCGACGAGTACTCGCGCGACGGGTGCACTCGGGCCCCGTGCGGCTCGGGCGGCGG 120
Db 61 ACGACCGACGAGTACTCGGCGCGACGGGTGCACTCGGGCCCCGTGCGGCTCGGGCGGCGG 120
Qy 121 GGCAGCAGTGGCGCGGTGTCGAACGTGGCTAGGCTGTCACGGGCTCTCTTCTTCAAC 180
Db 121 GGCAGCAGTGGCGCGGTGTCGAACGTGGCTAATGTGGTCCCGACGGCTTCTTCAAC 180
Qy 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGG 240
Db 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGG 240
Qy 241 TTCTGAGCGCGCTCAAGCGGTATCCAGGCTTCCGCCATCGCGGTCAAGGTGCAAGGC 300
Db 241 TTCTGAGCGCGCTCAAGCGGTATCCAGGCTTCCGCCATCGCGGTCCGAGGTGCGAGCG 300
Qy 301 AAGCGGAGATCGCGGCTTCTTCGCGCACGCCACGACGAGACCGGGCAATTTCTGTAC 360
Db 301 AAGCGGAGATTCGCGCTTCTTCGCGCATGTCAAGCGGTTCGCGGTCCGAGGTTCGCTAC 360
Qy 361 ATCAGCGAGATCGAGAGCAAGCGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420
Db 361 ATCAGCGAGATCAACAGAGCAAGCGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420
Qy 421 GCGCGGGCGAGAGTACTACGGCGCGCGCTGCGAGATCTGTTGGAATCAAACTAC 480
Db 421 GCGCGGGCGAGAGTACTACGGCGCGCGCTGCGAGATCTGTTGGAATCAAACTAC 480
Qy 481 GGGCGCGGGAGAGGACATCGGCTTCGACGGGCTGGGGACCCCGGAGGTTGGCGGG 540
Db 481 GGGCGCGGGAGAGGACATCGGCTTCGACGGGCTGGGGACCCCGGAGGTTGGCGGG 540
Qy 541 GAGCGGTGTTGGCTTCAAGGGCGGCTCTGTTCTGGATGAACAACGTCACCGTGTG 600
Db 541 GACCGGTGTTGGCTTCAAGGGCGGCTCTGTTCTGGATGAACAACGTCACCGTGTG 600
Qy 601 ATGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGCACCGG 660
Db 601 ATGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGCACCGG 660
Qy 661 AACAAACCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTC 720
Db 661 AACAAACCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTC 720
Qy 721 GCGTGCACCCAGGCGCCCAACCTCACTTGTGA 753
Db 721 GCGTGCACCCAGGCGCCCAACCTCACTTGTGA 753

RESULT 8
AAA96222
ID AAA96222 standard; cDNA; 1094 BP.
XX
AC AAA96222;
XX
XX 08-FEB-2001 (first entry)
XX
XX cDNA encoding a maize chitinase polypeptide designated ZmCh2.
XX
XX Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;
XX pathogen control; disease resistance; molecular marker; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 51..896
XX FT /*tag= a
XX FT /product= "chitinase"
XX
XX WO200056908-A2.
XX
XX 28-SEP-2000.
XX
```





QY 121 GGCAGCAGTGGCGGGTGGTGGCAACGTGGCTAGCGTGGTACCGGGCTCTTCTTCAAC 180  
DB |||||  
121 GGCAGCAGTGGCGGGTGGTGGCAACGTGGCTAGCGTGGTACCGGGCTCTTCTTCAAC 180  
QY 181 GGCATCAAGAACCAAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGG 240  
DB |||||  
181 GGCATCAAGAACCAAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGG 240  
QY 241 TTCTGAGCGCGTCAAGCGGTACCCAGGCTTGGCCCATGGCGGGTCAAGGTGACGGGC 300  
DB |||||  
241 TTCTGAGCGCGTCAAGCGGTACCCAGGCTTGGCCCATGGCGGGTCAAGGTGACGGGC 300  
QY 301 AAGCGGAGATCGCGCTTCTCGCGCACGCCACGACGACGCGGCACTTCTGTGTTAC 360  
DB |||||  
301 AAGCGGAGATCGCGCTTCTCGCGCACGCCACGACGACGCGGCACTTCTGTGTTAC 360  
QY 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCACTGCGGTGC 420  
DB |||||  
361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCACTGCGGTGC 420  
QY 421 GCCGGGGGAGAGTACTACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480  
DB |||||  
421 GCCGGGGGAGAGTACTACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480  
QY 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGCGGGTGGCGGG 540  
DB |||||  
481 GGGCGCGGGGAGGAGCCATCGGCTTCGACGGGCTCGGGGACCCCGGCGGGTGGCGGG 540  
QY 541 GACGCGGTGGTGGGTTCAAGCGCGGCTCTGGTTCTGGATGAACAACGTCACCGGTG 600  
DB |||||  
541 GACGCGGTGGTGGGTTCAAGCGCGGCTCTGGTTCTGGATGAACAACGTCACCGGTG 600  
QY 601 ATGCGGAGGGCTTGGCGGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGAACGGG 660  
DB |||||  
601 ATGCGGAGGGCTTGGCGGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGAACGGG 660  
QY 661 AACAAACCCGCCAGATGAACGGCGGCTCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
DB |||||  
661 AACAAACCCGCCAGATGAACGGCGGCTCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
QY 721 GCGGTGACCCAGGCGCCCAACTCACTTGCTGA 753  
DB GCGGTGACCCAGGCGCCCAACTCACTTGCTGA 753

## RESULT 10

ADS92683

ID ADS92683 standard; DNA; 765 BP.

XX AC ADS92683;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #31.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX KW Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR P-PSDB; ADS92684.

XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 67; 197pp; English.

PS The invention relates to chitinase polypeptides and the polynucleotides

XX encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression

CC cassette comprising a promoter operably linked to a chitinase

CC polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genusCC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing

CC plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polynucleotide of the invention.

XX

SQ Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

Query Match 94.5%; Score 711.8; DB 13; Length 765;

Best Local Similarity 96.9%; Pred. No. 1e-124;

Matches 741; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 1 TCGATGCGAGCACTCGCGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTCGGC 60

DB |||||

1 TCGATGCGAGCACTCGCGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTCGGC 60

QY 61 ACAACCCAGCACTCGCGCTGCCAGCTGCGGCGCCCGCTCGCGCTCGGGCGCGGC 120

DB |||||

61 ACAACCCAGCACTCGCGCTGCCAGCTGCGGCGCCCGCTCGCGCTCGGGCGCGGC 120

QY 121 GGCAGCAGTGGCGGC-----GGTGTGCGAACTGTGGTACGCTGTACCGGC 168

DB |||||

121 GGCAGCAGTGGCGGC-----GGTGTGCGAACTGTGGTACGCTGTACCGGC 180

QY 169 TCCTTCTTCAACGCATCAAGAACAGCGCGGAGCGGGTGCAGGGCAAGAACTTCTTAC 228

DB |||||

181 TCCTTCTTCAACGCATCAAGAACAGCGCGGAGCGGGTGCAGGGCAAGAACTTCTTAC 240

QY 229 ACCCGAGCGCGTTCTTCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTCA 288

DB |||||

241 ACCCGAGCGCGTTCTTCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTCA 300

QY 289 CAGGTGAGGGCAAGCGCGAGATCGCGCTTCTTCGCGCACGCGCACGACGACCGGG 348

DB |||||

301 CAGGTGAGGGCAAGCGCGAGATTTGCGGCTTCTTCGCGCACGCGCACGACGACCGGG 360

QY 349 CATTTCTGTTACATCAGCGAGATCAGCAAGAGCAACGCTTCTCGACCCCGACCAAGAGG 408

DB |||||

361 CATTTCTGTTACATCAGCGAGATCAGCAAGAGCAACGCTTCTCGACCCCGACCAAGAGG 420

QY 409 CAGTGGCGGTGCGCGCGGGGAGAACTACTACGGGCGCGGCGCGCTGCGAGATCTCGTGG 468

DB |||||

421 CAGTGGCGGTGCGCGCGGGGAGAACTACTACGGGCGCGGCGCGCTGCGAGATCTCGTGG 480

QY 469 AACTACAACTACGGGCGCGGAGGAGCACTCGGCTTCGACGGGCTCGGGGACCCCGGC 528

DB |||||

481 AACTACAACTACGGGCGCGGAGGAGCACTCGGCTTCGACGGGCTCGGGGACCCCGGC 540

QY 529 AGGTGGCGGGGAGCGCGGTTCGAGCGCGCTTCGAGCGCGCTCTGATCTGATCAACAAAC 588

DB |||||

541 AGGTGGCGGGGAGCGCGGTTCGAGCGCGCTTCGAGCGCGCTCTGATCTGATCAACAAAC 600

QY 589 GTGCAACCGTGTGATGCGCGCGGGCTTCGGCGCCACCATCAGGGCCATCAACGCGCGCTC 648

DB |||||

601 GTGCAACCGTGTGATGCGCGCGGGCTTCGGCGCCACCATCAGGGCCATCAACGCGCGCTC 660

QY 649 GAGTGGCGGGGAGCAACCCCGCCAGATGAAACGCGCGCTACTACAGCAGTAC 708

DB |||||

661 GAGTGGCGGGGAGCAACCCCGCCAGATGAAACGCGCGCTACTACAGCAGTAC 720

```
QY 709 TGGCGCAGCTCGCGCTGCAACCCAGGGGCCCAACCTCACTTCTGA 753
DB 721 TGGCGCAGCTCGCGCTGCAACCCAGGGGCCCAACCTCACTTCTGA 765

RESULT 11
ADS92669
ID ADS92669 standard; DNA; 753 BP.
XX AC ADS92669;
XX DT 02-DEC-2004 (first entry)
XX DE Chitinase variant polynucleotide #24.
XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX KW Heterodera.
XX OS Synthetic.
XX XX WO2004037194-A2.
XX PD 06-MAY-2004.
XX XX 22-OCT-2003; 2003WO-US033588.
XX PR 22-OCT-2002; 2002US-0420666P.
XX PR 06-NOV-2002; 2002US-00290086.
XX PR 14-MAR-2003; 2003US-00389432.
XX XX (VERD-) VERDIA INC.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX DR WPI; 2004-365417/34.
XX DR P-PSDB; ADS92670.
XX PT New chitinase polynucleotides and polypeptides, useful in producing
XX PS plants with enhanced resistance against a fungus or a nematode.
XX PS Claim 4; SEQ ID NO 53; 197pp; English.
XX XX The invention relates to chitinase polypeptides and the polynucleotides
XX CC encoding them. A method of enhancing plant resistance to a fungus or
XX CC nematode comprises introducing into a plant a recombinant expression
XX CC cassette comprising a promoter operably linked to a chitinase
XX CC polynucleotide of the invention. The plant is maize or soybean. The
XX CC fungus is from the genus Fusarium. The nematode is from the genus
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX CC plant resistance to a fungus or nematode. This sequence represents a
XX CC chitinase variant polynucleotide of the invention.
XX XX
XX SQ Sequence 753 BP; 141 A; 248 C; 254 G; 110 T; 0 U; 0 Other;

Query Match 94.5%; Score 711.4; DB 13; Length 753;
Best Local Similarity 96.5%; Pred. No. 1.2e-124;
Matches 727; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCGATGCGAAGTCTGGCTGCGAGCCAAACGATATGCTGCAGCAAGTTGCGGTACTGCGGC 60
DB 1 TCGATGCGAAGTCTGGCTGCGAGCCAAACGATATGCTGCAGCAAGTTGCGGTACTGCGGC 60
QY 61 ACAACCGACGAGTACTGCGGCGAGCGGTGCGAGTCCGCGCTGCGGCGGCGGC 120
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGAGTCCGCGCTGCGGCGGCGGC 120
QY 121 GGCAGCAGTGGCGGCGGTGTCGAACGTCGTCAGCGTCTGTCACCGGCTCTTCTTCAAC 180
DB 121 GGCAGCAGTGGCGGCGGTGTCGAACGTCGTCAGCGTCTGTCACCGGCTCTTCTTCAAC 180
QY 181 GGCATCAAGAACACGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTTACACCCGAGCGCG 240

DB 181 GGCATCAAGAACACGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTTACACCCGAGCGCG 240
QY 241 TTCTGAGCGCGCTCAAGGGGTACCCAGGGTTCGCCCATGCGCGGTCAACAGGTGCAGGGC 300
DB 241 TTCTGAGCGCGCTCAAGGGGTACCCAGGGTTCGCCCATGCGCGGTGCAGGTGCAGGGC 300
QY 301 AAGCGGAGATCGCGGCTCTTTCGCGCAGCCACGACGACGAGACCCGGGCACTTCTGTTAC 360
DB 301 AAGCGGAGATCGCGGCTCTTTCGCGCAGCCACGACGACGAGACCCGGGCACTTCTGTTAC 360
QY 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCCGTGC 420
DB 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCCGTGC 420
QY 421 GCCGCGGGCAGAACTACTACGGGCGCGCGCTGCAGATCTCTGTTGAACTACAACCTAC 480
DB 421 GCCGCGGGCAGAACTACTACGGGCGCGCGCTGCAGATCTCTGTTGAACTACAACCTAC 480
QY 481 GGGCCCGGGGAGGAGCATCGGCTTCGAGCGGGTCCGGGACCCCGGCGAGGTGGCGCGG 540
DB 481 GGGCCCGGGGAGGAGCATCGGCTTCGAGCGGGTCCGGGACCCCGGCGAGGTGGCGCGG 540
QY 541 GAGCGCGTGTGCGTTCAGAGCGGCGCTCTGTTCTGGAATGAACAACGTCACCGTGTG 600
DB 541 GAGCGCGTGTGCGTTCAGAGCGGCGCTCTGTTCTGGAATGAACAACGTCACCGTGTG 600
QY 601 ATGCGCGAGGGCTTCGGCGCCACCATCAGGGGCCATCAACGGCGCTCGAGTGCAGCGGG 660
DB 601 ATGCGCGAGGGCTTCGGCGCCACCATCAGGGGCCATCAACGGCGCTCGAGTGCAGCGGG 660
QY 661 AACAAACCCCGCCAGATGAACGGCGCGTCTGCTACTACAGGCGAGTACTGCGCGCAGCTC 720
DB 661 AACAAACCCCGCCAGATGAACGGCGCGTCTGCTACTACAGGCGAGTACTGCGCGCAGCTC 720
QY 721 GCGGTGCAACCCAGGGCCCAACCTCACTTGTCTGA 753
DB 721 GCGGTGCAACCCAGGGCCCAACCTCACTTGTCTGA 753

RESULT 12
ADS92665
ID ADS92665 standard; DNA; 753 BP.
XX AC ADS92665;
XX DT 02-DEC-2004 (first entry)
XX DE Chitinase variant polynucleotide #22.
XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX KW Heterodera.
XX OS Synthetic.
XX XX WO2004037194-A2.
XX PD 06-MAY-2004.
XX XX 22-OCT-2003; 2003WO-US033588.
XX PR 22-OCT-2002; 2002US-0420666P.
XX PR 06-NOV-2002; 2002US-00290086.
XX PR 14-MAR-2003; 2003US-00389432.
XX XX (VERD-) VERDIA INC.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX XX WPI; 2004-365417/34.
XX DR P-PSDB; ADS92666.
XX XX
```

PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 49; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

SQ Sequence 753 BP; 138 A; 238 C; 270 G; 107 T; 0 U; 0 Other;

Query Match 94.5%; Score 711.4; DB 13; Length 753;  
Best Local Similarity 96.5%; Pred. No. 1.2e-124;  
Matches 727; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 TCGATGAGAACTCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACCGAGAGTACTCGGCGAGCGGTGCGAGTCCAGTCCGCGCGCTCGGCGCGGC 120  
Db 61 ACGACCGAGAGTACTCGGCGAGCGGTGCGAGTCCAGTCCGCGCGCTCGGCGCGGC 120

Qy 121 GGCAGAGTGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 180  
Db 121 GGCAGAGTGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 180

Qy 181 GGCATCAAGAACCGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 240  
Db 181 GGCATCAAGAACCGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 240

Qy 241 TTCCTGAGCGCTGAGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 300  
Db 241 TTCCTGAGCGCTGAGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 300

Qy 301 AAGCGGAGATCGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 360  
Db 301 AAGCGGAGATCGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGCAAGTTTCGGCTACTGCGGC 420  
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGCAAGTTTCGGCTACTGCGGC 420

Qy 421 GCGCGGCGGAGAGTACTGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 480  
Db 421 GCGCGGCGGAGAGTACTGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 480

Qy 481 GGGCGCGGCGGAGAGTACTGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 540  
Db 481 GGGCGCGGCGGAGAGTACTGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 540

Qy 541 GACGCGGTGGCGTTCAGGCGGCGCTCTGGTTCGGATGAACAGCGTGCACCGGTG 600  
Db 541 GACGCGGTGGCGTTCAGGCGGCGCTCTGGTTCGGATGAACAGCGTGCACCGGTG 600

Qy 601 ATGCGCGAGGCTTTCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 660  
Db 601 ATGCGCGAGGCTTTCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 660

Qy 661 AACAAACCGGCGGAGTGAACCGGCGTACTGCGCTACTCAAGAGAGTACTGCGGCGGCGG 720  
Db 661 AACAAACCGGCGGAGTGAACCGGCGTACTGCGCTACTCAAGAGAGTACTGCGGCGGCGG 720

Qy 721 GCGCTGAGCGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 753  
Db 721 GCGCTGAGCGCGGCGGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 753

## RESULT 13

ADS92695 standard; DNA; 750 BP.

XX ADS92695;  
XX AC  
XX DT 02-DEC-2004 (first entry)  
XX DB Chitinase variant polynucleotide #37.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
XX *Heterodera*.  
XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92696.

XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 79; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus *Fusarium*. The nematode is from the genus  
XX *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.

SQ Sequence 750 BP; 140 A; 247 C; 256 G; 107 T; 0 U; 0 Other;

Query Match 94.1%; Score 708.2; DB 13; Length 750;  
Best Local Similarity 97.2%; Pred. No. 4.9e-124;  
Matches 732; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 TCGATGAGAACTCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACCGAGAGTACTCGGCGAGCGGTGCGAGTCCAGTCCGCGCGCTCGGCGCGGC 120  
Db 61 ACGACCGAGAGTACTCGGCGAGCGGTGCGAGTCCAGTCCGCGCGCTCGGCGCGGC 120

Qy 121 GGCAGAGTGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 180  
Db 121 GGCAGAGTGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 180

Qy 181 GGCATCAAGAACCGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 240  
Db 181 GGCATCAAGAACCGGCGGCTGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 240

Qy 241 TTCCTGAGCGCGGCTGAGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 300  
Db 241 TTCCTGAGCGCGGCTGAGCGGCTGCGGCAAACTATGCTGCGCAAGTTTCGGCTACTGCGGC 300



AC ADS92647;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #13.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Valpani N;  
XX  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92648.  
DR  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
PT  
XX  
XX Claim 4; SEQ ID NO 31; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 753 BP; 136 A; 247 C; 259 G; 111 T; 0 U; 0 Other;

Query Match 93.2%; Score 701.8; DB 13; Length 753;  
Best Local Similarity 95.8%; Pred. No. 7.8e-123;  
Matches 721; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTCGCGCTGCCAGCAAACTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
DB 1 TCGATGCAGAACTCGCGCTGCCAGCAAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60  
QY 61 ACAACCGACGAGTACTCGCGCGACGGGTGCCAGTCCAGTCCGGCCCGTCCCGCTCGGGCGGGC 120  
DB 61 ACGACCGACGAGTACTCGCGCGCGCGGTGCCAGTCCGGCCCGTCCCGCTCGGGCGGGC 120  
QY 121 GGCAGCAGTGCAGCGGTGTCGAACTGCTGCTAGCTGCTCAGCGGCTCCTTCTTCAAC 180  
DB 121 GGCAGCAGTGCAGCGGTGTCGAACTGCTGCTAGCTGCTCAGCGGCTCCTTCTTCAAC 180  
QY 181 GGCATCAAGAACACGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGGGCG 240  
DB 181 GGCATCAAGAACACGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGGGCG 240  
QY 241 TTCTGTAGCGCGGTCAAGGGCTA CCGAGGTTTCGCCCATGCGGGTCAAGTGCAGGGC 300  
DB 241 TTCTGTAGCGCGGTCAAGGGCTA CCGAGGTTTCGCCCATGCGGGTCCGAGGTGAGGGC 300  
QY 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCACGCCAGCAGAGCGGGCATTTCTGTAC 360  
DB 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCACGCCAGCAGAGCGGGCATTTCTGTAC 360

QY 361 ATCAGCGAGATCAGCAAGAGCAACGGCTACTGCGACCCGACCAAGAGGCAAGTGGCCGTGC 420  
DB 361 ATCAGCGAGATCAGCAAGAGCAACGGCTACTGCGACCCGACCAAGAGGCAAGTGGCCGTGC 420  
QY 421 GCCGCGGGCAGAAAGTACTACGGCGCGGCCCGCTGCGAGATCTCGTGGAACTACAACATAC 480  
DB 421 GCCGCGGGCAGAAAGTACTACGGCGCGGCCCGCTGCGAGATCTCGTGGAACTACAACATAC 480  
QY 481 GGCGCCGCGGGAGGAGACATCGGCTTCGAGCGGCTGGGGACCCCGGACGGGTGGCGCGG 540  
DB 481 GGCGCCGCGGGAGGAGGAGACATCGGCTTCGAGCGGCTGGGGACCCCGGACGGGTGGCGCGG 540  
QY 541 GAGCGCGTGGTGGCTTCAAGGGCGGGCTCTGGTTCGTGATGAACAACCGTGCACCGGTG 600  
DB 541 GAGCGCGTGGTGGCTTCAAGGGCGGGCTCTGGTTCGTGATGAACAACCGTGCACCGGTG 600  
QY 601 ATGCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGGCTCGAGTGGGACGGG 660  
DB 601 GTGCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGGCTCGAGTGGGACGGG 660  
QY 661 AACAAACCCCGCCAGATGAACGGCGCGCTACTTACAGCAGTACTTCCCGCAGCTC 720  
DB 661 AACAAACCCCGCCAGATGAACGGCGCGCTACTTACAGCAGTACTTCCCGCAGCTC 720  
QY 721 GGGCTCGACCCAGGGGCCCAACCTCAGTTGCTGA 753  
DB 721 GGGCTCGACCCAGGGGCCCAACCTCAGTTGCTGA 753

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Job time : 353.104 secs

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:35:31 ; Search time 116.87 Seconds  
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10542.593 Million cell updates/sec

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Perfect score: 753  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715.6	95.0	1094	4	US-09-522-714-1
2	384.6	51.1	1048	4	US-09-522-714-21
3	348.2	46.2	881	4	US-09-522-714-29
4	308.2	40.9	1116	4	US-09-522-714-31
5	200.4	26.6	1079	1	US-08-181-271A-37
6	200.4	26.6	1079	1	US-08-449-315-37
7	200.4	26.6	1079	1	US-08-444-803-37
8	200.4	26.6	1079	1	US-08-449-043-37
9	200.4	26.6	1079	1	US-08-456-265A-37
10	200.4	26.6	1079	1	US-08-455-416-37
11	200.4	26.6	1079	1	US-08-455-244-37
12	200.4	26.6	1079	1	US-08-454-876-37
13	200.4	26.6	1079	2	US-08-457-364-37
14	200.4	26.6	1079	2	US-08-456-262-37
15	200.4	26.6	1079	2	US-08-456-240-37
16	200.4	26.6	1079	2	US-08-455-736-37
17	200.4	26.6	1079	2	US-08-971-217-37
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20	163.6	21.7	1151	1	US-07-704-288C-2
21	163.6	21.7	1151	1	US-08-093-372-1
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23	154.4	20.5	1218	4	US-09-902-540-4667
24	154.4	20.5	29384	4	US-09-902-540-1229
25	148.2	19.7	816	4	US-09-266-965-73
26	148.2	19.7	53500	4	US-09-266-965-76
27	137.4	18.2	960	4	US-09-534-229C-8

28	129.6	17.2	1163	4	US-09-522-714-5	Sequence 5, Appli
29	127	16.9	1118	4	US-09-522-714-23	Sequence 23, Appli
30	126.8	16.8	1318	3	US-09-125-891-1	Sequence 1, Appli
31	123.8	16.4	972	4	US-09-534-229C-7	Sequence 7, Appli
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33	109.2	14.5	583	4	US-09-522-714-25	Sequence 25, Appli
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37	99.8	13.3	1619	4	US-09-522-714-11	Sequence 11, Appli
38	97.2	12.9	1013	4	US-09-522-714-19	Sequence 19, Appli
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41	89.2	11.8	952	1	US-08-449-315-38	Sequence 38, Appli
42	89.2	11.8	952	1	US-08-444-803-38	Sequence 38, Appli
43	89.2	11.8	952	1	US-08-449-043-38	Sequence 38, Appli
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45	89.2	11.8	952	1	US-08-455-416-38	Sequence 38, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-522-714-1

; Sequence 1, Application US/09522714

; Patent No. 6563020

; GENERAL INFORMATION:

; APPLICANT: Simmons, Carl R.

; APPLICANT: Valpani, Nasser

; TITLE OF INVENTION: Maize Chitinases and Their Use in

; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

; FILE REFERENCE: 1100

; CURRENT APPLICATION NUMBER: US/09/522,714

; CURRENT FILING DATE: 2000-03-10

; EARLIER APPLICATION NUMBER: 60/125,915

; EARLIER FILING DATE: 1999-03-24

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1094

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (51)...(893)

US-09-522-714-1

Query Match 95.0%; Score 715.6; DB 4; Length 1094;  
Best Local Similarity 97.5%; Pred. No. 7.3e-142;  
Matches 727; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy	6	GCAGAACTGCGGCTGCCAGACGATGCTGTCGAGCAAGTTCCGGCTACTCGCGCAAC 65
Db	149	GCAGAACTGCGGCTGCCAGACGATGCTGTCGAGCAAGTTCCGGCTACTCGCGCAAC 208
Qy	66	CGACGAGTACTGCGGCGACCGGGTCCAGTCCGGCCCGTGGCGCTCGGGCGCGCGCAG 125
Db	209	CGACGAGTACTGCGGCGACCGGGTCCAGTCCGGCCCGTGGCGCTCGGGCGCGCGCAG 268
Qy	126	CAGTGGCGGCGGTGGTGGCAAGTGGCTAGGCTGTCACCGGCTCCTTCTTCAACGGCAT 185
Db	269	CAGTGGCGGCGGTGGTGGCAAGTGGCTAGGCTGTCACCGGCTCCTTCTTCAACGGCAT 328
Qy	186	CAAGAACAGCGCGCGGAGCGGGTCCGAGGGCAAGAACTTCTACACCGGAGCGGTTCT 245
Db	329	CAAGAACAGCGCGCGGAGCGGGTCCGAGGGCAAGAACTTCTACACCGGAGCGGTTCT 388
Qy	246	GAGCGCGTCAAGCGGTACCCAGGCTTTCGCCCATGCGGGGTCAAGTGCAGGGCAAGCG 305
Db	389	GAGCGCGTCAAGCGGTACCCAGGCTTTCGCCCATGCGGGGTCAAGTGCAGGGCAAGCG 448
Qy	306	CGAGATCGCGCCTTCTTTCGCCCATGCGGGGTCAAGTGCAGGGCAAGTTCCTTACATCAG 365

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Db 449 CGAGATCGCCCTTCTTCGGCGACGCGCACGACGACCGGGCTTCTGCTACATCAG 508
Qy 366 CGAGATCAGCAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGCGCGTGC 425
Db 509 CGAGATCAAACAAGAGCAACGCTTACTGCGACCCGACCAAGAGGCAGTGGCGGTGCGCGC 568
Qy 426 GGGCGAGAGTACTACCGGCGCGCGCGCTGCGATCTCTGCGAACTTCAACTACGGGCC 485
Db 569 GGGCGAGAGTACTACCGGCGCGCGCGCTGCGATCTCTGCGAACTTCAACTACGGGCC 628
Qy 486 CGCGGAGGAGCATCGCTTTCGACGGGCTCGGGGACCCCGCGAGGCTGGCGCGGACGC 545
Db 629 CGCGGGGAGGCGCATCGCTTTCGACGGGCTCGGGGACCCCGCGAGGCTGGCGCGGACGC 688
Qy 546 CGTGGTGGCTTCAAGGCGCGCTCTGCTTCTGATGAACAACTGCAACCGTGTGATGCC 605
Db 689 CGTGGTGGCTTCAAGGCGCGCTCTGCTTCTGATGAACAGCGTGCACGCGGTGGTGCC 748
Qy 606 GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGGCGAGGACAA 665
Db 749 GCAGGGGTTGCGCGCCACCATCAGGGCCATCAACGGCGCGCTTCGAGTGGCGGAGACAA 808
Qy 666 CCGCGCCAGATGAACGGCGCATCGCTTACTACAGCAGTACTGCGCGCCAGCTCGGCGT 725
Db 809 CCGCGCCAGATGAACGGCGCGCTCGGCTACTACAGCAGTACTGCGCGCCAGCTCGGCGT 868
Qy 726 CGACCCAGGGCCCAACCTTCACTTGT 751
Db 869 CGACCCCGGGCCCAACCTTCACTTGT 894
```

## RESULT 2

```
US-09-522-714-21
; Sequence 21, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)...(854)
US-09-522-714-21
```

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Query Match 51.1%; Score 384.6; DB 4; Length 1048;
Best Local Similarity 72.5%; Pred. No. 3.9e-72;
Matches 549; Conservative 0; Mismatches 184; Indels 24; Gaps 3;

Qy 6 GCAGAACTCGCGTCCAGCCAAAGTATGCTGCAGCAAGTTTCGCTACTCGGCACAAAC 65
Db 116 GCAGAACTCGCGGTGCGGCTGTCTGCAAGCCGGTTTCGGGTACTCGGGACGGG 175
Qy 66 CGACAGTACTCGCGCAAGCGGTGCGAGTGGCGCCCGCTCGCGCGCGCGGCGGCGAG 125
Db 176 CGAGGACTACTCGCGCGCGGGTGCCACTCGGGCCCTCGCGCGCTGCGGAGACCAACAA 235
Qy 126 CAGTGGCGGGTGTGTGGAACGTTGGCTAGCGTGTGCTACCGGCTCTTCTTCAACGGCAT 185
Db 236 C-----GGTCCGTGGCCAGCATCTGTGACGCGCGGCTTCTTTCGACGCGCT 280
```

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Qy 186 CAAGAACAGGCGCGGAGCGGGTGCAGAGGCAAGAACTTCTACACCCGAGCGCGTTCCT 245
Db 281 CTTGCGCGCAGCGCGCGCTTCGTCGAGGCGCAACGGCTTCTACACCCGCGCGCTTCCT 340
Qy 246 GAGCGCGTCAAGCGGTACCCAGGCTTCGCCCTTTCGCGGTTCACAGTGCAGGCGAAGCG 305
Db 341 CGCGCGCGCGGTCTACTACCGGCTTCGCGCGCGCACCGGCAACCGTCGACGACTCCAAGCG 400
Qy 306 CGAGATCGCGCGCTTCTTCGCGCGACGCGCACGAGACCGGGCATTTCTGTACATCAG 365
Db 401 CGAGATCGCGCGCTTCTTCGCGCAACGCCAACACGAGACCATAAAGTTCTGCTACATCAA 460
Qy 366 CGAGAT---CAGCAAGAGCAACGCTTACTGCGACCCCGACCAAGAGGAGTGCGCGTGC 422
Db 461 CGAGATCGACGGCGCGAGCAAGAACTACTGCGACCGGAAACAACAGCAGTGGCGTGC 520
Qy 423 CGCGGGCAGAACTACTACGGGCGCGCGCTTCGATGAGATCTCTGTGAACTTCAACTACGG 482
Db 521 GCGCGGGAAGGGGTACTACGCGCGCGCGCGCTGCGAGATCTCTGTGAACTTCAACTACGG 580
Qy 483 GCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGGA 542
Db 581 GCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAG 640
Qy 543 CGCGGTGCTCGCGTTCAAGCGCGCGCTTCGATGAGTAAACAACTGATGAACTGACCGTGTGAT 602
Db 641 CGCGGTGCTCGCGTTCCGCTTCGCGCTTCGATGAGTAAACAACTGATGAACTGACCGTGTGAT 700
Qy 603 -----GCCGCGAGGGCTTCGCGCGCACCATGAGGGCCATCAACGCGCGCTCGAGTGC 656
Db 701 GGTCTCGCGCGAGGGCTTCGCGCGCACCATGAGGGCCATCAACGCGCGCTCGAGTGC 760
Qy 657 GCGGAAACAGCCCGCCAGATGAGCGCGCATCGGCTTACTACAGCAGTACTCGCGGCA 716
Db 761 CGGCAAGAACCCCAACTCCGTCACAAACCGGCTCGGCTTACTACAGCAGTACTCGCGGCA 820
Qy 717 GCTCGGCTCGACCCAGGCGCCCAACCTTCACTTGTCTGA 753
Db 821 TTTCGGGTGACCCCGGCAACCAACCTTCACTTGTCTGA 857
```

## RESULT 3

```
US-09-522-714-29
; Sequence 29, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(551)
US-09-522-714-29
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Query Match 46.2%; Score 348.2; DB 4; Length 881;
Best Local Similarity 77.5%; Pred. No. 1.8e-64;
Matches 435; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 194 AGCGCGGAGCGGTGCGAGGCGAAGAACTTCTACACCCGAGCGCGTTCCTGAGCGCG 253
Db 1 ATGCCGGAGTGTGTGCGAGGCGAGCGCTTCTACACGCGAAGCGCGTTCCTCGAGGCGCA 60
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QY	254	TC	AAGGCGT	AT	CC	AGGCTT	CG	CCCAT	TG	CGGGGT	CA	CGT	GC	AGGCG	CAAG	CCG	GAGAT	CG	313
DB	61	TC	CGCGGT	AT	CC	CGGGCT	TC	GCAT	TG	CGCGT	CC	GAGT	CG	AGCG	CAAG	CCG	GAGATT	CG	120
QY	314	CG	GCTTCT	TC	CG	CACGCC	CAC	GAC	GAG	AC	CGGGCA	TTT	CT	GT	TACAT	CA	CGGAGAT	CA	373
DB	121	CG	GCTTCT	TC	CG	GCAT	GT	CA	GC	AC	CGGAG	AT	TT	GT	GCT	TACAT	CA	ACGAGGTC	180
QY	374	GC	AAGAG	CA	CG	CTTA	CT	GC	CA	CCG	CA	CA	AG	GC	AG	CT	GC	CGCGGG	433
DB	181	AC	GTGGG	CA	AG	TACT	GC	CACT	TG	GA	CA	GT	GA	CA	GT	GA	CA	GT	240
QY	434	AG	TACT	AC	GGG	CGG	CG	CG	CT	GC	AG	AT	CT	CG	TG	AA	CT	TA	493
DB	241	GT	TACT	AC	GGG	CGG	CG	CG	CT	GC	AG	AT	CT	CG	TG	AA	CT	TA	300
QY	494	GG	GACAT	CG	GCTT	CG	A	CGGG	CT	CG	GGG	AC	CC	CG	G	AGG	TG	CGCGCG	553
DB	301	GG	AGCT	CGG	CTT	CG	A	CGGG	CT	GG	AG	AC	CC	CG	G	AG	CT	GGCG	360
QY	554	CG	TTCA	AGG	CG	CG	CT	CT	GT	GT	CG	AT	GA	AA	CA	CGT	GC	ACCG	613
DB	361	CG	TTCA	AGT	CG	CG	CT	CT	GT	GT	CG	AT	GA	AA	CA	CGT	GC	ACCG	420
QY	614	TC	GGCG	CA	CC	AT	C	AGG	CC	AT	CA	C	GGG	CG	CT	CG	AT	G	670
DB	421	TC	GGCG	CA	CC	AT	C	AGG	CC	AT	CA	C	GGG	CG	CT	CG	AT	G	480
QY	671	CC	CAG	AT	GA	AG	CG	CG	AT	CG	GT	ACT	CA	AG	CAG	T	ACT	CGCGCT	730
DB	481	CC	GAA	AT	GA	AG	CG	CG	GT	CT	CT	CT	CA	CT	CG	AT	CT	CG	540
QY	731	C	AGGG	CC	CA	AC	CT	CA	CT	TG	CT								751
DB	541	CG	GGCT	CG	AC	CT	C	AG	T	TG	CT								561

```

RESULT 4
US-09-522-714-31
; Sequence 31, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: intron
; LOCATION: (445) ... (512)
; NAME/KEY: CDS
; LOCATION: (42) ... (444)
; NAME/KEY: CDS
; LOCATION: (513) ... (922)
US-09-522-714-31

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116	CGAGAACTCGCGGGTCGGCTCGGGCCTGTGTCGACGCGGTTTCGGGTACTCGGGAGCGGG	17
125	CGACGAGTACTCGCGCGACGCGGTGCACTCGGGCCCCGTGCGCTCGGGCGCGCGGCGAG	125
176	CGAGGACTACTCGCGCGCGGGTGCACGTGCGGGCCCTGCGACGTGCGGAGACCAACAA	235
126	CAGTGGCGGCGGTGGTGGAACTGGGTGCTAGCGTGTGCTACCGGCTCTTCTTCAACGGCAT	185
236	C-----GGTCCGTGGCCAGCATCGTGACGCGCGGCTTCTTCGACGCGCT	280
186	CAAGAAACGAGGCCGCGGTGCGAGGCGAAGAACTTCTACACCGGAGCGCGTTCTCT	245
281	CCTCGCGAGCGCGCGCTCGTGGAGGCCAAACGGCTTCTACACCGCGGACGCTTCTCT	340
246	GAGCGCGTCAAGGCGTACACGAGCTTCGCGCCATGCGGGTCAAGGTGACGCGGCAAGCG	305
341	CGCGCGCGCGGCTACTACCGCGGTTTCGGCGCACCGGACCGTGCAGCATCTCCAAAGCG	400
306	CGAGATCGCGCGCTTCTTCGCGCACGCCACGCCAGAGAC-----	344
401	CGAGATCGCGCGCTTCTTCGGCAACGCCAACCCAGAGACCATAAGTACGTGCGAAACAAAC	460
345	-----CGGCGATTCTCTCT	357
461	CGAAGCTGTCAAGCTCTAGCTGTACTAATCAAGTTTGCAGTCTCTCGAGATTTCTGC	520
358	TACATCAGCGAGAT---CAGCAAGAGCAACGCTACTCGCACCCGACCAAGAGGCGAGTGG	414
521	TACATCAACGAGATCGAGCGGCCGAGCAAGAACTACTGGACCGGAAACAAACGCGAGTGG	580
415	CCGTGCGCGCGGGCGAGAGTACTACGGGCGCGGCCGCTGCGAGATCTCGTGGAACTTAC	474
581	CCGTGCGCAGCGCGGGAAGGGGTACTACGCGCGCGGCCGCTGCGAGATCTCTCTGGAATTC	640
475	AACCTACGGGCCCGCGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGCAGGGTG	534
641	AACCTACGGGCCCGCGGGGACAGATCGGCTTCGACGGGCTGGGGGACCCCGACGCGGTG	700
535	GCGCGGACGCGGTGTGGCTTCAAGGCGCGGCTCTGGTTCTTGATGAAACAAACGTGCAC	594
701	GCGCGACGCGGTGCTCGGTTCCGCTCCGGCTCTGGTACTGGATGAAACAAACGTGCAC	760
595	CGTGTGAT-----GCCGACGGCTTGGCGGCCACCATCAGGGCCATCAACGGCGCGCTC	648
761	GGGGCCATCGTCTCCGCGCAGGGTTCGGCGGCCACCATCAGGGCCATCAACGGCGCGCTC	820
649	GAGTGCAGCGGACAAACCCCGCCAGTGAACGGCGCATCGGTACTACAGCAGTAC	708
821	GAGTGCAGCGGACAAACCCCAATCTCGTCAACAAACCGCGCTGCTACTACAAAGCATTC	880
709	TGCCCGCAGCTCGCGTCGACCCAGGGCCCAACCTCACTTGTCTGA	753
881	TGCCAGGATTCGCGGTGACCCCGGGCAACAACTCACTGCTGA	925

RESULT 5

US-08-181-271A-37

; Sequence 37, Application US/08181271A

; Patent No. 5614395

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

```

RESULT 5
US-08-481-271A-37
? Sequence 37, Application US/08182171A
? Patent NO. 5614395
? GENERAL INFORMATION:
?
? APPLICANT: Ryals, John A.
? APPLICANT: Alexander, Danny C.
? APPLICANT: Beck, James J.
? APPLICANT: Duesing, John H.
? APPLICANT: Friedrich, Lealie B.
? APPLICANT: Goodman, Robert M.
? APPLICANT: Harms, Christian
? APPLICANT: Meins, Jr., Frederick
? APPLICANT: Montoya, Alice
? APPLICANT: Moyer, Mary B.
? APPLICANT: Neuhaus, Jean-Marc
? APPLICANT: Payne, George B.
? APPLICANT: Sperison, Christoph

```



APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,315  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIORITY DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-315-37  
Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTCCGCTACTCGGCGCACACC 66  
Db 93 CAAAACTGCGGTTGCGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTTACTTGTGGTACCGAC 152  
Qy 67 GACGAGTACTCGGCGACGCGGTGCAGTCGCGGCCCGTCGCGCTCGGCGCGGCGGCGAC 126  
Db 153 GATGCATACTCGGCGGTGTTGATGCCGATCAGTCTTGTAGAGGTAGTGGNACCCCGACC 212  
Qy 127 AGTGGCGGCGGTGGTGCAGACGTGGTACCGGTGCTCACCGGCTCTTCTTCAACGGGCATC 186  
Db 213 GGAGG-----GTGCGTGGTAGCATTGTGACACAAAGGTTCTTTAAACAATATT 260  
Qy 187 AAGAACCGAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGCTTCTG 246  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTCTACACCCGTCGACTCTTCGTT 320  
Qy 247 AGCGCGTCAAGCGTACCCAGGCTTCGCCATGCGCGGTCACAGGTGCGAGGCGAAGCGC 306  
Db 321 AACGCCGCTAATCTTCTCCCACTTTGCCAATCTCTGTAC-----CAGAGGT 368  
Qy 307 GAGATCGCGCCCTTCTTTCGCGCAGCCACGACGAGACCGGCGCATTTCTGTTACATCAGC 366  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCAGCAGACCGACATTTCTGCTACATAGAA 428  
Qy 367 GAGAT----CAGCAAGACCAACGCTACTGCGACCCGACCGGAGGCGAGTGGCCGTGGCC 423  
Db 429 GAGATTAAACGAGCAACACGTAATCTGCGCAGAGCAGCAACACAAATACCCATGTGCA 488  
Qy 424 GCGGGGCGAAGTACTACGCGCGCGCGCTGCGAGATCTGTTGGAATCACTACGAGTACGGG 483  
Db 489 CCGGAAAAGGCTACTTCGGTCTGGTCCGATCCAACTATCATGGAATCACTACGAGTACGGA 548  
Qy 484 CCGCGGGGAGGAGCATTCGGCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGCGGAC 543  
Db 549 GCGTGTGTCAAAGTCTCGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608  
Qy 544 GCGTGTGTGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTCGACCGTGTGATG 603  
Db 609 CCAACTGTAGCTTTTCAGGTCGGGTTTGTGGTATGAATAGCTAGTAAAGCCCGGTTCTG 668  
Qy 604 CCGCAGGCGTTTCGCGCCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGGAAC 663  
Db 669 AACCAAGGTTTGAGCCACCATTAGAGCTATTATGG---AATGGAAATGAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAACGCGCGCATCGGCTACTTACAAAGCAGTACTCCCGCCAGTCCGC 723  
Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGATGACTATATAGAGCTATTGTGGACACGCTTGGT 785  
Qy 724 GTCGACCCAGGGCCCAACCTCACTTCTGTA 753

Db 786 GTGACCCCTGCTCTTAACCTTAGTTGTAA 815

RESULT 7  
US-08-444-803-37  
; Sequence 37, Application US/08444803  
; Patent No. 5654414  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,803  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-444-803-37  
  
Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
  
Qy 7 CAGAACTGGCGTCCAGCAACGATATGTCGAGCAAGTTGGTCTACTCGCGGACACACC 66  
Db 93 CAAAACCTGGGTTGCGCTCCAAACCTCTGTTGCAGTCAGTTCTGTTTACTGTGTTACCGAC 152  
  
Qy 67 GACGAGTACTGCGCGACGGTCCAGTCGGGCGCGCTCGCGTCCGGCGCGCGCGGCGC 126  
Db 153 GATGCATACTGCGGTGTGGATCCGATCAGGTCCTTTAGAGGTAGTGGAAACCCCGACC 212  
  
Qy 127 AGTGGCGGCGGTGTCGAAACGTCGTCGTCACCGCTCTCTTCTTCAACGGCATC 186  
Db 213 GGAGG-----GTCGGTTCGGTAGCATTTGTGACACAGGTTCTTTAAACAATTT 260  
  
Qy 187 AAGAACCGCGCGGAGCGGTGCGAGGGCAAGAACTTCTTACACCGGAGCGGTTCTGTG 246  
Db 261 ATCAACCAAGCTGTAATGTTGCGCGGGGAAAAGATTCTACACCGCTGACTCTTTTCGTT 320  
  
Qy 247 AGCGCGTCAAGGCTACCCAGGCTTCGCCCATCGGGGTCACAGGTGCGAGGGCAAGCGC 306  
Db 321 AACGCGCTAATACTTTTCCCAACTTTGCCAATTTCTGTTCAC-----CAGACGT 368  
  
Qy 307 GAGATCGCCGCTTCTTCGCGCACGCCACCGACAGACCGGGCATTTCTGTTCATCAGC 366  
Db 369 GAAATTGCTACCATGTTGCTCATTTCACTCAAGACCGGACATTTCTGTACATAGAA 428  
  
Qy 367 GAGAT---CAGCAAGAACACGGCTACTGCGACCCGACCCGACAGGAGGAGTGGCGGTGCC 423  
Db 429 GAGATTAAACGAGCAACACGTAATACTACTGCGCAGACGACCAACACACATAATCCCATGTGCA 488  
  
Qy 424 GCGGGGCAAGTACTACGGGCGGCGCGCTCGAGATCTCGTGGAACTCAACTACGGG 483  
Db 489 CCGGGAAGAGGCTACTTTCGGTGTGGTCCGATCCAACTATCATGGAATCAACTACGGA 548  
  
Qy 484 CCGCGCGGAGGAGACATCGGCTTCGACGGCTCGGGGACCCCGGACAGGCGCGCGGAC 543  
Db 549 GCGTGTGTCAAAGTCTCGGTCTTGACCTTCTACGCCACCGCCGAACTTTGTGGGTAGCAAC 608  
  
Qy 544 GCGGTGTGGCGTTCAAGCGGCGGCTCTGTTCTTGGATGAACACAGTGCACCGGTGTATG 603

Db 609 CCAACTGTAGCTTTTCAGTCGGGTTTGTGGTTTGGATGATAGCGTAAGCGCGTTCGTG 668  
Qy 604 CCGCAGGCGCTTCGGCGCCACCACATCAGGCGCATCAACGCGCGCTCGAGTGGCGGGAAC 663  
Db 669 AACCAAGGGTTTGAGCGCCACATTTAGAGCTATTATGG--AATGGATGTAAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAAGCGCGCATCGGCTTACTACAGCAGTACTGCGCGCACGCTCGGC 723  
Db 726 AATTCCGCTGCAGTCAACGCAAGGATTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785  
Qy 724 GTGCACCCAGGCGCCCAACTCACTTGTCTGA 753  
Db 786 GTGACCTGTGCTTAACCTTAGTTGTAA 815

## RESULT 8

US-08-449-043-37  
; Sequence 37, Application US/08449043  
; Patent No. 5689044  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,043  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-449-043-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGNACTGCGCTGCCAGCCAAACGATGCTGCAGCAAGTTCCGGCTACTGCGGCACCAACC 66  
Db 93 CAAAACTGCGGTTGCGCTCCAAACCTCTGTTCAGTCAGTTCCGGTTACTGTGGTACCGAC 152  
Qy 67 GACGAGTACTGCGGCGACGGTGCAGTCGCGGCCCGTGCAGTCCGGCGCGGCGGCGAGC 126  
Db 153 GATGCATCTGCGGTGTTGGATGCCGATCAGGTCCTTGTAGAGGTAGTGGAAACCCCGACC 212  
Qy 127 AGTGGCGCGGTGGTGGCAACGTTGGTGTAGCGGTGTCAACCGGCTCCTTCTTCAACGGCATC 186  
Db 213 GGAGG-----GTGCGTGGTAGCATTTGTGACACAAGGTTTCTTTTAAACAATATT 260  
Qy 187 AAGNACCGCGCGGAGCGGTCGAGGGCAGCAAGTCTTCTACACCGGAGCGGCTCTCTG 246  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTCTACACCCGTGACTCTTTCTGTT 320  
Qy 247 AGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATCGCGGCTCACAGGTGCAGGGCAAGCGC 306  
Db 321 AACGCCCTAATACTTTTCCCACTTTTGCCAACTTCTGTAC-----CAGAGCT 368  
Qy 307 GAGATCGCGCGCTTCTTTCGCGCAGCCGCAACGAGACCGGGCATTTCTGTATCATCAGC 366  
Db 369 GAATTCGTACCATGTTTGTCTCAATTTCACTCACGAGACCGGACATTTCTGTACATAGAA 428  
Qy 367 GAGAT---CAGCAGAGCAACCGCTACTGCGACCCGACCAAGAGGAGTGCCTGCGGCC 423

Db 429 GAGATTAACGGAGCAACACACGTAACTACTGCGCAGAGCAGCAACACATAATCCCATGTGCA 488  
Qy 424 CGCGGGGAGAGTACTAGCGGGCGGGCGGCTCGATCTCGTGAAGTCACTAGCGG 483  
Db 489 CCGGAAAGAGCTACTTCGGTGGTGGTCCGATCACTATCACTGAAGTCACTAGCGG 548  
Qy 484 CCGCGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGGTGGCGCGGAC 543  
Db 549 GCGTGTGGTCAAAGTCTCGGCTTGAACCTTACGCCAGCCGGAATTTGGGTAGCAAC 608  
Qy 544 GCGGTGTGGCTTCAAGGGCGGCTCTGGTTCGTGATGAACAAAGTGCACCGGTGATG 603  
Db 609 CCAACTGTAGCTTTTCAGTGGGTTTGTGTTTGGATGAATAGCGTAAGCGCGGTTCTG 668  
Qy 604 CCGCAGGCTTCGGCGCCACCATCAGGCCCATCAAGCGGCGCTCGAGTGCAGCGGAAC 663  
Db 669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGG---AATGGAATGTAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAAGCGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGG 723  
Db 726 AATTCCGGTGCAGTCAACGCAAGGATGGATCTATAGAGCTATTGTGGACAGCTTGGT 785  
Qy 724 GTCAGCCAGGCGCCAACTCACTTGTCTGA 753  
Db 786 GTGACCCCTGGTCTCACTTGTGTCTAA 815

## RESULT 9

US-08-456-265A-37  
; Sequence 37, Application US/08456265A  
; Patent No. 5767369  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Ryals, John A.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Stinson, Jeffrey R.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,265A  
; FILING DATE: 31-MAY-95  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/181,271  
; FILING DATE: 13-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-456-265A-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGAACTGCGGCTGCCAGCCAAACGTAATGCTGAGCAAGTTTCGGCTACTGCGGCACAAAC 66  
Db 93 CAAAACCTGCGGTTGGCTCCAAACCTCTGTTGCAGTCAGTTTCGGTTACTGTTGGTACCGAC 152  
Qy 67 GACGAGTACTCGCGGACGGTGCAGTCCGAGTCCGCTCGGCGCGCTCGGCGGGCGGCGGAGC 126  
Db 153 GATGCATACCTGCGGTGTTGGATGCCGATCAGGTCCTTTGTAGAGTAGTGGAAACCCCGACC 212  
Qy 127 AGTGGCGGCGGTGTTGCGAAACGTTGCGGTAGCTGCTCACCGCTCTCTTCTTCAACCGCATC 186  
Db 213 GGAGG-----GTGCGTGGTAGGATGTTGTGACACAAAGTTTCTTAAACAATTT 260  
Qy 187 AAGAACCAAGCCCGGAGCGGGTGGAGGGCAAGAACTTTCTACACCCCGAGCGCGTTCTG 246  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGGAAAAGATTCTACACCCCGTGAATCTTTTGGTT 320  
Qy 247 AGCGCGGTCAAGGGTACCCAGGTTTCGCCATGGCGGGTTCACAGGTGCAGGGGCAAGCGC 306  
Db 321 AACGCGCTAATACTTTTCCCAACTTTGCCAAATTTCTGTTC-----CAGACGT 368  
Qy 307 GAGATCGCGCTTCTTTCGGCGCAGCCACGCAAGAGCCGGGCAATTTCTGTTCATCAGC 366  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTTCACTCAGCAGACCGGACATTTCTGTACATAGAA 428  
Qy 367 GAGAT---CAGCAAGCAAGCGCTACTGCGACCCGCAAGAGGAGTGGCGCGTGGCGCC 423

Db 429 GAGATTACGGAGCAGACAGTAACTACCTCCAGAGCAGCAACACATATCCCATGTGCA 488  
Qy 424 CGGGGCGAGAGTACTACGGGCGGCGCGCTGCGAGATCTCGTGGAACTACAACCTACGGG 483  
Db 489 CGGGGAAAGGCTACTTCGGTGGTCCGATCCAACCTATCATGGAACCTACAACCTACGGA 548  
Qy 484 CCGGGGGGAGGAGCATCGCTTCAGCGGCTCGGGGACCCCGGAGCGGTGGCGGGGAC 543  
Db 549 GCGTGTGCTCAAGTCTCGGCTTGGACCTTCTACGCCAGCCCGAACTTTGTGGGTAGCAAC 608  
Qy 544 GCGGTGGTGGGCTTCAAGCGGCGCTCTGGTTCGGATGAACAACGTCACCGTGTGATG 603  
Db 609 CCAACTGTAGCTTTCAGGTCGGTTTGGTTTGGATGAATAGGTAAGCGCGGTCTG 668  
Qy 604 CGCAGGCGCTTGGCGCCACCATCAGCGGCCATCAACGGCGCGCTCGAGTGGGACGGGAAC 663  
Db 669 AACCAAGGTTTGGAGCCACCATTAGAGCTATTAATGG--AATGGAATGAACGGTGGT 725  
Qy 664 AACCCGCGCAGATGAACCGCGCATCGGCTACTACAAGCAGTACTGCGCGCAGCTCGGC 723  
Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785  
Qy 724 GTCCAGCCAGGCGCCCAACCTCACTTGCTGA 753  
Db 786 GTGACCTGTCTCAACCTTAGTTGCTAA 815

## RESULT 10

US-08-455-416-37  
; Sequence 37, Application US/08455416  
; Patent No. 577200

## GENERAL INFORMATION:

; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,416  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-455-416-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGAACTGCGCTCCAGCAAGCAACGATATGTCGAGCAAGTTCGCTACTCGGGCACAACC 66  
Db 93 CAAAACTGCGGTTTCGCTCCAAACCTCTGTTGCAGTCAGTTCGTTTACTGTGGTACCGAC 152  
Qy 67 GACGAGTACTGCGGCGACGGTGCAGTCGCGGCCGTCGCTCGGGCGGGCGGCGAC 126  
Db 153 GATGCATACCTGCGGTGTTGATGCCGATCAGTTCCTTGTAGAGTAGTGGNACCCCGACC 212  
Qy 127 AGTGGCGCGGTGGTGGCAACGTCGTCACCGGCTCTCTTCTCAACGGCATC 186  
Db 213 GGAGG-----GTCCGTCGGTAGCATTTGTGACACAAAGGTTTCTTTAAACAATAT 260  
Qy 187 AAGAACACAGCCCGGAGCGGTCGGAGGGCAAGNACTTCTACACCCGAGCGGCTTCTG 246

Db 261 ATCAACAGCTGTGTAATGTTGCGCGGGAAGAATTTACACCGGTGACTCTTTTCGTT 320  
Qy 247 AGCCCGGTCAAGCGTACCCAGGTTTCCGCCATGCGCGGTACAGGTGCGAGGCAAGCGC 306  
Db 321 AACCGCGTAAATCTTTCCCAACTTTTCCCAATTTCTGTTAC-----CAGACGT 368  
Qy 307 GAGATCGCGGCTTTCTCGGCGACGCCACGACGACGACCGGCAATTTCTGTTACATCAGC 366  
Db 369 GAAATGCTACCATGTTGCTCATTTCACTCAGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 367 GAGAT---CAGCAAGAGCAACCCCTACTGCGACCCGACCAAGAGGCGAGTGGCCGTGGCC 423  
Db 429 GAGATTAACGAGCAACACGTAACCTACTGCGCAGAGCAGCAACACATAATCCCATGTGCA 488  
Qy 424 GCGGGCGAAGTACTACGCGCGCGCGCGCTGCGATCTGTTGGAATCAACTACACTACGG 483  
Db 489 CCGGAAAGGCTACTTTCGTCGTTGCGGTCCGATCCAACTATCATGGAATCAACTACGGA 548  
Qy 484 CCGCGGGAGGACATCGGCTTCGAGGGCTCGGCGACCCCGCAGGCGCGCGGAC 543  
Db 549 GCGTGTGTTCAAGTCTCGGCTTGAACCTTCTAGCCAGCCCGAACTTGTGGGTAGCAAC 608  
Qy 544 GCGTGTGCGGTTCAAGCGCGCGCTCTGTTCTGATGAACAACGTCACCGGTGATG 603  
Db 609 CCAACTGTAGCTTTCAAGTCTCGGTTTGTGGTTTGGATGAATAGCGTAAGCGCGTCTG 668  
Qy 604 CCGCAGGCTTCGCGCGCCACCATCAGGCGCATCAGCGCGGCTCGAGTGGAGCGGAC 663  
Db 669 AACCAAGGTTTGGAGCCACCATTAGAGCTATTAATG---AATGGAATGTAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAACGCGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGC 723  
Db 726 AATTCGGTGCAGTCAACGCAAGATTTGGATCTATAGAGCTATTTGGACACTTGGT 785  
Qy 724 GTCGACCCAGGCGCCAACTCACTTGTGTA 753  
Db 786 GTGACCCCTGCTCTTAACCTTAGTTGCTAA 815

RESULT 11  
US-08-455-244-37  
Sequence 37, Application US/08455244  
Patent No. 5789214

GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Steinson, Jeffrey R.  
APPLICANT: Ukenes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,244  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-244-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

Qy 7 CAGAACTGCGGCTGCCAGCCAAACGTATGCTGTCGAGCAAGTTTCGGCTACTCGCGGCAACCC 66



Db 93 CAAMACTCGGTTCCGCTCAAACTCTGTTGAGTCAGTTTCGTTACTGTTGTTACCGAC 152  
Qy 67 GACGAGTACTCGCGGAGCGGTGCGAGTTCGCGGCGCGCTCGCGCTCGCGGCGCGGCGGAGC 126  
Db 153 GATGCATACTCGGTTGTTGATGCGGATCCGATCAGTCTCTGTAGAGTAGTGAACCCCGACC 212  
Qy 127 AGTGGCGGCGGTGTTGCGAAGCTGGTACGCTGCTCACCCTCTCTTCTTCAACGGGATC 186  
Db 213 GGAGG-----GTGCGTGGTAGCATTTGTGACACAAAGGTTTCTTTTAAACAATATT 260  
Qy 187 AAGAACAGGCGCGGAGCGGTGCGGAGCGGGAAGAACTTCTACACCCGAGCGGCTTCTG 246  
Db 261 ATCAACCAAGTGTATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTTCGTT 320  
Qy 247 AGCGCGTCAAGGCTTACCAAGGTTTCGCCCATGCGCGGCTCACAGGTCAGGCGCAAGCGC 306  
Db 321 AACCGCGTAATACTTTCGCCAACTTTCGCCAACTTCTGTTAC-----CAGACGT 368  
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Qy 367 GAGAT---CAGCAAGAGCAACCGCTACTCTGCGACCCGACAGGAGGAGTGGCGCTGCGCC 423  
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Qy 424 GCGGGGAGAGTACTACGCGCGCGCGCTGCGAGATCTGTTGGAATCAACTACACTACGGG 483  
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Db 669 AACCAAGGTTTGGAGCCACCATTAGAGCTATTAAATGG---AATGGAATGAACGGTGGT 725  
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Db 726 AATTCCGGTTCAGTCAACGCAAGGATTTGGATCTATAGAGCTATTGTGGACAGCTTGGT 785  
Qy 724 GTGACCCAGGCGGCAACCTCCTCCTGCTGA 753  
Db 786 GTGACCTGCTCCTAACCTTAGTTGCTAA 815

## RESULT 12

US-08-454-876-37

; Sequence 37, Application US/08454876

; Patent No. 5804693

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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; APPLICATION NUMBER: US/08/454,876  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
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; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
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; APPLICATION NUMBER: US 07/848,506  
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:





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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-262-37

Query Match      26.68; Score 200.4; DB 2; Length 1079;
Best Local Similarity 58.58; Pred. No. 2:5e-33;
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

QY 7 CAGAACTGCGGCTCCAGCAAAAGTATGTCGACGAAGTTTCGGCTACTCGGGCACAAC 66
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 93 CAARACTGCGGTTGCGCTCCAAACTCTGTTCAGTCAGTTCGTTACTGTTACCGAC 152
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GACGAGTACTCGCGGACGGGTGCGAGTCGGGCGCGCTCGCGCTCGGGCGGGCGGCGAC 126
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 153 GATGCATACCTCGCGTGTGGATCCGATCAGTCTTGTAGAGGTAGTGAACCCCGACC 212
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 AGTGGCGGCGGTGTGGCAAGTCGTAGCTAGCTGCTCACCGCTCTCTTCAACGGCATC 186
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QY 213 GGAGG-----GTGGTTCGTAGCATTTGTGACACAGGTTTCTTAAACATATT 260-
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QY 187 AAGAACGAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACCCGCGAGCGGTTCTGT 246
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 261 ATCAACCAAGCTGTAATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTTGTT 320
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 247 AGCCCGTCAAGGCTACCCAGGCTTCCGCCATCGCGGTCACAGTGCAGGGCAAGGC 306
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 321 AACCCCGCTAATACTTTCCCAACTTTGCCAAATTCTGTAC-----CAGACGT 368
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 307 GAGATCGCGCTTCTTCGCGCACGCCAGCGACGAGACCGGGCATTTCTGTATCATCAGC 366
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QY 369 GAAATGCTACCATGTTTGCTCATTTCTACGAGACCGGACATTTCTGCTACATAGAA 428
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 GAGAT---CAGCAAGAGCAACCGCTACTTGCACCCGACCCGACAGAGCGAGTGCCTGCGCC 423
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QY 429 GAGATTAAAGGAGCAACAGCTAATCTGTCGAGAGCGAGCAACACAAATACCCATGTGCA 488
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 CGCGGGCAGAGTACTACGGCGCGCGCGCTGAGATCTGTGGAATCACTACACTAGGG 483
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QY 489 CCGGAAAGGCTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 CCCGCGGAGGAGCATCGGCTTCGACGGGCTCGAGGACCCCGGACCGGCGCGGAC 543
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 549 CGGTGTGCTCAAGTCTCGCTTGTGACCTTCTACGCGACCCGACCTTGTGGTAGCAAC 608
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QY 544 CCGGTGTGCGGTTCAAGCGCGCGCTCTGTTCTGGATGAACAACTGTCACCGTGTGATG 603
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DB 609 CCAACTGTAGCTTTTCAGTCCGGTTTGTGGATGAATAGCGTAAGCGCGGTTCTG 668
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DB 669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTATATGG---AATGGAATGTAACGGTGT 725
QY 664 AACCCCGCCAGATGAACGCGGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGC 723
DB 726 AATTCGGTGCAGTCAACGCAAGGATTGGATCTATAGAGCTATTATTGTGACAGCTTGGT 785
QY 724 GTCGACCCAGGCGCCCAACCTCACTTCTCTGA 753
DB 786 GTGACCCCTGGTCTTAACCTTAGTTGCTAA 815
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## RESULT 15

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US-08-456-240-37
; Sequence 37, Application US/08456240
; Patent No. 5856154
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,240
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 35,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-240-37

Query Match      26.6%; Score 200.4; DB 2; Length 1079;
Best Local Similarity 58.5%; Pred. No. 2.5e-33;
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

Qy      7  CAGAACTGCGGCTGCCAGCCAAACGATATGTCGAGCAAGTTCCGCTACTCGGCGCACCAACC 66
Db      93  CAAAACCTGCGGTTGCGCTCCAAACCTCTGTTGCAGTCAGTTTCGGTTTACTGTGTGTACCGAC 152

Qy      67  GACGAGTACTGCGGCGAGCGGTGCCAGTCGCGGCCCGCTCGGCGCGCGCGCGCAGC 126
Db      153  GATGCATACCTGCGGTGTGGATGCCGATCAGGTCCTTTGTAGAGGTAGTGGAAACCCCGACC 212

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Qy      604  CCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGGAGCGGAAC 663
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Qy      724  GTCGACCCAGGCGCCCAACCTCACTTGTCTGA 753
Db      786  GTGACCCCTGGTCTTAACCTTAGTTGCTAA 815
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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

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Database : Published Applications NA:\*

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- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	753	19	US-10-692-367-69 Sequence 69, Appl
2	732.2	97.2	753	19	US-10-692-367-51 Sequence 51, Appl
3	729.2	96.8	750	18	US-10-389-432B-51 Sequence 51, Appl
4	725.8	96.4	753	19	US-10-692-367-55 Sequence 55, Appl
5	722.8	96.0	750	18	US-10-389-432B-55 Sequence 55, Appl
6	722.6	96.0	753	19	US-10-692-367-77 Sequence 77, Appl
7	719.4	95.5	753	19	US-10-692-367-81 Sequence 81, Appl
8	717.8	95.3	753	19	US-10-692-367-35 Sequence 35, Appl
9	717.2	95.2	1037	17	US-10-425-114-19751 Sequence 19751, A
10	716.2	95.1	753	19	US-10-692-367-43 Sequence 43, Appl
11	715.6	95.0	1094	15	US-10-304-928-1 Sequence 1, Appl

12	714.8	94.9	750	18	US-10-389-432B-35	Sequence 35, Appl
13	714.6	94.9	753	19	US-10-692-367-21	Sequence 21, Appl
14	713.2	94.7	750	18	US-10-389-432B-43	Sequence 43, Appl
15	711.8	94.5	765	19	US-10-692-367-67	Sequence 67, Appl
16	711.6	94.5	750	18	US-10-389-432B-21	Sequence 21, Appl
17	711.4	94.5	753	19	US-10-692-367-49	Sequence 49, Appl
18	711.4	94.5	753	19	US-10-692-367-53	Sequence 53, Appl
19	708.4	94.1	750	18	US-10-389-432B-49	Sequence 49, Appl
20	708.4	94.1	750	18	US-10-389-432B-53	Sequence 53, Appl
21	708.2	94.1	750	19	US-10-692-367-79	Sequence 79, Appl
22	701.8	93.2	753	19	US-10-692-367-31	Sequence 31, Appl
23	701.8	93.2	753	19	US-10-692-367-57	Sequence 57, Appl
24	698.8	92.8	750	18	US-10-389-432B-31	Sequence 31, Appl
25	698.8	92.8	750	18	US-10-389-432B-57	Sequence 57, Appl
26	697.8	92.7	771	19	US-10-692-367-47	Sequence 47, Appl
27	696.4	92.5	774	19	US-10-692-367-71	Sequence 71, Appl
28	694.8	92.3	768	18	US-10-389-432B-47	Sequence 47, Appl
29	694.6	92.2	771	19	US-10-692-367-73	Sequence 73, Appl
30	689.8	91.6	771	19	US-10-692-367-61	Sequence 61, Appl
31	689	91.5	753	19	US-10-692-367-27	Sequence 27, Appl
32	686.8	91.2	768	18	US-10-389-432B-61	Sequence 61, Appl
33	686.6	91.2	771	19	US-10-692-367-83	Sequence 83, Appl
34	686	91.1	750	18	US-10-389-432B-27	Sequence 27, Appl
35	685	91.0	771	19	US-10-692-367-59	Sequence 59, Appl
36	683.6	90.8	774	19	US-10-692-367-65	Sequence 65, Appl
37	682	90.6	768	18	US-10-389-432B-59	Sequence 59, Appl
38	680.6	90.4	771	18	US-10-389-432B-65	Sequence 65, Appl
39	675.6	89.7	774	19	US-10-692-367-63	Sequence 63, Appl
40	674.2	89.5	1277	18	US-10-425-115-65712	Sequence 65712, A
41	672.6	89.3	771	18	US-10-389-432B-63	Sequence 63, Appl
42	672.4	89.3	774	19	US-10-692-367-45	Sequence 45, Appl
43	671.2	89.1	780	19	US-10-692-367-39	Sequence 39, Appl
44	671.2	89.1	780	19	US-10-692-367-75	Sequence 75, Appl
45	669.4	88.9	771	18	US-10-389-432B-45	Sequence 45, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-692-367-69  
; Sequence 69, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpari, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(753)  
US-10-692-367-69

```
Query Match      100.0%; Score 753; DB 19; Length 753;
Best Local Similarity 100.0%; Pred. No. 7.9e-189; Indels 0; Gaps 0;
Matches 753; Conservative 0; Mismatches 0;

Qy 1 TCGATGAGAACTCGCGCTGCGAGCAAAAGTATGCTGCGAGCAAGTTGCGTACTGCGGC 60
Db 1 TCGATGAGAACTCGCGCTGCCAGCAAAAGTATGCTGCGAGCAAGTTGCGTACTGCGGC 60

Qy 61 ACAACCGAGAGTACTCGCGGCGAGGTCGAGTGCAGTTCGCGGCGCGTCCGCTCGGGCGGCG 120
Db 61 ACAACCGAGAGTACTCGCGGCGAGGTCGAGTGCAGTTCGCGGCGCGTCCGCTCGGGCGGCG 120

Qy 121 GGCAGAGTTCGCGGCGGTGTCGCAAGTGGCTAGCGTTCGTCACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGAGTTCGCGGCGGTGTCGCAAGTGGCTAGCGTTCGTCACCGGCTCTCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240
Db 181 GGCATCAAGAACACGAGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240

Qy 241 TTCTGAGCGCGTCAAGGCGTACCGAGGCTTCCGCGTTCGCGGCTCAGAGTGCAGGCG 300
Db 241 TTCTGAGCGCGTCAAGGCGTACCGAGGCTTCCGCGTTCGCGGCTCAGAGTGCAGGCG 300

Qy 301 AAGCGGAGATTCGCGGCTTCTTCGCGCAGCGACGAGACCGGCGCATTTCTGTTAC 360
Db 301 AAGCGGAGATTCGCGGCTTCTTCGCGCAGCGACGAGACCGGCGCATTTCTGTTAC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGCGCAAGAGGCGAGTGCCTGTC 420
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGCGCAAGAGGCGAGTGCCTGTC 420

Qy 421 GCCCGGCGGAGAGTACTAGCGGCGCGCGCTCGAGATCTCTGCGAATCAACTAC 480
Db 421 GCCCGGCGGAGAGTACTAGCGGCGCGCGCTCGAGATCTCTGCGAATCAACTAC 480

Qy 481 GGGCGCGGCGGAGGAGATCGCGCTTCGAGCGGCTCGGGGACCCCGCGAGGTCGCGCG 540
Db 481 GGGCGCGGCGGAGGAGATCGCGCTTCGAGCGGCTCGGGGACCCCGCGAGGTCGCGCG 540

Qy 541 GACGCGGTGTCGCGTTCAAGCGGCGCTCTGTTCTGCGATGAACAACGTCACCGTGTG 600
Db 541 GACGCGGTGTCGCGTTCAAGCGGCGCTCTGTTCTGCGATGAACAACGTCACCGTGTG 600

Qy 601 ATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 660
Db 601 ATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 660

Qy 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGCTC 720
Db 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGCTC 720

Qy 721 GGCCTGCAACCCAGGCGCGCAACCTCACTTGTGTA 753
Db 721 GGCCTGCAACCCAGGCGCGCAACCTCACTTGTGTA 753
```

## RESULT 2

```
US-10-692-367-51
; Sequence 51, Application US/10692367
; Publication No. US2005050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
```

```
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-51
```

```
Query Match      97.2%; Score 732.2; DB 19; Length 753;
Best Local Similarity 98.3%; Pred. No. 2.4e-183; Indels 0; Gaps 0;
Matches 740; Conservative 0; Mismatches 13;

Qy 1 TCGATGAGAACTCGCGCTGCCAGCAAAAGTATGCTGCGAGCAAGTTGCGTACTGCGGC 60
Db 1 TCGATGAGAACTCGCGCTGCCAGCAAAAGTATGCTGCGAGCAAGTTTGGCTACTGCGGC 60

Qy 61 ACAACCGAGAGTACTCGCGGCGAGGTCGAGTGCAGTTCGCGGCGCGTCCGCTCGGGCGGCG 120
Db 61 ACAACCGAGAGTACTCGCGGCGAGGTCGAGTGCAGTTCGCGGCGCGTCCGCTCGGGCGGCG 120

Qy 121 GGCAGAGTTCGCGGCGGTGTCGCAAGTGGCTAGCGTTCGTCACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGAGTTCGCGGCGGTGTCGCAAGTGGCTAGCGTTCGTCACCGGCTCTCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240
Db 181 GGCATCAAGAACACGAGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240

Qy 241 TTCTGAGCGCGTCAAGGCGTACCGAGGCTTCCGCGTTCGCGGCTCAGAGTGCAGGCG 300
Db 241 TTCTGAGCGCGTCAAGGCGTACCGAGGCTTCCGCGTTCGCGGCTCAGAGTGCAGGCG 300

Qy 301 AAGCGGAGATTCGCGGCTTCTTCGCGCAGCGACGAGACCGGCGCATTTCTGTTAC 360
Db 301 AAGCGGAGATTCGCGGCTTCTTCGCGCAGCGACGAGACCGGCGCATTTCTGTTAC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGCGCAAGAGGCGAGTGCCTGTC 420
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGCGCAAGAGGCGAGTGCCTGTC 420

Qy 421 GCCCGGCGGAGAGTACTAGCGGCGCGCGCTCGAGATCTCTGCGAATCAACTAC 480
Db 421 GCCCGGCGGAGAGTACTAGCGGCGCGCGCTCGAGATCTCTGCGAATCAACTAC 480

Qy 481 GGGCGCGGCGGAGGAGATCGCGCTTCGAGCGGCTCGGGGACCCCGCGAGGTCGCGCG 540
Db 481 GGGCGCGGCGGAGGAGATCGCGCTTCGAGCGGCTCGGGGACCCCGCGAGGTCGCGCG 540

Qy 541 GACGCGGTGTCGCGTTCAAGCGGCGCTCTGTTCTGCGATGAACAACGTCACCGTGTG 600
Db 541 GACGCGGTGTCGCGTTCAAGCGGCGCTCTGTTCTGCGATGAACAACGTCACCGTGTG 600

Qy 601 ATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 660
Db 601 ATGCGCGAGGCTTCGCGGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 660

Qy 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGCTC 720
Db 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGCTC 720

Qy 721 GGCCTGCAACCCAGGCGCGCAACCTCACTTGTGTA 753
```



```
Db 721 GGCCTGACCCAGGCGCCCACTCACTTGCTGA 753
|||||
US-10-389-432B-51
; Sequence 51, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/23_G4 nucleic acid
US-10-389-432B-51

Query Match 96.8%; Score 729.2; DB 18; Length 750;
Best Local Similarity 98.3%; Pred. No. 1.5e-182;
Matches 737; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTCGCGCTGCGACCAAACTATGTCGACGAGTTTCGGCTACTCGGC 60
Db 1 TCGATGACAGAACTCGCGCTGCGACCAAACTATGTCGACGAGTTTCGGCTACTCGGC 60
Qy 61 ACAACCGACGAGTACTCGCGCGACGGTGCAGTGCAGGCGCGCTCGCGCTCGCGCGGC 120
Db 61 ACACCGACGAGTACTCGCGCGACGGTGCAGTGCAGGCGCGCTCGCGCTCGCGCGGC 120
Qy 121 GGCAGAGTGCAGGCGGTGTCGAACTGTCGAGGCTTCCAGGCTTCTTCTTCAAC 180
Db 121 GGCAGAGTGCAGGCGGTGTCGAACTGTCGAGGCTTCTTCTTCAAC 180
Qy 181 GGCATCAAGAACCAAGCGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 240
Db 181 GGCATCAAGAACCAAGCGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 240
Qy 241 TTCTGAGCGCGGTCAAGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 300
Db 241 TTCTGAGCGCGGTCAAGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 300

Db 721 GGCCTGACCCAGGCGCCCACTCACTTGCTGA 753
|||||
US-10-692-367-55
; Sequence 55, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-55

Query Match 96.4%; Score 725.8; DB 19; Length 753;
Best Local Similarity 97.7%; Pred. No. 1.2e-181;
Matches 736; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTCGCGCTGCGACCAAACTATGTCGACGAGTTTCGGCTACTCGGC 60
Db 1 TCGATGACAGAACTCGCGCTGCGACCAAACTATGTCGACGAGTTTCGGCTACTCGGC 60
Qy 61 ACAACCGACGAGTACTCGCGCGACGGTGCAGTGCAGGCGCGCTCGCGCGCGGC 120
Db 61 ACAACCGACGAGTACTCGCGCGACGGTGCAGTGCAGGCGCGCTCGCGCGCGGC 120
Qy 121 GGCAGAGTGCAGGCGGTGTCGAACTGTCGAGGCTTCTTCTTCAAC 180
Db 121 GGCAGAGTGCAGGCGGTGTCGAACTGTCGAGGCTTCTTCTTCAAC 180
Qy 181 GGCATCAAGAACCAAGCGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 240
Db 181 GGCATCAAGAACCAAGCGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 240
Qy 241 TTCTGAGCGCGGTCAAGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 300
Db 241 TTCTGAGCGCGGTCAAGCGGTGTCGAGGCGCGGCTTCTTCTTCAAC 300
```



```
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-77

Query Match      96.0%; Score 722.6; DB 19; Length 753;
Best Local Similarity 97.5%; Pred. No. 8.2e-181;
Matches 734; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTCGCGCTGCGGCGAGCAAACTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGCTGCGGCGAGCAAACTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACCGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 120
Db 61 ACACCGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 120

Qy 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 240
Db 181 GGCATCAAGAACACGAGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 240

Qy 241 TTCTGTAGCGCGCTCAAGGCGTACCCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 300
Db 241 TTCTGTAGCGCGCTCAAGGCGTACCCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 300

Qy 301 AAGCGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 360
Db 301 AAGCGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 360

Qy 361 ATCAGCGAGATCAGCAAGACGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 420
Db 361 ATCAGCGAGATCAGCAAGACGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 420

Qy 421 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 480
Db 421 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 480

Qy 481 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 540
Db 481 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 540

Qy 541 GACGCGGCTGGTGGCGTTCAAGCGGCGCTTCTGCTTCTGATGAACAACTGCGGCGGCGG 600
Db 541 GACGCGGCTGGTGGCGTTCAAGCGGCGCTTCTGCTTCTGATGAACAACTGCGGCGGCGG 600

Qy 601 ATGCGCGAGGCTTTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 ATGCGCGAGGCTTTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

Qy 661 AACAAACCCCGCCAGATGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 AACAAACCCCGCCAGATGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720

Qy 721 GCGGTCGACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 753
Db 721 GCGGTCGACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 753
```

## RESULT 7

```
US-10-692-367-81
; Sequence 81, Application US/10692367
; Publication No. US200500595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
```

```
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-81
```

```
Query Match      95.5%; Score 719.4; DB 19; Length 753;
Best Local Similarity 97.2%; Pred. No. 5.7e-180;
Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTCGCGCTGCGGCGAGCAAACTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGCTGCGGCGAGCAAACTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACCGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 120
Db 61 ACACCGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 120

Qy 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 240
Db 181 GGCATCAAGAACACGAGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 240

Qy 241 TTCTGTAGCGCGCTCAAGGCGTACCCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 300
Db 241 TTCTGTAGCGCGCTCAAGGCGTACCCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 300

Qy 301 AAGCGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 360
Db 301 AAGCGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 360

Qy 361 ATCAGCGAGATCAGCAAGACGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 420
Db 361 ATCAGCGAGATCAGCAAGACGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 420

Qy 421 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 480
Db 421 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 480

Qy 481 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 540
Db 481 GCGCGGCGGCGAGAACTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGCTCCTTCTTCAAC 540

Qy 541 GACGCGGCTGGTGGCGTTCAAGCGGCGCTTCTGCTTCTGATGAACAACTGCGGCGGCGG 600
Db 541 GACGCGGCTGGTGGCGTTCAAGCGGCGCTTCTGCTTCTGATGAACAACTGCGGCGGCGG 600

Qy 601 ATGCGCGAGGCTTTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 ATGCGCGAGGCTTTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

Qy 661 AACAAACCCCGCCAGATGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 AACAAACCCCGCCAGATGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
```

Qy 661 AACAAACCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTAGTACTGCGGCCAGCTC 720  
Db 661 AACAAACCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTAGTACTGCGGCCAGCTC 720  
Qy 721 GCGGTGACCCAGGCGCCAAACCTCACCTTGCTGA 753  
Db 721 GCGGTGACCCAGGCGCCAAACCTCACCTTGCTGA 753

## RESULT 8

US-10-692-367-35  
; Sequence 35, Application US/10692367  
; Publication No. US200500595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 54916200320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; NAME/KEY: CDS  
; LOCATION: (1)...(753)  
US-10-692-367-35

Query Match 95.3%; Score 717.8; DB 19; Length 753;  
Best Local Similarity 97.1%; Pred. No. 1.5e-179;  
Matches 731; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Qy 1 TCGATGAGAACTCGCGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTCGCGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
Qy 61 AACACGACGAGTACTCGCGGACGGGTGCGAGTCCGCGCCGCTCGCGGCGCGGC 120  
Db 61 ACGACCGACGAGTACTCGCGGACGGGTGCGAGTCCGCGCCGCTCGCGGCGCGGC 120  
Qy 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGGCTAGCGTTCGTCACGGGCTCCTTCTTCAAC 180  
Db 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGGCTAGCGTTCGTCACGGGCTCCTTCTTCAAC 180  
Qy 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACCCCGAGGCGG 240  
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACCCCGAGGCGG 240  
Qy 241 TTCTGAGCGCGGTCAAGCGGTACCCAGGCTTCGCCCATATGCGGGTTCACAGTGCAGGGC 300  
Db 241 TTCTGAGCGCGGTCAAGCGGTACCCAGGCTTCGCCCATATGCGGGTTCACAGTGCAGGGC 300  
Qy 301 AAGCGCAGATCGCGGCTTCTTCGCGACGCCACGACGAGCGGSCATTTCTGTATAC 360  
Db 301 AAGCGCAGATCGCGGCTTCTTCGCGACGCCACGACGAGCGGSCATTTCTGTATAC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTACTTCGGAACCCGACCCGAGGCGAGTGGCCGTGC 420  
Db 361 ATCAACGAGATCAACAGAGCAACGCTACTTCGGAACCCGACCCGAGGCGAGTGGCCGTGC 420  
Qy 421 GCGCGGGGCGAGAAGTACTACGGCGCGCGCGTGCAGATCTCGTGGAACTACAACCTAC 480  
Db 421 GCGCGGGGCGAGAAGTACTACGGCGCGCGCGTGCAGATCTCGTGGAACTACAACCTAC 480  
Qy 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTGGGGACCCCGGACGGGTGGCGGG 540  
Db 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTGGGGACCCCGGACGGGTGGCGGG 540  
Qy 541 GACGCGGTGCTGGCGTTCAAGCGCGCGCTCTGGTTCTGATGAACAAACGTCGACCGTGTG 600  
Db 541 GACGCGGTGCTGGCGTTCAAGCGCGCGCTCTGGTTCTGATGAACAAACGTCGACCGTGTG 600  
Qy 601 ATGCGCAGGGCTTCGGCGCCACATCAGGGCCCATCAACGGCGGCTCGAGTGGAGCGGG 660  
Db 601 ATGCGCAGGGCTTCGGCGCCACATCAGGGCCCATCAACGGCGGCTCGAGTGGAGCGGG 660  
Qy 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTTACAAGCAGTACTTCCCGCAGCTC 720  
Db 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTTACAAGCAGTACTTCCCGCAGCTC 720  
Qy 721 GCGGTGACCCAGGCGCCAAACCTCACCTTGCTGA 753  
Db 721 GCGGTGACCCAGGCGCCAAACCTCACCTTGCTGA 753

## RESULT 9

US-10-425-114-19751  
; Sequence 19751, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19751  
; LENGTH: 1037  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-014-E10\_FLI  
US-10-425-114-19751

Query Match 95.2%; Score 717.2; DB 17; Length 1037;  
Best Local Similarity 97.6%; Pred. No. 2.2e-179;  
Matches 728; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Qy 6 GCAGAACTCGGGTGCAGCCAAACGATGCTGCAGCAAGTTTCGGCTACTGCGGCAAC 65  
Db 124 GCAGAACTCGGGTGCAGCCAAACGATGCTGCAGCAAGTTTCGGCTACTGCGGCAAC 183  
Qy 66 CGACGAGTACTTCGCGGACGGGTGCCAGTGGGCGCCGCTGCGGCGCGGCGGCGAG 125  
Db 184 CGACGAGTACTTCGCGGACGGGTGCCAGTGGGCGCCGCTGCGGCGCGGCGGCGAG 243  
Qy 126 CAGTGGCGCGGTGTCGAAAGTGGCTAGCGTTCACCGGCTCCTTCTTCAACGGGAT 185  
Db 244 CAGTGGCGCGGTGTCGAAAGTGGCTAGCGTTCACCGGCTCCTTCTTCAACGGGAT 303  
Qy 186 CAGAAACCGCGGAGCGGTCGAGGGCAGAACTTCTACACCGGCGGCGGTTCCT 245  
Db 304 CAGAGCCAGCGCGGAGCGGTCGAGGGCAGAACTTCTACACCGGCGGCGGTTCCT 363

```
Qy 246 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGGCGGGTCA CAGGTGCAAGGCAAGCG 305
|
|
|
Db 364 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGGCGGGTCA CAGGTGCAAGGCAAGCG 423
|
|
|
Qy 306 CGAGATCGCGCGCTTCGCGCGACGCCACGACGAGACCGGGCATTTCTGTTACATCAG 365
|
|
|
Db 424 CGAGATCGCGCGCTTCGCGCGACGCCACGACGAGACCGGGCATTTCTGTTACATCAG 483
|
|
|
Qy 366 CGAGATCAGCAGAGCAACGCGCTACTGCGACCCGACCAAGAGGCGAGTGGCGCGCGCGC 425
|
|
|
Db 484 CGAGATCAACAGAGCAACGCGCTACTGCGACCCGACCAAGAGGCGAGTGGCGCGCGCGC 543
|
|
|
Qy 426 GGGCAGAGTACTACGGGCGCGCGCGCTCGAGATCTCGTGGAACTTACAACTACGGGCGC 485
|
|
|
Db 544 GGGCAGAGTACTACGGGCGCGCGCGCTCGAGATCTCGTGGAACTTACAACTACGGGCGC 603
|
|
|
Qy 486 CGCGGGGAGGACATCGCGCTTCGACGCGCTCGGGGACCCCGGACGGGTGGCGCGGACGC 545
|
|
|
Db 604 CGCGGGGAGGACATCGCGCTTCGACGCGCTCGGGGACCCCGGACGGGTGGCGCGGACGC 663
|
|
|
Qy 546 CGTGTGCGCTTCAAGCGCGCGCTCTGGTCTTGGATGAACAACTGACACCGTGTGATGCC 605
|
|
|
Db 664 CGTGTGCGCTTCAAGCGCGCGCTCTGGTCTTGGATGAACAACTGACACCGTGTGATGCC 723
|
|
|
Qy 606 GCAGGCTTCGCGCGCACCATCAGGCGCATCAACGGCGCGCTCGAGTGGCGAGGAAACAA 665
|
|
|
Db 724 GCAGGCTTCGCGCGCACCATCAGGCGCATCAACGGCGCGCTCGAGTGGCGAGGAAACAA 783
|
|
|
Qy 666 CCGCGCCAGATGAACGGCGCATCGGCTACTACAAGCAGTACTGCGCCAGCTCGGCGT 725
|
|
|
Db 784 CCGCGCCAGATGAACGGCGCATCGGCTACTACAAGCAGTACTGCGCCAGCTCGGCGT 843
|
|
|
Qy 726 CGACCCGAGGCGCCCAACCTCACTTGTCT 751
|
|
|
Db 844 CGACCCGAGGCGCCCAACCTCACTTGTCT 869
|
|
|
```

## RESULT 10

```
US-10-692-367-43
; Sequence 43, Application US/10692367
; Publication No. US2005005959A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-43
```

```
Query Match 95.1%; Score 716.2; DB 19; Length 753;
Best Local Similarity 96.9%; Pred. No. 4e-179;
Matches 730; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 TCGATGCAAGAACTCGCGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
|
|
|
Db 1 TCGATGCAAGAACTCGCGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
|
|
|
Qy 61 ACAAACGACGAGTACTGCGCGCGACGGGTGCGAGTTCGAGTTCGCGCGCGTCCGCTCGCGCGCGC 120
|
|
|
Db 61 ACGACCGACGAGTACTGCGCGCGACGGGTGCGAGTTCGAGTTCGCGCGCGTCCGCTCGCGCGCGC 120
|
|
|
Qy 121 GCGAGCAGTTCGCGCGCGTTCGAGAACTGCTAGCGTTCGAGTTCGCGCGCGTCCGCTTCCTTCAAC 180
|
|
|
Db 121 GCGAGCAGTTCGCGCGCGTTCGAGAACTGCTAGCGTTCGAGTTCGCGCGCGTCCGCTTCCTTCAAC 180
|
|
|
Qy 181 GGCATCAAGAACCAAGCGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCGAGGCGCG 240
|
|
|
Db 181 GGCATCAAGAACCAAGCGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCGAGGCGCG 240
|
|
|
Qy 241 TTCTGAGCGCGCTCAAGCGGTACCCAGGTTACCCAGGTTTCGCCCATGCGCGGTCAAGTGCAGGCGC 300
|
|
|
Db 241 TTCTGAGCGCGCTCAAGCGGTACCCAGGTTACCCAGGTTTCGCCCATGCGCGGTCCGAGTGCAGGCGC 300
|
|
|
Qy 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCAACGCCACGACGAGACCGGGCATTTCTGTGTAC 360
|
|
|
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCATGTTCGCGCAACGCCACGAGACCGGGCATTTCTGTGTAC 360
|
|
|
Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCGCTACTGCGACCCGACCAAGAGGCGAGTGGCGCGTGC 420
|
|
|
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCGCTACTGCGACCCGACCAAGAGGCGAGTGGCGCGTGC 420
|
|
|
Qy 421 GCGCGCGGCGAGAACTACTACGCGCGCGCGCTGCGAGATCTGCTGGAACCTACAACTAC 480
|
|
|
Db 421 GCGCGCGGCGAGAACTACTACGCGCGCGCGCTGCGAGATCTGCTGGAACCTACAACTAC 480
|
|
|
Qy 481 GGGCGCGCGGAGGAGCATCGGCTTCGAGCGGCTTCGAGCGGCTCGGGGACCCCGGAGGGTGGCGCG 540
|
|
|
Db 481 GGGCGCGCGGAGGAGCATCGGCTTCGAGCGGCTTCGAGCGGCTCGGGGACCCCGGAGGGTGGCGCG 540
|
|
|
Qy 541 GAGCGCGTGGTGGCGTTCAAGGGCGCGCTCTGCTGTTCTGGATGAACAACTGCAACCGTGTG 600
|
|
|
Db 541 GAGCGCGTGGTGGCGTTCAAGGGCGCGCTCTGCTGTTCTGGATGAACAACTGCAACCGTGTG 600
|
|
|
Qy 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCAGCGG 660
|
|
|
Db 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCAGCGG 660
|
|
|
Qy 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCGCGCGAGTTC 720
|
|
|
Db 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCGCGCGAGTTC 720
|
|
|
Qy 721 GGGTTCGACCCAGGCGCCCAACCTCACTTGTCTGA 753
|
|
|
Db 721 GGGTTCGACCCAGGCGCCCAACCTCACTTGTCTGA 753
|
|
|
```

## RESULT 11

```
US-10-304-928-1
; Sequence 1, Application US/10304928
; Publication No. US20030101484A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100D
; CURRENT APPLICATION NUMBER: US/10/304,928
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/522,714
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/125,915
; PRIOR FILING DATE: 1999-03-24
```

; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-10-304-928-1

Query Match 95.0%; Score 715.6; DB 15; Length 1094;  
Best Local Similarity 97.5%; Pred. No. 5.8e-179;  
Matches 727; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 6 GCAGAACTGGCGCTGCCAGCCAAACGATGCTGCAGCAAGTTGGCTACTGCGGCACAAC 65  
Db 149 GCAGAACTGGCGCTGCCAGCCAAACGATGCTGCAGCAAGTTGGCTACTGCGGCAGAC 208  
Qy 66 CGACGAGTACTGCGCGCACGGGTGCCAGTGGGGCCCGTGGCGCTCGGGCGCGCGCGGAG 125  
Db 209 CGACGAGTACTGCGCGCACGGGTGCCAGTGGGGCCCGTGGCGCTCGGGCGCGCGGAG 268  
Qy 126 CAGTGGCGCGGTGGTGCAGACGTGGCTAGCGTCTCACCGGCTCTTCTTCAACGGCAT 185  
Db 269 CAGTGGCGCGGTGGTGCAGACGTGGCTAGCGTCTCACCGGCTCTTCTTCAACGGCAT 328  
Qy 186 CAAGAAACAGCGCCGGGAGCGGTGCGAGGGCAAGACTTCTACACCGGAGCGGTTCCT 245  
Db 329 CAAGAGCCAGCGCCGGGAGCGGTGCGAGGGCAAGACTTCTACACCGGAGCGGTTCCT 388  
Qy 246 GAGCGCGTCAAGCGCTACCCAGCGTTTCGCCATGGCGGGTACAGGTGAGGGCAAGCG 305  
Db 389 GAGCGCGTCAAGCGCTACCCAGCGTTTCGCCATGGCGGGTACAGGTGAGGGCAAGCG 448  
Qy 306 CGAGATCGCGCGCTTCTTGGCGCACGCGACGACAGACCGGGCATTTCTGTATCATCAG 365  
Db 449 CGAGATCGCGCGCTTCTTGGCGCACGCGACGACAGACCGGGCATTTCTGTATCATCAG 508  
Qy 366 CGAGATCAGCAGACGCGCTACTGGACCCGACCAAGAGGAGTGGCGGTGGCGGC 425  
Db 509 CGAGATCAACAGAGCAACGCGCTACTGGACCCGACCAAGAGGAGTGGCGGTGGCGGC 568  
Qy 426 GGGCGAGAGTACTACGGCGCGCGCGCTGCGAGTCTCGTGGAACTACAACTACGGGCG 485  
Db 569 GGGCGAGAGTACTACGGCGCGCGCGCTGCGAGTCTCGTGGAACTACAACTACGGGCG 628  
Qy 486 CGCGGGAGGAGCAATCGGCTTTCGACCGGCTCGGGGACCCCGGACGGGTGGCGGGAGCG 545  
Db 629 CGCGGGAGGAGCAATCGGCTTTCGACCGGCTCGGGGACCCCGGACGGGTGGCGGGAGCG 688  
Qy 546 CGTGGTGGCTTCAAGGGCGCTCTGGTCTGATGAAACAACTGACCGTGGATGCC 605  
Db 689 CGTGGTGGCTTCAAGGGCGCTCTGGTCTGATGAAACAACTGACCGTGGATGCC 748  
Qy 606 GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGGCAAGGGAACAA 665  
Db 749 GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGGCGGGGAACAA 808  
Qy 666 CCGCGCCAGATGAACCGCGCATCGGCTACTAAGCAGTACTGCGCGCATAGCTCGGGGT 725  
Db 809 CCGCGCCAGATGAACCGCGCATCGGCTACTAAGCAGTACTGCGCGCATAGCTCGGGGT 868  
Qy 726 CGACCCAGGGCCCACTTCTTCT 751  
Db 869 CGACCCAGGGCCCACTTCTTCT 894

RESULT 12  
US-10-389-432B-35  
; Sequence 35, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 750  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: rl AH8 nucleic acid  
US-10-389-432B-35

Query Match 94.9%; Score 714.8; DB 18; Length 750;  
Best Local Similarity 97.1%; Pred. No. 9.3e-179;  
Matches 728; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Qy 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTGGCTACTGCGGC 60  
Qy 61 ACAACCGACGAGTACTGCGCGCACGGGTGCGAGTGGGGCCCGTGGCGCTCGGGCGCGGC 120  
Db 61 ACACCGACGAGTACTGCGCGCACGGGTGCGAGTGGGGCCCGTGGCGCTCGGGCGCGGC 120  
Qy 121 GCGAGAGTGGCGCGCGTGGTGCAGACGTTAGCGTCTCACCGGCTCTTCTTCAAC 180  
Db 121 GCGAGAGTGGCGCGCGTGGTGTGAACGTTGGTGTGAGCGTCTCACCGGCTCTTCTTCAAC 180  
Qy 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCCGAGGCGCG 240  
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCCGAGGCGCG 240  
Qy 241 TTCTGAGCGCTTCAAGGCGTACCAGGTTTCCGCCATGCGCGGTTCAGAGTGCAGGGC 300  
Db 241 TTCTGAGCGCTTCAAGGCGTACCAGGTTTCCGCCATGCGCGGTTCAGAGTGCAGGGC 300  
Qy 301 AAGCGGAGATCGCGCTTCTTTCGCGCACCGCACGAGACCCGCGCATTTCTGTAC 360  
Db 301 AAGCGGAGATCGCGCTTCTTTCGCGCACCGCACGAGACCCGCGCATTTCTGTAC 360  
Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGGTGC 420  
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGGTGC 420  
Qy 421 GCGCGGGGAGAACTACTACGGCGCGCGCTGCGATCTCTGTTGGAATCTCAACTAC 480  
Db 421 GCGCGGGGAGAACTACTACGGCGCGCGCTGCGATCTCTGTTGGAATCTCAACTAC 480  
Qy 481 GGGCGCGGGGAGGAGCATCGGCTTTCGAGCGGCTGGGAGACCCCGGAGGTTGGCGCGG 540  
Db 481 GGGCGCGGGGAGGAGCATCGGCTTTCGAGCGGCTGGGAGACCCCGGAGGTTGGCGCGG 540  
Qy 541 GAGCGCGTGGTGGCTTCAAGGGCGGCTCTGTTCTGATGAAACAACTGTCACCGGTGTG 600  
Db 541 GAGCGCGTGGTGGCTTCAAGGGCGGCTCTGTTCTGATGAAACAACTGTCACCGGTGTG 600  
Qy 601 ATGCGCGAGGGCTTGGCGCCACCATCAGGGCCATCAACGGCGCTCTGAGTGGAGAGCGG 660  
Db 601 ATGCGCGAGGGCTTGGCGCCACCATCAGGGCCATCAACGGCGCTCTGAGTGGAGAGCGG 660  
Qy 661 AACAAACCCCGCAGATGAACGCGCATCGGCTACTTACAGCAGTACTTCCCGCAGCTC 720  
Db 661 AACAAACCCCGCAGATGAACGCGCATCGGCTACTTACAGCAGTACTTCCCGCAGCTC 720

QY 721 GCGTCGACCCAGGGCCCAACCTCACTTGC 750  
Db 721 GCGTCGACCCAGGGCCCAACCTCACTTGC 750

## RESULT 13

US-10-692-367-21  
; Sequence 21, Application US/10692367  
; Publication No. US200500595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; NAME/KEY: CDS  
; LOCATION: (1)...(753)  
US-10-692-367-21

Query Match 94.9%; Score 714.6; DB 19; Length 753;  
Best Local Similarity 96.8%; Pred. No. 1.1e-178;  
Matches 729; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1 TCGATGCAGAACTCGCGCTGCGCAGCAAAAGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGCGGTGCGCGTCTGCTGCGCGCTTTCGGGTACTGCGGC 60  
QY 61 ACACCGGACGAGTACTGCGGCGACGGGTGCCAGTCCGAGTCCGGCCCGTCCGGCGCGGC 120  
Db 61 ACACCGGACGAGTACTGCGGCGACGGGTGCCAGTCCGAGTCCGGCCCGTCCGGCGCGGC 120  
QY 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGTCACCGGCTCTTCTTCAAC 180  
Db 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGTCACCGGCTCTTCTTCAAC 180  
QY 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGC 240  
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGC 240  
QY 241 TTCCTGAGCGGCTCAAGCGGTACCCAGGCTTTCGCGCATGGCGGGTCAAGGTGACGGC 300  
Db 241 TTCCTGAGCGGCTCAAGCGGTACCCAGGCTTTCGCGCATGGCGGGTTCAGGTGACGGC 300  
QY 301 AAGCGGAGATCGCGGCTTCTTCGCGCAGCGCAGCAGAGACCGGSCATTTCTGTAC 360  
Db 301 AAGCGGAGATCGCGGCTTCTTCGCGCAGCGCAGCAGAGACCGGSCATTTCTGTAC 360  
QY 361 ATCAGCGAGATCAGCAAGAACGCTTACTGCGACCGGACCAAGAGGACGTGGCGCTGC 420  
Db 361 ATCAGCGAGATCAGCAAGAACGCTTACTGCGACCGGACCAAGAGGACGTGGCGCTGC 420

QY 421 GCCCGGGGAGAACTACTAGCGGCGCGGCCGCTGCAGATCTCGTGGAACTACAACTAC 480  
Db 421 GCCCGGGGAGAACTACTAGCGGCGCGGCCGCTGCAGATCTCGTGGAACTACAACTAC 480  
QY 481 GGGCCCGCGGGAGGACATCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTTGGCGCG 540  
Db 481 GGGCCCGCGGGAGGACATCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTTGGCGCG 540  
QY 541 GACGCGGTGGTGGCTTCAAGGCGCGCTTCGGTTCGTGATGAACAACGTGCACCGTGTG 600  
Db 541 GACGCGGTGGTGGCTTCAAGGCGCGCTTCGGTTCGTGATGAACAACGTGCACCGTGTG 600  
QY 601 ATGCGCGAGGGCTTCGGGCGCCACCATCAGGCGCCATCAACGGCGGCTCGAGTGCACCG 660  
Db 601 ATGCGCGAGGGCTTCGGGCGCCACCATCAGGCGCCATCAACGGCGGCTCGAGTGCACCG 660  
QY 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
Db 661 AACAAACCCCGCCAGATGAACGCGCGGCTCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
QY 721 GCGTCGACCCAGGGCCCAACCTCAGTTCGTGA 753  
Db 721 GCGTCGACCCAGGGCCCAACCTCAGTTCGTGA 753

## RESULT 14

US-10-389-432B-43  
; Sequence 43, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 750  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: 4N1/95\_H3 nucleic acid  
US-10-389-432B-43

Query Match 94.7%; Score 713.2; DB 18; Length 750;  
Best Local Similarity 96.9%; Pred. No. 2.5e-178;  
Matches 727; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 1 TCGATGCAGAACTCGCGCTGCGCAGCAAAAGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGCGCTGCGCAGCAAAAGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60  
QY 61 ACACCGGACGAGTACTGCGGCGACGGGTGCCAGTCCGAGTCCGGCCCGTCCGGCGCGGC 120  
Db 61 ACACCGGACGAGTACTGCGGCGACGGGTGCCAGTCCGAGTCCGGCCCGTCCGGCGCGGC 120  
QY 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGTCACCGGCTCTTCTTCAAC 180  
Db 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGTCACCGGCTCTTCTTCAAC 180  
QY 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGC 240  
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGC 240  
QY 241 TTCCTGAGCGGCTCAAGGGGTACCCAGGCTTTCGCCCATGCGCGGTTCAGGTCAGGGC 300

```
Db 241 TTCTGAGCGCGTCAAGGCGTACCAGGCTTCCGCCATGCGGCTCCGAGTCCGAGCGC 300
Qy 301 AAGCGGAGATCGCGCGCTTCTCGCGACGCCACGACGAGACCGGGCATTTCTGTATC 360
Db 301 AAGCGGAGATCGCGCGCTTCTCGCGCATGTCAAGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 ATCAGCGAGATCAGGAGAGCAAGCGCTTCTCGCGACCGGCGGCGGCGGCGGCGGCGG 420
Db 361 ATCAGCGAGATCAACAAGAGCAAGCGCTTCTCGCGACCGGCGGCGGCGGCGGCGGCGG 420
Qy 421 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Qy 481 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 481 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Qy 541 GAGCGCGTGTGGCGTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 541 GAGCGCGTGTGGCGTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Qy 601 ATGCGCGAGGCGTTCGCGCGCACCATCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 ATGCGCGAGGCGTTCGCGCGCACCATCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Qy 661 AACACCGCGCGCGAGATGAACGCGCGCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 AACACCGCGCGCGAGATGAACGCGCGCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Qy 721 GCGCTGCGACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750
Db 721 GCGCTGCGACCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750
```

## RESULT 15

```
US-10-692-367-67
; Sequence 67, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(765)
US-10-692-367-67
```

Query Match 94.5%; Score 711.8; DB 19; Length 765;  
Best Local Similarity 96.9%; Pred. No. 5.8e-178;

```
Matches 741; Conservative 0; Mismatches 12; Indels 12; Gaps 1;
Qy 1 TCGATGCGAAGTCTGCGGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTCGGCG 60
Db 1 TCGATGCGAAGTCTGCGGCTGCCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTCGGCG 60
Qy 61 ACAACCGAGTACTGCGGCGGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 120
Db 61 ACAACCGAGTACTGCGGCGGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 120
Qy 121 GGCAGCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 168
Db 121 GGCAGCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180
Qy 169 TCCTTCTTCAACCGCATCAAGAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 228
Db 181 TCCTTCTTCAACCGCATCAAGAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
Qy 229 ACCCGAGCGCGTTCCTGAGCGCGGCTCAAGCGCGTACCCAGGCGTTCGCGGCGGCGGCGGCG 288
Db 241 ACCCGAGCGCGTTCCTGAGCGCGGCTCAAGCGCGTACCCAGGCGTTCGCGGCGGCGGCGGCG 300
Qy 289 CAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
Db 301 CAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 349 CATTTCTGTTACATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
Db 361 CATTTCTGTTACATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Qy 409 CAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 468
Db 421 CAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Qy 469 AACTACAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 528
Db 481 AACTACAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Qy 529 AGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 588
Db 541 AGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Qy 589 GTGCACCGTGTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 648
Db 601 GTGCACCGTGTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
Qy 649 GAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 708
Db 661 GAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Qy 709 TGCGCGCAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 753
Db 721 TGCGCGCAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 765
```

Search completed: May 23, 2005, 17:32:11

Job time : 388.609 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:20:11 ; Search time 2155.94 Seconds  
(without alignments)  
13294.634 Million cell updates/sec

Title: US-10-692-367-69

Perfect score: 753

Sequence: 1 tcgatgcagaaactgcgctg.....ggcccaactcactgtgtga 753

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsel1:\*

9: gb\_gsel2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
C 1	663.4	88.1	855	4	BG837663 Zm10_01e1
2	643	85.4	1179	3	AY103546 Zea_mays
3	619.6	82.3	767	7	C0524416 3530_1_16
4	599.6	79.6	737	6	CD435649 EL01N0364
5	598.6	79.5	958	4	BG837479 Zm10_10h0
6	550.8	73.1	710	6	CD443492 EL01N0427
7	546.8	72.6	837	7	CN133023 OX1_9_D11
8	536.8	71.3	628	4	BM736454 952051A06
9	533.2	70.8	625	5	BM895383 952073H05
10	526.6	69.9	820	6	CD995497 QB825f07
11	526.6	69.4	578	6	CD994156 QB813f07
12	521.2	69.2	575	6	CD994132 QB813e04
13	520.6	69.1	578	6	CD994454 QB815f08
14	519.6	69.0	741	6	CD994869 QB818d07
15	519.6	69.0	753	6	CD994885 QB818e05
16	508.6	67.5	754	6	CD995176 QB820h11
17	502.4	66.7	647	6	CA197556 SCBPAD106
18	498.8	66.2	550	6	CF001565 QB84f06.x
19	498.8	66.2	559	6	CD999920 QB810a02
20	498.8	66.2	562	6	CF000010 QB811a02
21	498.8	66.2	562	6	CF000228 QB813e12
22	498.8	66.2	562	6	CF000357 QB815b09
23	498.8	66.2	562	6	CF000565 QB817b11
24	498.8	66.2	562	6	CF000643 QB818a05

25	498.8	66.2	573	6	CF000161	CF000161 QB812g06.
26	498.8	66.2	573	6	CF000412	CF000412 QB815g11.
27	498.8	66.2	574	6	CD999947	CD999947 QB810c07.
28	498.8	66.2	574	6	CF000325	CF000325 QB814g11.
29	498.8	66.2	587	6	CF002068	CF002068 QB8f07.x
30	498.8	66.2	587	6	CF002109	CF002109 QB8h11.x
31	498.8	66.2	606	6	CF001250	CF001250 QB82a02.x
32	498.8	66.2	606	6	CF001262	CF001262 QB82b02.x
33	498.8	66.2	606	6	CF001900	CF001900 QB87c09.x
34	498.8	66.2	742	6	CF001316	CF001316 QB82e05.p
35	497.8	66.1	573	6	CF000017	CF000017 QB811a12.
36	497.8	66.0	603	6	CF001775	CF001775 QB86c07.x
37	497.2	66.0	627	6	CF001901	CF001901 QB87c10.x
38	497.2	66.0	641	6	CF011507	CF011507 QB8jhl1.x
39	497.2	66.0	695	6	CF014634	CF014634 QBL17d09.
40	497.2	66.0	746	6	CF001249	CF001249 QB82a02.p
41	497.2	66.0	751	6	CF014225	CF014225 QBL14a03.
42	494.6	65.7	626	6	CF001317	CF001317 QB82e05.x
43	494	65.6	585	6	CF002103	CF002103 QB8h06.x
44	494	65.6	647	6	CF011391	CF011391 QB8b07.x
45	494	65.6	744	6	CF000853	CF000853 QB81a05.p

## ALIGNMENTS

RESULT 1  
BG837663/c 855 bp mRNA linear EST 25-MAY-2001

LOCUS Zm10\_01e10.A Zm10.AAFC\_ECORC\_Fusarium\_graminearum\_corn\_silk Zea  
DEFINITION Zea\_mays CDNA Clone Zm10\_01e10, mRNA sequence.

ACCESSION BG837663  
VERSION BG837663.1 GI:14203986  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 855)  
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A., Sprout,D., and Tinker,N.A.  
TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum  
JOURNAL Unpublished (2001)  
COMMENT Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agricuture and Agri-food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6, CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-6566  
Email: harrielj@agr.gc.ca

## FEATURES

source  
1..855  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="CO388"  
/db\_xref="taxon:4577"  
/clone="Zm10\_01e10"  
/tissue\_type="Silk"  
/dev\_stage="4-5 days post-silk emergence"  
/clone\_lib="Zm10\_AAFC\_ECORC\_Fusarium\_graminearum\_corn\_silk"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was



Qy 525 CGGAGGCGCGCGGAGCGCGTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAA 584  
|  
Db 688 CAACAGGCTGCGCGAGGAGCGCGTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAA 747  
|  
Qy 585 CAAGTCGACCGTGTGATCGCGAGGCTTCCGGCGCCACCATCAAGGCGCATCAACGCGCG 644  
|  
Db 748 CAAGTCGACCGTGTGATCGCGAGGCTTCCGGCGCCACCATCAAGGCGCATCAACGCGCG 807  
|  
Qy 645 GCTCAGTGGCAACCGGCAACCGCGCCAGATGAACGCGCGCATCGGCTACTACAAGCA 704  
|  
Db 808 CCTCAGTGGCAACCGGCAACCGCGCCAGATGAACGCGCGCATCGGCTACTACAAGCA 867  
|  
Qy 705 GTACTGCGCGCGCTCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 751  
|  
Db 868 GTACTGCGCGCGCTCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 914  
|

## RESULT 3

CO524416

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

EST

EST

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EST

EST

EST

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Query Match 82.3%; Score 619.6; DB 7; Length 767;  
Best Local Similarity 97.8%; Pred. No. 7.6e-122;  
Matches 628; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 6 GCAGAACTGGCGCTGCGCGAGCAAAACGATGCTGCGAGCAAGTTGCGGTACTGCGGCAAC 65  
Db 126 GCAGAACTGGCGCTGCGCGAGCAAAACGATGCTGCGAGCAAGTTGCGGTACTGCGGCAAC 185  
Qy 66 CGACGAGTACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGCGG 125  
Db 186 CGACGAGTACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGG 245  
Qy 126 CAGTGGCGCGGCTGCTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
Db 246 CAGTGGCGCGGCTGCTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305  
Qy 186 CAGAACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGGCTGCT 245  
Db 306 CAGAACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGGCTGCT 365  
Qy 246 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCGCCATGCGCGGCTCACAGTGCAGGCGCAAG 305  
Db 366 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCGCCATGCGCGGCTCGCGAGTGCAGGCGCAAG 425  
Qy 306 CGAGATCGCGCGCTTCTTTCGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365  
Db 426 CGAGATCGCGCGCTTCTTTCGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485  
Qy 366 CGAGATCGCAAGAGCAACCGCTTCTGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 425  
Db 486 CGAGATCAACAAGAGCAACCGCTTCTGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 545  
Qy 426 GGGGAGAGTACTACGCGCGCGCGCTGCGAGTCTGCTGGAATACAACTACGAGCGCC 485  
Db 546 GGGGAGAGTACTACGCGCGCGCGCTGCGAGTCTGCTGGAATACAACTACGAGCGCC 605  
Qy 486 CGCGGGAGAGGACATCGCGCTTTCGACCGGCTCGCGGAGCCCGCGGAGGCTGCGCGGAGCG 545  
Db 606 CGCGGGAGAGGACATCGCGCTTTCGACCGGCTCGCGGAGCCCGCGGAGGCTGCGCGGAGCG 665  
Qy 546 CTTGCTGCTGCTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605  
Db 666 CTTGCTGCTGCTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725  
Qy 606 GCAGGCGCTTCCGCGCGCGCGCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAGTCTGCG 647  
Db 726 GCAGGCGCTTCCGCGCGCGCGCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAGTCTGCG 767

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3530\_1.161.1 row: E column: 12.

Location/Qualifiers

1. 767

/organism="Zea mays"

/mol type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue type="multiple"

/dev stage="varies by tissue"

/lab hosts="DH10B"

/clone.lib="3530 - Full length cDNA library created by

Invitrogen from multiple tissues"

/note="Organ: silks, husks, ears, pollen, shoot tips,

leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT

6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery

Project contracted with Invitrogen to produce a

normalized, full length library in a pSport vector. This

is a Gateway compatible vector, permitting clone movement

to new vector backbones for expression in diverse host

cells using recombination rather than restriction enzymes.

Details of the vector and sequencing primers are available

at ZmDB in the EST library description tables. poly(A) +

mRNA was prepared by Invitrogen, and equimolar amounts of

RNA from each of the 12 tissue samples were mixed together

for selection of mRNA with a 5' cap. After synthesis of

cDNA, a normalization step was conducted against the

mixture of RNA sources. This step effected a 20X to 80X

reduction in common transcript types. Tissues prepared: 1.

just emerging silks; 2. inner husks from ears of sample

#1; 3. 20 day aleurone; 4. immature tassels, stages from

1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

## ORIGIN

Query Match 82.3%; Score 619.6; DB 7; Length 767;  
Best Local Similarity 97.8%; Pred. No. 7.6e-122;  
Matches 628; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 6 GCAGAACTGGCGCTGCGCGAGCAAAACGATGCTGCGAGCAAGTTGCGGTACTGCGGCAAC 65  
Db 126 GCAGAACTGGCGCTGCGCGAGCAAAACGATGCTGCGAGCAAGTTGCGGTACTGCGGCAAC 185  
Qy 66 CGACGAGTACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGG 125  
Db 186 CGACGAGTACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGG 245  
Qy 126 CAGTGGCGCGGCTGCTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185  
Db 246 CAGTGGCGCGGCTGCTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305  
Qy 186 CAGAACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGGCTGCT 245  
Db 306 CAGAACTGCGCGGAGCGGCTGCCAGTCCGCGCCCGCTGCCGCTCGCGCGCGCGGCTGCT 365  
Qy 246 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCGCCATGCGCGGCTCACAGTGCAGGCGCAAG 305  
Db 366 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCGCCATGCGCGGCTCGCGAGTGCAGGCGCAAG 425  
Qy 306 CGAGATCGCGCGCTTCTTTCGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365  
Db 426 CGAGATCGCGCGCTTCTTTCGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485  
Qy 366 CGAGATCGCAAGAGCAACCGCTTCTGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 425  
Db 486 CGAGATCAACAAGAGCAACCGCTTCTGCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 545  
Qy 426 GGGGAGAGTACTACGCGCGCGCGCTGCGAGTCTGCTGGAATACAACTACGAGCGCC 485  
Db 546 GGGGAGAGTACTACGCGCGCGCGCTGCGAGTCTGCTGGAATACAACTACGAGCGCC 605  
Qy 486 CGCGGGAGAGGACATCGCGCTTTCGACCGGCTCGCGGAGCCCGCGGAGGCTGCGCGGAGCG 545  
Db 606 CGCGGGAGAGGACATCGCGCTTTCGACCGGCTCGCGGAGCCCGCGGAGGCTGCGCGGAGCG 665  
Qy 546 CTTGCTGCTGCTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605  
Db 666 CTTGCTGCTGCTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725  
Qy 606 GCAGGCGCTTCCGCGCGCGCGCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAGTCTGCG 647  
Db 726 GCAGGCGCTTCCGCGCGCGCGCTGCGAGTCTGCGAGTCTGCGAGTCTGCGAGTCTGCG 767

## RESULT 4

CD435649

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

EST

EST

EST

EST

CD435649 737 bp mRNA linear EST 03-JUN-2003  
EL01N0364B04.b Endosperm\_3 Zea mays cDNA, mRNA sequence.

CD435649

CD435649.1

GI:31351292

EST

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 737)

Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its comparison to the rice genome

Genome Res. 14 (10), 1932-1937 (2004)

Contact: Lai, Jinsheng

Dr. Joachim Messing's lab

Waksman Institute, Rutgers University

190 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@waksman.rutgers.edu

Seq primer: T3.

Location/Qualifiers

1. 737

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W22"

/db\_xref="taxon:4577"

/tissue\_type="Endosperm of 7-23DAP"

/clone\_lib="Endosperm\_3"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI"

ORIGIN

Query Match 79.6%; Score 599.6; DB 6; Length 737;

Best Local Similarity 96.0%; Pred. No. 1.4e-117;

Matches 641; Conservative 0; Mismatches 14; Indels 13; Gaps 2;

2;

6 GCAGAACTCGCGTCCAGCAACAGTATCTGTCAGCAAGTTCGGCTACTCGGCACAAC 65

82 GCAGAACTCGCGTCCAGCAACAGTCTGTCAGCAAGTTCGGCTACTCGGCACGAC 141

66 CGACGAGTACTGCGCGCACGCGTGCACAGTGGCGCCGCTGCGCTCGCGCGCGCGCAG 125

142 CGACGAGTACTGCGCGCACGCGTGCACAGTGGCGCCGCTGCGCTCGCGCGCGC 193

126 CAGTGGCGCGGTGCTCGCAAGTGGTCTAGGTCTGTCACCGGCTCTTCTTCAACGGCAT 185

194 ----GGCGCGCGGTGCTCGCAAGTGGTCTAGGTCTGTCACCGGCTCTTCTTCAACGGCAT 249

186 CAAGAACACGCGCGGAGCGGTGTCGAGGCAAGAACTTCTACACCGGAGCGGTTCTCT 245

250 CAAGAACACGCGCGGAGCGGTGTCGAGGCAAGAACTTCTACACCGGAGCGGTTCTCT 309

246 GAGCGCGCTCAAGCGCTACCGAGCTTTCGCCCATGGCGGGTTCACAGTGCAGGCGCAAGCG 305

310 GAGCGCGCTCAAGCGCTACCGAGCTTTCGCCCATGGCGGGTTCGAGTGCAGGCGCAAGCG 369

306 CGAGATCGCGCTTCTTCGGCGACGCGCAGCAGCAGCGGAGATTTCTGTATCATCAG 365

370 CGAGATCGCGCTTCTTCGGCGACGCGCAGCAGCAGCGGAGATTTCTGTATCATCAG 429

366 CGAGATCAGCAGCAGCAGCAGCTACTGCGACCCGACCAAGGCGAGTGGCGCGCGC 425

430 CGAGATCAAGAGCAGCAGCAGCTACTGCGACCCGACCAAGGCGAGTGGCGCGCGC 489

426 GGGGCGAGAAGTACTACCGCGCGCGCGCGCTGCAGATCTCTGTGAACCTACAACTACGCGGC 485

490 GGGGCGAGAAGTACTACCGCGCGCGCGCGCTGCAGATCTCTGTGAACCTACAACTACGCGGC 549

486 CGCGGGAGGGAATCTCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTTGGCGGGGACGC 545

550 CGCGGGAGGGAATCTCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTTGGCGGGGACGC 609

546 CGTGGTGGCGTTCAAGCGCGGCTCTGTGTTCTGTGATGAACAACTGTGAC - CGTGTGATGC 604

610 CGTGGTGGCGTTCAAGCGCGGCTCTGTGTTCTGTGATGAACAACTGTGACCGGGGTGGTGC 669

605 CGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCTCGAGTGCAGCGGGAACA 664

670 CGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCTCGAGTGCAGCGGGAACA 729

665 ACCCGGCC 672

730 ACCCGGCC 737

RESULT 5

EG837479

LOCUS

DEFINITION

Zm10\_10h09\_A Zm10\_AAFCECORC\_Fusarium\_graminearum\_corn\_silk Zea

mays cDNA clone Zm10\_10h09, mRNA sequence.

EG837479

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 958)

Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D., and Tinker, N.A.

Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum

Unpublished (2001)

Contact: Harris, Linda J.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA

Tel: (613) 759-1314

Fax: (613) 759-6566

Email: harrisjl@agr.gc.ca.

Location/Qualifiers

1. 958

/organism="Zea mays"

/mol\_type="mRNA"

/db\_xref="taxon:4577"

/clone="Zm10\_10h09"

/tissue\_type="Silk"

/dev\_stage="4-5 days post-silk emergence"

/clone\_lib="Zm10\_AAFCECORC\_Fusarium\_graminearum\_corn\_silk"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel. RNA from five silk channels was pooled."

ORIGIN

Query Match 79.5%; Score 598.6; DB 4; Length 958;

Best Local Similarity 89.9%; Pred. No. 2.3e-117;

Matches 683; Conservative 6; Mismatches 56; Indels 15; Gaps 4;

6 GCAGAACTCGCGTCCAGCAACAGTATCTGTCAGCAAGTTCGGCTACTCGGCACAA 64

31 GCAGAACTCGCGTCCAGCAACAGTATCTGTCAGCAAGTTCGGCTACTCGGCACGA 90

65 CCAGCAGTACTCGCGCGACGCGGTGCGAGTCCGCGCCCGTCCGCTCGCGCGCGCGGCA 124

91 CCAGCAGTACTCGCGCGACGCGGTGCGAGTCCGCGCCCGTCCGCTCGCGCGCGCGGCG 150

125 GCAGTGGCG-----GGGTGGTGCAGACGTGGCTAGCTCGTCAACCGGCTCTCT 172

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Db 151 SCGGCGCGGAGCGGAGGCGAGTGGCGGTGCGACGTGGCTAAAGTGGTCAAGCGCGGT 210
QY 173 TCTTCAACGGGATCAAGAACACAGGCGCGGAGCGGTGCGAGGAGCAAGAACTTCTACACCC 232
Db 211 TCTTCAACGGGATCAAGAACACAGGCGCGGAGCGGTGCGAGGAGCAAGAACTTCTACACCC 270
QY 233 GGAGCGGTTCTCGAGCGCGTCAAGCGTCAAGCGTACCCAGGCTTCGCCATGGCGGTCAAGG 292
Db 271 GGAGCGGTTCTCGAGCGCGTCAAGCGTCAAGCGTACCCAGGCTTCGCCATGGCGGTCAAGG 329
QY 293 TGCAGGGCAAGCGGAGATCGCGCTTCTTTCGGCGACGCGCACGACGAGACCGGGCAT 352
Db 330 TGCAGGGCAAGCGGAGATCGCGCTTCTTTCGGCGACGCGCACGACGAGACCGGACAT 389
QY 353 TCTGTACATCAGCGAGATCAGAGAGCAAGCGCTACTCGGACCCGACCAAGAGGAGT 412
Db 390 TCTGTACATCAGCGAGATCAACAGAGCAACGCTACTTCGACGCAAGCAACAGGCGAT 449
QY 413 GGCGTCCGCGCGGCGGAGGAGATCGGCTTTCGACGGGCTCGGGACCCCGGCAAGG 472
Db 450 GGCGTCCGCGCGGCGGAGGAGTACTACGGGCGGCGCTCGGACATCTCGTGGAACT 509
QY 473 ACAACTACGGGCGCGCGGAGGAGATCGGCTTTCGACGGGCTCGGGACCCCGGCAAGG 532
Db 510 ACAACTACGGGCGCGCGGAGGAGATCGGCTTTCGACGGGCTCGGGACCCCGGCAAGG 569
QY 533 TGGCGGGAGCGCGTGGTGGTTCAAGGCGGCGCTCTCGTTCGTGATGAACAAAGTGC 592
Db 570 TGGCGGAGGAGCGCGTGTATCGGTTCAAGAGCGGCGCTCTCGTTCGTGATGAACAAAGTGC 629
QY 593 ACCGTGTGATCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAAGCGCGCTCGAGT 652
Db 630 ACCGTGTGATCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAAGCGCGCTCGAGT 689
QY 653 GCGACGGGAACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCC 712
Db 690 GCAACGGGACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCC 749
QY 713 GCGAGTGGGCTGACACCA-GGGCCCAACTCACTTGGCT 751
Db 750 AGCMCTCCGCTGACCCAGGGGCCCAACGCTCACTTGGCT 789

RESULT 6
CD443492
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 710)
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Freelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
1..710
/organism="Zea mays"
/mol_type="mRNA"

FEATURES
source
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ORIGIN
Query Match 73.1%; Score 550.8; DB 6; Length 710;
Best Local Similarity 97.4%; Pred. No. 3.5e-107;
Matches 571; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 6 GCAGAACTCGCGGTGCGGACCAACGATATGCTGCGAGCAAGTTCGGCTACTCGGCAACAC 65
Db 125 GCAGAACTCGCGGTGCGGACCAACGATATGCTGCGAGCAAGTTCGGCTACTCGGCAACAC 184
QY 66 CGACGAGTACTGCGGGGACCGGTCGAGTCCGCGCCGCTGCGCTCG---GGCGCGCGG 122
Db 185 CGACGAGTACTGTTGGCGAGCGGTCGAGTCCGCGCCGCTGCGGCGCGGCGGCGG 244
QY 123 CAGCAGTGGCGCGGTGCGAAAGTGGTACGCTGCTCAGCGGCTCTTCTTCAACGG 182
Db 245 CGCAGTGGTGGCGGTGCTGCAACGTTAGCGTCTCAGCAGCTCTTCTTCAACGG 304
QY 183 CATCAAGAACCGCGGAGCGGTCGAGGGCAAGACTTCTACACCCGAGCGCGTT 242
Db 305 CATCAAGAACCGCGGAGCGGTCGAGGGCAAGACTTCTACACCCGAGCGCGTT 364
QY 243 CTTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCGCCATGGCGGTCACAGGTGCGAGGCAA 302
Db 365 CTTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCGCCATGGCGGTCGAGGTGCGAGGCAA 424
QY 303 GCGCAGATCGCGCTTCTTCGCGCAAGCGTACGCGAGAGACCGGCGCATTTCTGTTCAT 362
Db 425 GCGCAGATCGCGCTTCTTCGCGCAAGCGTACGCGAGAGACCGGCGCATTTCTGTTCAT 484
QY 363 CAGCGAGATCAGCAAGGCAACCGCTACTCGGACCCGACCAAGAGGAGTGGCGTGGCG 422
Db 485 CAGCGAGATCAGCAAGGCAACCGCTACTCGGACCCGACCAAGAGGAGTGGCGTGGCG 544
QY 423 CCGCGGCGGAGGAGTACTACGCGGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGG 482
Db 545 CCGCGGCGGAGGAGTACTACGCGGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGG 604
QY 483 GCGCGGCGGAGGAGTACTACGCGGCTTCGAGCGGCTCGGAGACCCCGGAGGCTGGCGGGA 542
Db 605 GCGCGGCGGAGGAGTACTACGCGGCTTCGAGCGGCTCGGAGACCCCGGAGGCTGGCGGGA 664
QY 543 GCGCGTGGTGGCGTTCAGAGCGGCGCTCTGGTTCTGGATGAACAAAC 588
Db 665 GCGCGTGGTGGCGTTCAGAGCGGCGCTCTGGTTCTGGATGAACAAAC 710

RESULT 7
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 837)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9.D11.b1.A002
Contact: Cordonnier-Pratt MM

CN133023 837 bp mRNA linear EST 01-APR-2004
OX1_9.D11.g1.A002 Oxidatively-stressed leaves and roots Sorghum
bicolor cDNA clone OX1_9.D11.A002 5', mRNA sequence.
CN133023
CN133023.1 GI:45963543
EST.
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 837)
Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9.D11.b1.A002
Contact: Cordonnier-Pratt MM
```

Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.

Seq primer: Sug5 (CTTGTGCTCTAAAGCTCGG).

#### FEATURES

Location/Qualifiers  
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/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="OX1\_9\_D11\_A002"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Oxidatively-stressed leaves and roots"  
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1:  
XhoI; Site 2: XhoI; The library was prepared from polyA+  
RNA from oxidatively stressed, hydroponically grown  
sorghum seedlings. At 8 days of age, growth medium was  
supplemented with hydrogen peroxide to 0.003% and leaves  
were misted with 10 uM methyl viologen. Leaves and roots  
were harvested at 3, 12 and 27 hr after treatment and all  
tissue pooled. Double-stranded cDNA was cloned  
unidirectionally into different DraIII sites of the  
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,  
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA  
insert."

#### ORIGIN

Query Match 72.6%; Score 546.8; DB 7; Length 837;  
Best Local Similarity 87.2%; Pred. No. 2.5e-106;  
Matches 628; Conservative 0; Mismatches 77; Indels 15; Gaps 2;  
Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGCTGCAGCAAGTTCGGCTACTCGGCAACAAC 65  
Db 133 GCAGAACTACGGCTGCCAGGAGGTACTGCTGCAGCAAGTTCGGCTACTCGGCAACAAC 192  
Qy 66 CGACGAGTACTGCGGCGAGCGGGTCCAGTGCAGGCGCCGCTCGGCGCGCGCGGCGAG 125  
Db 193 CGACGAGTACTGCGGCGAGCGGGTCCAGTGCAGGCGCCGCTCGGCGCGCGCGAGCA- 251  
Qy 126 CAGTGGCGGCGGTGTCGACAGTGGCTAGCGTCTCACCGGCTCTTCTTCAACGGCAT 185  
Db 252 -----GTGGAGGTGGAAACGTGGCTGGGGTGTTCACCGACGATCTTCAACAGCAT 303  
Qy 186 CAAGAACCGAGCGCGGAGCGGTCGAGGGCAAGAACTTCTACACCGGAGCGGCTTCCT 245  
Db 304 CAAGAACCGAGCGCGGAGCGGTCGAGGGCAAGAACTTCTACACCGGAGCGGCTTCCT 363  
Qy 246 GAGCGCGTCAAGCGGTACCCAGGCTTCGCCATTCGGCGGTTCAGAGTGCAGGCGAGCG 305  
Db 364 GAGCGCGCGCGAGCGGTACCAAGGCTTCG-----GTGGCAGGTTCGGTGCAGGCGAAGCG 417  
Qy 306 CGAGATCGCGGCTTCTTCGCGCAGCGCCAGCAGCAGCGGCGGATTTCTGTATCATCAG 365  
Db 418 CGAGATCGCGGCTTCTTCGCGCAGCATCACCAGCAGACCGGACATTTCTGTATCATCAG 477  
Qy 366 CGAGATCAGCAAGAGCAACGCTTACTGCGACCCCGACCAAGAGCGAGTGGCGTGGCGGC 425  
Db 478 CGAGATCAACAAGAACACGCTTACTGCGACTCGAGCAACAGGCGAGTGGCGGTGGCGGC 537  
Qy 426 GGGGAGAGTACTACGGGCGGCGCGCGCTCGAGATCTCGTGGAACTACAATACGAGGCC 485  
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Qy 486 CGCGGGGAGGACATCGGCTTCGACGGGCTCGGGACCCCGCAGGCTGGCGGGACGC 545  
Db 598 TGCGGGAGGACATCGGCTTCGACGGGCTTCGGACCCCGCAGGCTGGCGGGACGC 657  
Qy 546 CGTGTGGCGCTTCAAGACGGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTGATGCC 605  
Db 658 CGTGTGGCGCTTCAAGACGGCGCTCTGGTTCTGGACCAACAACGTCACCGGGTGTATGTC 717  
Qy 606 GCAGGCTTCGGCGCCACCATCAGGCGCATCAAGGGCGCTCGAGTGCAGCGGAGCAA 665  
Db 718 GCAGGCTTCGGCGCCACCATCAGGCGCATCAAGGGCGCTTCGAGTGCAGCGGAGCAA 777  
Qy 666 CCCGCCCGACATCAAGCGCGCATCGGCTACTACTCAAGCAGTACTGCCCGCAGCTCGGCGT 725  
Db 778 TACTGCCAGATCAAGCGGGGTGGCTACTACTACAGCAGTACTGCCAGCAGCTCGGCGT 837  
RESULT 8  
BM736454  
LOCUS  
DEFINITION  
952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
mays cDNA, mRNA sequence.  
ACCESSION  
BM736454  
VERSION  
BM736454.1 GI:19057787  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 628)  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 952051 row: A column: 06.  
FEATURES  
Location/Qualifiers  
1..628  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth  
phases"  
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/clone\_lib="952 - BMS tissue from Walbot Lab (reduced  
rRNA)"  
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and Universal Riboclone cDNA Synthesis System  
(Promega). cDNA was synthesized using both random and  
oligo(dT) primers in separate reactions and equipped with  
EcoRI adaptors. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-directionally cloned  
into EcoRI-digested pUC19 vector. Blue/white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

#### ORIGIN

Query Match 71.3%; Score 536.8; DB 4; Length 628;  
Best Local Similarity 93.0%; Pred. No. 3.4e-104;  
Matches 573; Conservative 0; Mismatches 42; Indels 1; Gaps 1;  
Qy 136 GGTGGTCGAAACGTGGCTAGCGTCGCCCGGCTCTTCTTCAACGGCATCAAGAACG 195

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Db 3 GGGCGGGGAACTGGCTTACGT GCGAGCAGCGGTTCTTCAACGGGATCAAGAACAG 61
Qy 196 GCGGGAGCGGGTCCGAGGGCAAGAACTTTACACCCGAGCGGTTCTTCTGAGCGCGTC 255
Db 62 GCGGGAGCGGGTCCGAGGGCAAGAACTTTACACCCGAGCGGTTCTTCTGAGCGCGTC 121
Qy 256 AAGCGGTACCCAGCGTTCCCATGCGGGTCAAGGTGAGGCAAGCGGAGATGCGC 315
Db 122 AACAACTACCCGGGCTTCGCCATGCGGGAGCGAGGTGGAGGCAAGCGGAGATGCGC 181
Qy 316 GCCTTTCTCGCGCACGCCACACAGAGACCGGGCATTTCTGTATCATCAGCGAGATCAGC 375
Db 182 GCCTTTCTCGCGCACGTCACGACGAGACCGGACATTTCTGTATCATCAGCGAGATCAAC 241
Qy 376 AAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCGGGCGAGAAG 435
Db 242 AAGAGCAACGCTTACTGCGACCGCAAGCAACAGGCAAGTGGCGCGTGGCGGGCGAGAAG 301
Qy 436 TACTACGGCGCGCGCGCTGCAGATCTCGTGGAACTACAACTACGGCGCGCGGGGAGG 495
Db 302 TACTACGGCGCGCGCGCTGCAGATCTCGTGGAACTACAACTACGGCGCGCGGGGAGG 361
Qy 496 GACATCGGCTTCGACGCGGCTCGGGACCCCGCAGGGTGGCGCGGAGCGCGTGTGGCG 555
Db 362 GACATCGGCTTCGACGCGGCTCGCGACCCCAAGAGGTTGGCGGAGCGCGTGTATCGG 421
Qy 556 TTCAAGCGCGCGCTCTGTTCTGATGAACAACTGCAACCGTGTGATGCCAGCGGCTTC 615
Db 422 TTCAAGCGCGCGCTCTGTTCTGATGAACAACTGCAACCGTGTGATGCCAGCGGCTTC 481
Qy 616 GCGCGCACCATCAGGCGCATCAAGCGCGCTCGAGTGCAGCGGAAACACCCCGCGCAG 675
Db 482 GCGCGCACCATCAGGCGCATCAAGCGCGCTCGAGTGCAGCGGAAACACCCCGCGCAG 541
Qy 676 ATGAACCGCGCATCGGCTACTACAAGCAGTACTGCGCGCGAGCTCGGCTCGACCCAGGG 735
Db 542 ATGAACCGCGCGCTGCGCTACTACAGCAGTACTGCGCGCGAGCTCGGCTCGACCCAGGG 601
Qy 736 CCCAACTCACTTCT 751
Db 602 CCCAACTCACTTCT 617
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RESULT 9  
BM895383  
LOCUS 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
DEFINITION BM895383 625 bp mRNA linear EST 11-MAR-2002  
may8 cDNA, mRNA sequence.

ACCESSION BM895383  
VERSION BM895383.1 GI:19350851  
KEYWORDS EST.  
SOURCE Zea mays

## ORGANISM

Zea mays  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 625)  
AUTHORS Walbot,V.  
TITLE Zea mays

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

CONTACT Walbot V

DEPARTMENT OF Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952073 row: H column: 05.

Location/Qualifiers

1..625

/organism="Zea mays"

/mol\_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
/notes="vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

## ORIGIN

Query Match 70.8%; Score 533.2; DB 5; Length 625;  
Best Local Similarity 92.1%; Pred. No. 2e-103;  
Matches 573; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

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Qy 119 GCGGACAGTGGCGGCGGTGGTGGAACTGGGTAGCTGTCAACGGCTCTCTTCTTCA 178
Db 5 GCTGTGCGGAGGAGTGGCGGTGCGAACTGGGTAAAG-GGTCAGGACGCTTCTTCA 63
Qy 179 ACGCATCAAGAACCCAGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCG 238
Db 64 ACGCATCAAGAACCCAGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCG 123
Qy 239 CGTTCTGAGCGCGTCAAGGCGTACCAGGCTTTCGCCCATGGCGGCTCAAGGTGCA 298
Db 124 GCTTCTGAGCGCGTCAAGAACTACCGGGCTTTCGCCCATGGCGGAGGTGGAGG 183
Qy 299 GCAAGCGGAGATCGCGCTTCTTCGCGACGCGCACGAGACCGGGGATTTCTGTT 358
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Qy 359 ACATCAGCGAGATCAGCAAGAGCAACGCTTACTCGGACCGGACCAAGAGGAGTGG 418
Db 244 ACATCAGCGAGATCAGCAAGAGCAACGCTTACTCGGACGAGCAAGCAAGGCGGT 303
Qy 419 GCGCGCGGCGCAGAGTACTACGGCGCGCGCTGCGAGATCTCGTGGAACTACAACT 478
Db 304 GCGCGCGGCGCAGAGTACTACGGCGCGCGCTGCGAGATCTCGTGGAACTACAACT 363
Qy 479 ACGGCGCGGAGGAGGACATCGGCTTTCAGCGGCTTCGGGAGCCCGGAGGTGGCG 538
Db 364 ACGGCGCGGAGGAGGACATCGGCTTTCAGCGGCTTCGGGAGCCCAACAGGAGTGG 423
Qy 539 GGGACGCGGTGGCGCTTCAAGCGCGCGCTTCTGATGAAACAACTGACACCGTG 598
Db 424 AGGACGCGGTGATCGGCTTCAAGACGCGCTTCTGATGAAACAACTGACACCGTG 483
Qy 599 TGATGCGCAGGCGTTCGGCGCCACCATCAGGGGCATCAACGGCGCTCGAGTGCAG 658
Db 484 TGATGCGCAGGCGTTCGGCGCCACCATCAGGGGCATCAACGGCGCTCGAGTGCAG 543
Qy 659 GGAACAAACCCCGCCAGATGAACCGCGGATTCGGCTACTACAGCAGTACTGCGCG 718
Db 544 GGAACAAACCCCGCCAGATGAACCGCGGCTTCGGCTACTACAGCAGTACTGCGCG 603
Qy 719 TCGCGCTCGACCCAGGCGCCAA 740
Db 604 TCGCGCTCGACCCAGGCGCCAA 625
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RESULT 10  
CD995497  
LOCUS

CD995497 820 bp mRNA linear EST 16-JUL-2003

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DEFINITION QBB25f07.xg QBB Zea mays cDNA clone QBB25f07, mRNA sequence.
ACCESSION CD995497
VERSION CD995497.1 GI:32855816
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 820)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..820
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            /mol_type="mRNA"
            /cultivar="F2"
            /db_xref="taxon:4577"
            /clone="QBB25f07"
            /tissue_type="embryo"
            /clone_lib="QBB"
ORIGIN
    Query Match 69.9%; Score 526.6; DB 6; Length 820;
    Best Local Similarity 96.6%; Pred. No. 5e-102;
    Matches 538; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 195 GCGCGGAGCGGGTGCAGAGGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGT 254
Db 45 GCGCGTGCAGCGGTGCAGAGGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGT 104
Qy 255 CAAGCGGTACCCAGGCTTCGCCCATGCGGGTCAAGTGCAGGCGAGGCAAGCGAGATCGC 314
Db 105 CAAGCGGTACCCAGGCTTCGCCCATGCGGGTCAAGTGCAGGCGAGGCAAGCGAGATCGC 164
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Db 225 CAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGGGGCGAGAA 284
Qy 435 GTACTAGCGGCGCGCGCGCTGCGAGATCTCGTGAACTAACAATACGGGCCCGCGGGAG 494
Db 285 GTACTAGCGGCGCGCGCGCTGCGAGATCTCGTGAACTAACAATACGGGCCCGCGGGAG 344
Qy 495 GGACATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGC 554
Db 345 GGCATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGC 404
Qy 555 GTTCAAGCGCGCGCTCTGTTCTGGATGAACAAGTGCACCGTGTGATGCGCGAGGGCTT 614
Db 405 GTTCAAGCGCGCGCTCTGTTCTGGATGAACAAGTGCACCGTGTGATGCGCGAGGGTC 464
Qy 615 CGGCGCAACATCAGGGGCATCAACGGCGCGCTCGAGTGCAGCGGGAACAACCCCGCCCA 674
Db 465 CGGCGCAACATCAGGGGCATCAACGGCGCGCTCGAGTGCAGCGGGAACAACCCCGCCCA 524
Qy 675 GATGAACGCGGCTCGGCTACTCAAGCAGTACTTGGCCGAGTCTCGGCTCGACCCAGG 734
Db 525 GATGAACGCGGCTCGGCTACTCAAGCAGTACTTGGCCGAGTCTCGGCTCGACCCAGG 584
Qy 735 GCCCAACCTCACTTGTCT 751
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Db 585 GCCCAACCTCACTTGTCT 601
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CD994156 578 bp mRNA linear EST 16-JUL-2003
QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA sequence.
ACCESSION CD994156
VERSION CD994156.1 GI:32854475
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 578)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
    Location/Qualifiers
        1..578
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="F2"
            /db_xref="taxon:4577"
            /clone="QBB13f07"
            /tissue_type="embryo"
            /clone_lib="QBB"
ORIGIN
    Query Match 69.4%; Score 522.6; DB 6; Length 578;
    Best Local Similarity 96.6%; Pred. No. 3.6e-101;
    Matches 534; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 199 GGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGTCAAG 258
Db 1 GGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGTCAAG 60
Qy 259 GCGTACCCAGGCTTCGCCCATGCGGGTCAAGTGCAGGCGAGCGCGAGATCGCGCC 318
Db 61 GCGTACCCAGGCTTCGCCCATGCGGGTCAAGTGCAGGCGAGCGCGAGATCGCGCC 120
Qy 319 TTCTTCGCGACGCGCACGACGAGACCGGCATTTCTGTATCATCAGCAGATCAGCAAG 378
Db 121 TTCTTCGCGACGCGCACGACGAGACCGGCATTTCTGTATCATCAGCAGATCAGCAAG 180
Qy 379 AGCAACCGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCGGGGCGAGAGTAC 438
Db 181 AGCAACCGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGGGGCGAGAGTAC 240
Qy 439 TAGCGGCGCGCGCGCTGCGAGATCTCGTGAACTAACAATACGGGCCCGCGGGAGGAG 498
Db 241 TAGCGGCGCGCGCGCTGCGAGATCTCGTGAACTAACAATACGGGCCCGCGGGAGGAG 300
Qy 499 ATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGTGGC 558
Db 301 ATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGTGGC 360
Qy 559 AAGCGCGCGCTCTGTTCTGGATGAACAAGTGCACCGTGTGATGCGCGAGGGCTTCGGC 618
Db 361 AAGCGCGCGCTCTGTTCTGGATGAACAAGTGCACCGTGTGATGCGCGAGGGCTTCGGC 420
Qy 619 GCGCAACCTCAAGGCGCATCAAGCGGCGCGCTCGAGTGCAGCGGGAACAACCCCGCCAG 678
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Df 421 GCCACCACGGGCCATCAACGGGCCCTCGAGTGGCGGGGAACAACCCCGCCAGATG 480

Qy 679 AACGGCGCATCGGTACTATAAGCAGTACTGCGCCAGCTCGGGTGCAGCCAGGGCCC 738

Df 481 AACGGCGCGTGGGTACTATACAGGCGAGTACTGCGCCAGCTCGGGTGCAGCCCGGGCCC 540

Qy 739 AACCTCACTTGT 751

Df 541 AACCTCACTTGT 553

RESULT 12

CD994132

LOCUS

DEFINITION

QBB13604.xg QBB Zea mays cDNA clone QBB13604, mRNA sequence.

ACCESSION

CD994132

VERSION

CD994132.1 GI:32854451

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 575)

AUTHORS

Genoplante.

TITLE

Genoplante, a major partnership french program in plant genomics

JOURNAL

Unpublished (2003)

COMMENT

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1..575

/organism="Zea mays"

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/tissue\_type="embryo"

/clone\_lib="QBB"

ORIGIN

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Best Local Similarity 96.7%; Pred. No. 7.1e-101;

Matches 532; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 202 AGCGGTGCGAGGCAAGAACTTTACACCGGAGCGGTTCTGAGCGCGTCAAGGCG 261

Df 1 AGCGGTGCGAGGCAAGAACTTTACACCGGAGCGGTTCTGAGCGCGTCAAGGCG 60

Qy 262 TACCAGGCTTCGCCCATGGCGGCTCACAGTGCAGGCGAGCCGAGATCGCGCTTC 321

Df 61 TACCAGGCTTCGCCCATGGCGGCTCGAGGTGCGAGGTGAGGCGAGATCGCGCTTC 120

Qy 322 TTCGCGCAGCGCAGCAGACCGCGGCAATTTCTGTTACATCAGCGAGATCAGCAAGAGC 381

Df 121 TTCGCGCAGCGCAGCAGACCGCGGCAATTTCTGTTACATCAGCGAGATCAGCAAGAGC 180

Qy 382 AACGCTTACTCGACCCGACCAAGAGGAGTGGCGCGTGGCGCGCGGAGGAGTACTAC 441

Df 181 AACGCTTACTCGACCCGAGCAGAGGAGTGGCGCGTGGCGCGCGGAGGAGTACTAC 240

Qy 442 GGGCGCGCGCTCGAGATCTCTGGAATCTACAACTACCGGCGCGGAGGAGGAGTATC 501

Df 241 GGGCGCGCGCTCGAGATCTCTGGAATCTACAACTACCGGCGCGGAGGAGGAGTATC 300

Qy 502 GCGTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGAGGAGGAGTGGCGGTTCAAG 561

Df 301 GCGTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGAGGAGGAGTGGCGGTTCAAG 360

Qy 562 GCGGCGCTCTGGTTCTGATGAAACAAGTGCACCGTGTGATGCCGAGGGCTTCGGCGCC 621

Df 361 GCGGCGCTCTGGTTCTGATGAAACAAGTGCACCGTGTGATGCCGAGGGTTCGGCGCC 420

Qy 622 ACCATCAGGGCCATCAACGGCGCGTCTGAGTGCAGCGGAACAACCCCGCCAGATGAAC 681

Df 421 ACCACCGGGCCATCAACGGCGCGTCTGAGTGCAGCGGAACAACCCCGCCAGATGAAC 480

Qy 682 GCGGCATCGGCTACTACAAGCAGTACTGCGCGCAGCTCGGCGTGCAGCCAGGGCCCAAC 741

Df 481 GCGGCGTGGCTACTACAGGCACTACTGCGCGCAGCTCGGCGTGCAGCCCGGGCCCAAC 540

Qy 742 CTCACCTTGT 751

Df 541 CTCACCTTGT 550

RESULT 13

CD994454

LOCUS

DEFINITION

QBB15f08.xg QBB Zea mays cDNA clone QBB15f08, mRNA sequence.

ACCESSION

CD994454

VERSION

CD994454.1 GI:32854773

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 578)

AUTHORS

Genoplante.

TITLE

Genoplante, a major partnership french program in plant genomics

JOURNAL

Unpublished (2003)

COMMENT

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

Location/Qualifiers

1..578

/organism="Zea mays"

/mol\_type="mRNA"

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ORIGIN

Query Match 69.1%; Score 520.6; DB 6; Length 578;

Best Local Similarity 96.4%; Pred. No. 9.5e-101;

Matches 532; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 200 GAGCGGGTGGAGGGCAAGAACTTTACACCGGAGCGGTTCTGAGCGCGTCAAGG 259

Df 6 GAGCGGGTGGAGGGCAAGAACTTTACACCGGAGCGGTTCTGAGCGCGTCAAGG 65

Qy 260 GGTACCCAGGCTTCGCCCATGGCGGTTCAAGTGCAGGCGAGCGGAGATCGCGCT 319

Df 66 GGTACCCAGGCTTCGCCCATGGCGGTTCAAGTGCAGGCGAGCGGAGATCGCGCT 125

Qy 320 TCTTGGCGCAGCGCAGCAGAGCGGGATTTCTGTTACATCAGCGAGATCAGCAAGA 379

Df 126 TCTTGGCGCAGCGCAGCAGAGCGGGATTTCTGTTACATCAGCGAGATCAGCAAGA 185

Qy 380 GCAACGCTTACTCGACCCCGACCAAGAGGAGTGGCGGCGTGGCGGCGAGGAGTACT 439

Df 186 GCAACGCTTACTCGACCCCGACCAAGAGGAGTGGCGGCGTGGCGGCGAGGAGTACT 245

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DB 246 ACGGGCGCGCCGCTGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGAGGACGA 305
QY 500 TCGGCTTCGACGGGCTCGGGGACCCCGCAGGGTGGCGGGGACGCCGTTGTCGCGTTCA 559
DB 306 TCGGCTTCGACGGGCTCGGGGACCCCGCAGGGTGGCGGGGACGCCGTTGTCGCGTTCA 365
QY 560 AGGGCGGCTCTGGTTCTGATGTAACAACTGCAACCGTGTGATGTCGCGAGGGCTTCGGCG 619
DB 366 AGGGCGGCTCTGGTTCTGATGTAACAACTGCAACCGTGTGATGTCGCGAGGGTTCGGCG 425
QY 620 CCACATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGA 679
DB 426 CCACATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGA 485
QY 680 ACGCGCATCGGCTACTACAAGCAGTACTCGCCAGCTCGGGTTCGACCCAGGGCCCA 739
DB 486 ACGCGCATCGGCTACTACAAGCAGTACTCGCCAGCTCGGGTTCGACCCAGGGCCCA 545
QY 740 ACCTCACTTGT 751
DB 546 ACCTCACTTGT 557

RESULT 14
CD994869
LOCUS CD994869 741 bp mRNA linear EST 16-JUL-2003
DEFINITION QB18d07.xg QBB Zea mays cDNA clone QB18d07, mRNA sequence.
ACCESSION CD994869
VERSION CD994869.1 GI:32855188
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 741)
AUTHORS Genoplatte.
TITLE Genoplatte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).
FEATURES
Location/Qualifiers
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Best Local Similarity 96.5%; Pred. No. 1.6e-100;
Matches 531; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 202 AGCGGTTCGAGGGCAGAACTTCTACACCGGAGCGGTTCTCTAGCGCGCTCAAGCG 261
DB 1 AGCGGTTCGAGGGCAGAACTTCTACACCGGAGCGGTTCTCTAGCGCGCTCAAGCG 60
QY 262 TACCCAGGCTTCGCCCATGGCGGGTTCAGGTGCAGGGCAAGCGAGATCGCGCTTC 321
DB 61 TACCCAGGCTTCGCCCATGGCGGGTTCAGGTGCAGGGCAAGCGAGATCGCGCTTC 120
QY 322 TTCGCGACGCCACGACGAGACCGGGCATTTCTGTTATCATCGAGATCAGCAAGAGC 381
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DB 121 TTCGCGACGCCACGACGAGACCGGGCATTTCTGCTATCATCAGCGAGATCAACAAGAGC 180
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DB 181 AACGCTTACTGCAACCCGACCAAGAGGAGTGGCGCGCGCGGAGAGTACTAC 240
QY 442 GGGCGGGCGCGCTGCAGATCTCTGTGAACTACAACACTACGGGCGCGGGAGGAGCATC 501
DB 241 GGGCGGGCGCGCTGCAGATCTCTGTGAACTACAACACTACGGGCGCGGGAGGAGCATC 300
QY 502 GGCTTCGACGGGCTCGGGGACCCCGCAGGGTGGCGGGGACGCCGTTGTTCAAG 561
DB 301 GGCTTCGACGGGCTCGGGGACCCCGCAGGGTGGCGGGGACGCCGTTGTTCAAG 360
QY 562 GCGGCGCTCTGGTTCTGGATGAACACGTGCAACCGTGTGATGTCGAGGGCTTCGGCGCC 621
DB 361 GCGGCGCTCTGGTTCTGGATGAACACGTGCAACCGTGTGATGTCGAGGGCTTCGGCGCC 420
QY 622 ACCATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGAAACAAACCCCGCAGATGAAC 681
DB 421 ACCATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGAAACAAACCCCGCAGATGAAC 480
QY 682 GCGCGCATCGGCTACTACAAGCAGTACTCGCGCGAGTTCGCGCGTTCGACCCAGGGCCCAAC 741
DB 481 GCGCGCATCGGCTACTACAAGCAGTACTCGCGCGAGTTCGCGCGTTCGACCCAGGGCCCAAC 540
QY 742 CTCACCTTGT 751
DB 541 CTCACCTTGT 550

RESULT 15
CD994885
LOCUS CD994885 753 bp mRNA linear EST 16-JUL-2003
DEFINITION QB18e05.xg QBB Zea mays cDNA clone QB18e05, mRNA sequence.
ACCESSION CD994885
VERSION CD994885.1 GI:32855204
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 753)
AUTHORS Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT 1 (bases 1 to 753)
Genoplatte.
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 96.5%; Pred. No. 1.6e-100;
Matches 531; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 202 AGCGGTTCGAGGGCAGAACTTCTACACCGGAGCGGTTCTCTAGCGCGCTCAAGCG 261
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Db      1 AGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGGTTCTTGAGCGCGTCAAGCG 60
Qy      262 TACCCAGGCTTCGCCCATGCGGCTCAAGGTGAGGGCAAGCGCGAGATGCGCGCTTC 321
Db      61 TACCCAGGCTTCGCCCATGCGGCTCGAGGTGAGGGCAAGCGCGAGATGCGCGCTTC 120
Qy      322 TTGCGGCAAGCGGCAAGCGGCGGCTTCGTTACATCAGCGGAGATCAGCAAGGC 381
Db      121 TTGCGGCAAGCGGCAAGCGGCGGCTTCGTTACATCAGCGGAGATCAGCAAGGC 180
Qy      382 AACGCTACTGCGACCGGACCAAGAGGAGTGGCGCTGCGCGCGGGGAGAGTACTAC 441
Db      181 AACGCTACTGCGACCGGAGCAAGAGGAGTGGCGCTGCGCGCGGGGAGAGTACTAC 240
Qy      442 GGGCGGCGCGCTGCGAGATCTGTGGAATTAACAATAAGGCGCGGGAGGGACATC 501
Db      241 GGGCGGCGCGCTGCGAGATCTGTGGAATTAACAATAAGGCGCGGGAGGGCCATC 300
Qy      502 GGCTTCGACGGGCTCGGGGACCGCGGAGGTGGCGGAGCGCGTGTGGCGTTCAAG 561
Db      301 GGCTTCGACGGGCTCGGGGACCGCGGAGGTGGCGGAGCGCGTGTGGCGTTCAAG 360
Qy      562 GCGGCGCTCTGGTTCTGATGAACAAAGTGCACCGTGTGATGCGCAGGGCTTCGGCGCC 621
Db      361 GCGGCGCTCTGGTTCTGATGAACAGCGTGCACGGGTTGTCGCGAGGGTTTCGGCGCC 420
Qy      622 ACCATCAGGCGCATCAACGGCGCGCTCGAGTGCACGGGAAACAACCGCGCCAGATGAAC 681
Db      421 ACCACAGGCGCATCAACGGCGCGCTCGAGTGCAGGGGAAACAACCGCGCCAGATGAAC 480
Qy      682 GCGGCGATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTTCGACCCAGGGCCCCAAC 741
Db      481 GCGGCGATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTTCGACCCAGGGCCCCAAC 540
Qy      742 CTCACCTGCT 751
Db      541 CTCACCTGCT 550
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-692-367-70

Perfect score: 1408

Sequence: 1 SMQNCQPNVCCSKFYCG.....GYKQYRQLGVDPGNLTC 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1377	97.8	250	8	ADS92668 Chitinase
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10	1351	96.0	250	8	ADS92666 Chitinase
11	1351	96.0	281	3	AAB18894 A maize C
12	1350	95.9	250	8	ADS92670 Chitinase
13	1349	95.8	256	8	ADS92690 Chitinase
14	1348	95.7	250	8	ADS92638 Chitinase
15	1348	95.7	256	8	ADS92664 Chitinase
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17	1342	95.3	256	8	ADS92678 Chitinase
18	1341	95.2	250	8	ADS92652 Chitinase
19	1336.5	94.9	249	8	ADS92696 Chitinase
20	1335.5	94.9	257	8	ADS92682 Chitinase
21	1335	94.8	256	8	ADS92700 Chitinase
22	1328.5	94.4	257	8	ADS92646 Chitinase
23	1328.5	94.4	257	8	ADS92650 Chitinase
24	1325.5	94.1	259	8	ADS92656 Chitinase
25	1324.5	94.1	259	8	ADS92692 Chitinase

26	1323	94.0	250	8	ADS92674	AdS92674 Chitinase
27	1322.5	93.9	257	8	ADS92662	AdS92662 Chitinase
28	1321.5	93.9	257	8	ADS92680	AdS92680 Chitinase
29	1319	93.7	250	8	ADS92648	AdS92648 Chitinase
30	1318.5	93.6	257	8	ADS92628	AdS92628 Chitinase
31	1314.5	93.4	269	8	ADS92634	AdS92634 Maize chi
32	1312	93.2	250	8	ADS92644	AdS92644 Chitinase
33	1309.5	93.0	257	8	ADS92654	AdS92654 Chitinase
34	1303	92.4	270	8	ADS92636	AdS92636 Maize chi
35	1300.5	92.4	257	8	ADS92640	AdS92640 Chitinase
36	1285	91.3	256	8	ADS92658	AdS92658 Chitinase
37	1283.5	91.2	257	8	ADS92624	AdS92624 Chitinase
38	1271.5	90.3	255	8	ADS92617	AdS92617 Maize chi
39	1265.5	89.9	280	8	ADS92635	AdS92635 Maize chi
40	1258.5	89.4	280	8	ADS92633	AdS92633 Maize chi
41	1255	89.1	254	8	ADS92642	AdS92642 Chitinase
42	1253	89.0	258	8	ADS92632	AdS92632 Chitinase
43	1245	88.4	258	8	ADS92620	AdS92620 Chitinase
44	1244.5	88.4	251	8	ADS92630	AdS92630 Chitinase
45	1242.5	88.2	251	8	ADS92622	AdS92622 Chitinase

## ALIGNMENTS

## RESULT 1

ADS92686

ID ADS92686 standard; protein; 250 AA.

XX ADS92686;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polypeptide #32.

XX Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX N-PSDB; ADS92685.

XX New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

XX Claim 3; SEQ ID NO 70; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprising introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.

XX Sequence 250 AA;

Query Match	100.0%;	Score 1408;	DB 8;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.6e-115;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SMQCGQPNVCCSKFCYCGTTDEYCGDGCQSGP	CRSGGGSSGGGGANVASVVTG	SFFN 60
Db	1	SMQCGQPNVCCSKFCYCGTTDEYCGDGCQSGP	CRSGGGSSGGGGANVASVVTG	SFFN 60
Qy	61	G1KNQAGSGEGKNFYTRSAFLSAVKAYPGFAHGS	OVQGRKRETAAPFAHATHETGHFCY	120
Db	61	G1KNQAGSGEGKNFYTRSAFLSAVKAYPGFAHGS	OVQGRKRETAAPFAHATHETGHFCY	120
Qy	121	ISEISKNAYCDPTKRWPCAAGOKYGRGP	QLISWNNYGPAGRDIGFDGLGDPGRVAR	180
Db	121	ISEISKNAYCDPTKRWPCAAGOKYGRGP	QLISWNNYGPAGRDIGFDGLGDPGRVAR	180
Qy	181	DAVVAFKAALWFMMNNVHRVMPQFGATIRAI	NGALECDGNNPAQMNARIGYTKQYCRQL	240
Db	181	DAVVAFKAALWFMMNNVHRVMPQFGATIRAI	NGALECDGNNPAQMNARIGYTKQYCRQL	240
Qy	241	GVDPGPNLTC	250	
Db	241	GVDPGPNLTC	250	

RESULT 2	
AD92668	
ID	ADS92668 standard; protein; 250 AA.
XX	
AC	ADS92668;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Chitinase variant polypeptide #23.
XX	
KW	Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX	
OS	Synthetic.
XX	
PN	WO2004037194-A2.
XX	
PD	06-MAY-2004.
XX	
PF	22-OCT-2003; 2003WO-US033588.
XX	
PR	22-OCT-2002; 2002US-0420666P.
PR	06-NOV-2002; 2002US-00290086.
PR	14-MAR-2003; 2003US-00389432.
XX	
PA	(VERD-) VERDIA INC.
PA	(PION-) PIONEER HI-BRED INT INC.
PI	Muller ML, True T, Simmons CR, Yalpani N;
XX	
DR	WPI; 2004-365417/34.
DR	N-PSDB; ADS92667.
XX	
PT	New chitinase polynucleotides and polypeptides, useful in producing
PT	plants with enhanced resistance against a fungus or a nematode.
XX	
PS	Claim 3; SEQ ID NO 52; 197pp; English.
XX	
CC	The invention relates to chitinase polypeptides and the polynucleotides
CC	encoding them. A method of enhancing plant resistance to a fungus or
CC	nematode comprises introducing into a plant a recombinant expression
CC	cassette comprising a promoter operably linked to a chitinase
CC	polynucleotide of the invention. The plant is maize or soybean. The
CC	fungus is from the genus Fusarium. The nematode is from the genus
CC	Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC	plant resistance to a fungus or nematode. This sequence represents a
CC	chitinase variant polypeptide of the invention.
XX	

SQ Sequence 250 AA;  
 Query Match 97.8%; Score 1377; DB 8; Length 250;  
 Best Local Similarity 97.2%; Pred. No. 8.6e-113;  
 Matches 243; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 1 SMQCGQPNVCSKFGYCGTTDEYCGDGCQGPCRSGGGSGGGGGANVASVVTGSGFN 60  
 Db 1 SMQCGQPNVCSKFGYCGTTDEYCGDGCQGPCRSGGGSGGGGGANVASVVTGSGFN 60  
  
 Qy 61 GIKNOAGSGCEGKNFYTRSAPLSAVKAYPGFAHGSSQVQCKREIAAFFAHATHETGHFCY 120  
 Db 61 GIKSQAGSGCEGKNFYTRSAPLSAVKAYPGFAHGSSQVQCKREIAAFFAHATHETGHFCY 120  
  
 Qy 121 ISEISKSNAYCDPTKROWPCAAGKQKYYGRGFLQISWNYNYPGAGRDIGFPGGLGDPGRVAR 180  
 Db 121 ISEINKSNAYCDPTKROWPCAAGKQKYYGRGFLQISWNYNYPGAGRAIGFPGGLGDPGRVAR 180  
  
 Qy 181 DAVVAFKAALWFWMNNVHRVYMPQGFATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240  
 Db 181 DAVVAFKAALWFWMNNVHRVYMPQGFATIRAINGALECGNNPAQMNARVGYTRQYCRQL 240  
  
 Qy 241 GVDPGPNLTC 250  
 Db 241 GVDPGPNLTC 250  
  
 RESULT 3  
 ADS92698  
 ID ADS92698 standard; protein; 250 AA.  
 XX  
 AC ADS92698;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #38.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
 XX  
 OS Synthetic.  
 OS  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 XX 22-OCT-2003; 2003WO-US033588.  
 PF  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR  
 PR 06-NOV-2002; 2002US-00290086.  
 PR  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 PA  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 DR  
 DR N-PSDB; ADS92697.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 ET  
 XX Claim 3; SEQ ID NO 82; 197pp; English.  
 PS  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus Fusarium. The nematode is from the genus  
 CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

```
XX  Sequence 250 AA;
SQ
Query Match      97.4%; Score 1372; DB 8; Length 250;
Best Local Similarity 97.2%; Pred. No. 2.4e-112;
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDBYCGDGCOSGCRSGGGSGGGGANVASVVTGFFN 60
Db 1 SMQNGCOPNVCCSKFGYCGTTDBYCGDGCOSGCRSGGGSGGGGANVASVVTDAFFN 60
Qy 61 GIKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETGFCY 120
Db 61 GIKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETGFCY 120
Qy 121 ISEISKSNAAYCDPTKQWPCAAGQKYGRGRLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEINKSNAYCDPTKQWPCAAGQKYGRGRLQISWNNYGPAGRAIGFDGLGDPGRVAR 180
Qy 181 DAVAFKAAALWFMNNVHRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
Db 181 DAVAFKAAALWFMNNVHRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
Qy 241 GVDPGNLTC 250
Db 241 GVDEGNLTC 250

RESULT 4
ADS92684
ID ADS92684 standard; protein; 254 AA.
XX
AC ADS92684;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polypeptide #31.
XX
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR N-PSDB; ADS92683.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 3; SEQ ID NO 68; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polypeptide of the invention.
XX
SQ Sequence 254 AA;
Query Match      97.0%; Score 1366; DB 8; Length 254;
Best Local Similarity 95.7%; Pred. No. 8.1e-112;
Matches 243; Conservative 3; Mismatches 4; Indels 4; Gaps 1;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDBYCGDGCOSGCRSGGGSGGGGANVASVVTG 56
Db 1 SMQNGCOPNVCCSKFGYCGTTDBYCGDGCOSGCRSGGGSGGGGANVASVVTG 60
Qy 57 SPFNGIKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETG 116
Db 61 SPFNGIKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETG 120
Qy 117 HFCYISISKSNAAYCDPTKQWPCAAGQKYGRGRLQISWNNYGPAGRDIGFDGLGDPG 176
Db 121 HFCYISEINKSNAYCDPTKQWPCAAGQKYGRGRLQISWNNYGPAGRAIGFDGLGDPN 180
Qy 177 RVARDAVAFKAAALWFMNNVHRVMPQFGATIRAINGALECDGNPQMNARIGYYKQY 236
Db 181 RVAQDAVAFKAAALWFMNNVHRVMPQFGATIRAINGALECDGNPQMNARVGYKQY 240
Qy 237 CRQLGVDPGNLTC 250
Db 241 CRQLGVDPGNLTC 254

RESULT 5
ADS92694
ID ADS92694 standard; protein; 250 AA.
XX
AC ADS92694;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polypeptide #36.
XX
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR N-PSDB; ADS92693.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 3; SEQ ID NO 78; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
```

CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 250 AA;  
Query Match 96.8%; Score 1363; DB 8; Length 250;  
Best Local Similarity 96.0%; Pred. No. 1.5e-111;  
Matches 240; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGGANNVAVVTGSFFN 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGGANNVAVVTGSFFN 60  
QY 61 GIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCY 120  
DB 61 GIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCY 120  
QY 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180  
DB 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180  
QY 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
DB 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
QY 241 GVDPGPNLTC 250  
DB 241 GVDPGPNLTC 250

## RESULT 6

ADSS2672  
ID ADS92672 standard; protein; 250 AA.  
XX AC ADS92672;  
XX AC  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #25.  
XX  
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
FR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR N-PSDB; ADS92671.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 56; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus

CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 250 AA;

Query Match 96.6%; Score 1360; DB 8; Length 250;  
Best Local Similarity 96.0%; Pred. No. 2.7e-111;  
Matches 240; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGGANNVAVVTGSFFN 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGGANNVAVVTGSFFN 60  
QY 61 GIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCY 120  
DB 61 GIKNOAGSGCEGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCY 120  
QY 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180  
DB 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180  
QY 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
DB 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
QY 241 GVDPGPNLTC 250  
DB 241 GVDPGPNLTC 250

## RESULT 7

ADSS2660  
ID ADS92660 standard; protein; 250 AA.  
XX AC ADS92660;  
XX AC  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #19.  
XX  
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
FR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR N-PSDB; ADS92659.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 44; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus



CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 250 AA;

Query Match 96.4%; Score 1358; DB 8; Length 250;  
 Best Local Similarity 95.6%; Pred. No. 4e-111;  
 Matches 239; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGANVASVVTGSFEN 60  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGANVANVTDFFN 60

QY 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETGHFCY 120  
 DB 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFPAHATHETGHFCY 120

QY 121 ISEISKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRDIGFDGLGDPGRVAR 180  
 DB 121 ISEISKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRAIGFDGLGDPGRVAR 180

QY 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGYTKQYCKQL 240  
 DB 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGYTKQYCKQL 240

QY 241 GVDGPNLTC 250  
 DB 241 GVDGPNLTC 250

# RESULT 8

ADS92688  
 ID ADS92688 standard; protein; 257 AA.

XX AC ADS92688;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #33.

XX KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR N-ESDB; ADS92687.

XX FT New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 3; SEQ ID NO 72; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides

XX CC encoding them. A method of enhancing plant resistance to a fungus or

XX CC nematode comprises introducing into a plant a recombinant expression

CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 257 AA;

Query Match 96.4%; Score 1357.5; DB 8; Length 257;  
 Best Local Similarity 94.2%; Pred. No. 4.6e-111;  
 Matches 242; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGG-----CGANVASV 53  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGGGSGGANVANV 60

QY 54 VTGSPFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATH 113  
 DB 61 VTDAFNGIKSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATH 120

QY 114 ETGHFCYIISISKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRDIGFDGLG 173  
 DB 121 ETGHFCYIISISKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRAIGFDGLG 180

QY 174 DPCRVARDAVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGY 233  
 DB 181 DPCRVARDAVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGY 240

QY 234 KOYCRQLGVDGPNLTC 250  
 DB 241 KOYCRQLGVDGPNLTC 257

# RESULT 9

ADS92618

ID ADS92618 standard; protein; 248 AA.

XX AC ADS92618;

XX DT 02-DEC-2004 (first entry)

XX DE Maize chitinase B polypeptide #1.

XX KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*;  
 XX maize; chitinase B; plant.

XX OS Zea mays.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX PT New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Disclosure; SEQ ID NO 2; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides

XX CC encoding them. A method of enhancing plant resistance to a fungus or

XX CC nematode comprises introducing into a plant a recombinant expression

CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC maize chitinase B polypeptide of the invention.  
 XX  
 SQ Sequence 248 AA;

Query Match 96.0%; Score 1351; DB 8; Length 248;  
 Best Local Similarity 96.0%; Pred. No. 1.6e-110;  
 Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 QNCCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFNGI 62  
 DB 1 QNCCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFNGI 60  
 QY 63 KNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAFAHATHETHGFCYIS 122  
 DB 61 KSOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAFAHATHETHGFCYIS 120  
 QY 123 EISKSNAICDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRDIGFDGLDGPGRVARD 182  
 DB 121 EINKSNAYCDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRAIGFDGLDGPGRVARD 180  
 QY 183 VVAFKAALWFMMNNVHVRVMPQGFATIRAINGALECCDGNPQNMNARIQYKQYCRQLGV 242  
 DB 181 VVAFKAALWFMMNSVHGVVQGFATIRAINGALECCGNNPQNMNARVGYRYQYCRQLGV 240  
 QY 243 DPGPNLTC 250  
 DB 241 DPGPNLTC 248

RESULT 10  
 ADS92666  
 ID ADS92666 standard; protein; 250 AA.  
 AC  
 AC ADS92666;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #22.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 FA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 FI  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92665.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 FT plants with enhanced resistance against a fungus or a nematode.  
 PT  
 XX  
 XX Claim 3; SEQ ID NO 50; 197pp; English.  
 PS  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 250 AA;

Query Match 96.0%; Score 1351; DB 8; Length 250;  
 Best Local Similarity 94.8%; Pred. No. 1.7e-110;  
 Matches 237; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFN 60  
 DB 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFN 60  
 QY 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKREIAAFAHATHETHGFCY 120  
 DB 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGTEVEGKREIAAFAHATHETHGFCY 120  
 QY 121 ISEISKSNAICDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRDIGFDGLDGPGRVAR 180  
 DB 121 ISEISKSNAICDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRAIGFDGLDGPGRVAR 180  
 QY 181 DAVVAFKAALWFMMNNVHVRVMPQGFATIRAINGALECCDGNPQNMNARIQYKQYCRQL 240  
 DB 181 DAVVAFKAALWFMMNSVHGVVQGFATIRAINGALECCGNNPQNMNARVGYRYQYCRQL 240  
 QY 241 GVDPGPNLTC 250  
 DB 241 GVDPGPNLTC 250

RESULT 11  
 AABI8894  
 ID AABI8894 standard; protein; 281 AA.  
 AC  
 AC AABI8894;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE A maize chitinase polypeptide designated ZmCh2.  
 XX  
 KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;  
 KW pathogen control; disease resistance; molecular marker.  
 XX  
 OS Zea mays.  
 XX  
 FN WO200056908-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 09-MAR-2000; 2000WO-US006121.  
 XX  
 PR 24-MAR-1999; 99US-0125915P.  
 XX  
 XX (PION-) PIONEER HI-BRED INT INC.  
 FA  
 XX Simmons CR, Yalpani N;  
 FI  
 XX WPI; 2000-628269/60.  
 DR N-PSDB; AAA96222.  
 XX  
 XX New maize chitinase genes encoding seven chitinases of glucosyl hydrolase  
 FT family 19 are useful for enhancing disease resistance in crop plants by  
 PT modulating its expression in plants.  
 XX  
 XX Claim 11; Page 65-66; 96pp; English.  
 PS  
 XX The present sequence represents a maize chitinase polypeptide. The  
 CC specification describes glucosyl hydrolase family 19 chitinases

CC (AAB18994, AAB18996, AAB18999, and AAB18902-05), and glucosyl hydrolase  
 CC family 18 chitinases (AAB18995, AAB18997-98 and AAB18900-01). The level of  
 CC chitinase in plants can be modulated to enhance disease resistance in  
 CC crop plants and for control of pathogens. The chitinase polynucleotides  
 CC are also useful as molecular markers for genotype in a plant, and for  
 CC sequence shuffling  
 XX  
 SQ Sequence 281 AA;

Query Match 96.0%; Score 1351; DB 3; Length 281;  
 Best Local Similarity 96.0%; Pred. No. 1.9e-110;  
 Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFNGI 62  
 Db 34 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFNGI 93  
 Qy 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETGHFCYIS 122  
 Db 94 KSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETGHFCYIS 153  
 Qy 123 EISKSNAYCDPTKRWPCAAQKYYGRGLQISWNYNYGPAGRDIGFDGLGDPGRVARDA 182  
 Db 154 EINKSNAYCDPTKRWPCAAQKYYGRGLQISWNYNYGPAGRAIGFDGLGDPGRVARDA 213  
 Qy 183 VVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQNNARIGYYKQYCRQLGV 242  
 Db 214 VVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQNNARIGYYKQYCRQLGV 273  
 Qy 243 DPGPNLTC 250  
 Db 274 DPGPNLTC 281

RESULT 12  
 ADS92670  
 ID ADS92670 standard; protein; 250 AA.  
 XX  
 AC ADS92670;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #24.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92669.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 54; 197pp; English.  
 XX  
 CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus Fusarium. The nematode is from the genus  
 CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 250 AA;

Query Match 95.9%; Score 1350; DB 8; Length 250;  
 Best Local Similarity 94.4%; Pred. No. 2e-110;  
 Matches 236; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFN 60  
 Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFN 60  
 Qy 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETGHFCY 120  
 Db 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETGHFCY 120  
 Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180  
 Db 121 ISEINKSNAYCDPTKRWPCAAQKYYGRGLQISWNYNYGPAGRDIGFDGLADPNRVAQ 180  
 Qy 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQNNARIGYYKQYCRQL 240  
 Db 181 DAVIAFKSALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQNNARVGYRQYCRQL 240  
 Qy 241 GVDPGPNLTC 250  
 Db 241 GVDPGPNLTC 250

RESULT 13  
 ADS92690  
 ID ADS92690 standard; protein; 256 AA.  
 XX  
 AC ADS92690;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #34.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92689.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 74; 197pp; English.  
 XX  
 CC The invention relates to chitinase polypeptides and the polynucleotides

CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 256 AA;  
Query Match 95.8%; Score 1349; DB 8; Length 256;  
Best Local Similarity 93.8%; Pred. No. 2.6e-110;  
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;  
QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGG-----GGANVASV 54  
DB 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGSGGANVASV 60  
QY 55 TGSFFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHE 114  
DB 61 TDSFFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHE 120  
QY 115 TGHFICYISEISKSNAAYCDPTKRWPCAAGQKYYGRGLQISWNNYNGPAGRDIGFDGLGD 174  
DB 121 TGHFICYINEINKSNAYCDPTKRWPCAAGQRYGRGLQISWNNYNGPAGRAIGFDGLGD 180  
QY 175 PGRVARDAVAFKAALFWNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYK 234  
DB 181 PGRVARDAVAFKAALFWNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYK 240  
QY 235 QYCRQLGVDPGNLTC 250  
DB 241 QYCRQLGVDPGNLTC 256

RESULT 14  
ADS92638  
ID ADS92638 standard; protein; 250 AA.  
XX  
AC ADS92638;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #8.  
XX  
KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR  
DR N-PSDB; ADS92637.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 22; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 250 AA;  
Query Match 95.7%; Score 1348; DB 8; Length 250;  
Best Local Similarity 95.2%; Pred. No. 3e-110;  
Matches 238; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGSGGANVASVVTGSFFN 60  
DB 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGSGGANVASVVTGSFFN 60  
QY 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHEGHFCY 120  
DB 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHEGHFCY 120  
QY 121 ISBISKSNAAYCDPTKRWPCAAGQKYYGRGLQISWNNYNGPAGRDIGFDGLGDGPRVAR 180  
DB 121 ISBISKSNAAYCDPTKRWPCAAGQKYYGRGLQISWNNYNGPAGRAIGFDGLGDGPRVAR 180  
QY 181 DAVVAFKAALFWNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
DB 181 DAVVAFKAALFWNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
QY 241 GVDPGPNLTC 250  
DB 241 RVDPGPNLTC 250

RESULT 15  
ADS92664  
ID ADS92664 standard; protein; 256 AA.  
XX  
AC ADS92664;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #21.  
XX  
KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR  
DR N-PSDB; ADS92663.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 48; 197pp; English.  
XX

XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 256 AA;  
  
Query Match 95.7%; Score 1348; DB 8; Length 256;  
Best Local Similarity 93.8%; Pred. No. 3.1e-110;  
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;  
  
Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSGGSGG-----GGANVASV 54  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSGGSGGSGGSGGSGG 60  
  
Qy 55 TGSFNGIKNQAGSGCGKFNFTSAFLSAVKAYPGFAHGSQVQKREIAAFPFAHATHE 114  
Db 61 TGSFNGIKNQAGSGCGKFNFTSAFLSAVKAYPGFAHGSQVQKREIAAFPFAHVTHE 120  
  
Qy 115 TGHEFCYISEISKSNAYCDPTKRWPCAAGQKYGRGPIQISWNYNYPAGRDIGFDGLGD 174  
Db 121 TGHPRIYISEVKNKNAYCDPTKRWPCAAGQKYGRGPIQISWNYNYPAGRAIGFDGLGD 180  
  
Qy 175 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNPNPQMNARIGYK 234  
Db 181 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALECGNPNPQMNARVGYR 240  
  
Qy 235 QYCRQLGVDPGPNLTC 250  
Db 241 QYCRQLGVDPGPNLTC 256

Search completed: May 24, 2005, 12:50:20  
Job time : 114.905 secs

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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:41:36 ; Search time 30.572 Seconds  
(without alignments)  
610.437 Million cell updates/sec

Title: US-10-692-367-70

Perfect score: 1408

Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYKQYCRQLGVDPGPNLTC 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgm2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	96.0	281	4	US-09-522-714-2
2	861	61.2	271	4	US-09-522-714-22
3	685.5	48.7	183	4	US-09-522-714-30
4	627.5	44.6	328	3	US-07-791-931-5
5	621.5	44.1	310	1	US-07-704-288C-6
6	621.5	44.1	310	1	US-08-379-259-6
7	621.5	44.1	330	1	US-07-704-288C-8
8	621.5	44.1	330	1	US-08-379-259-8
9	621	44.1	310	3	US-07-791-931-6
10	620	44.0	324	1	US-08-047-413-11
11	620	44.0	324	3	US-08-229-050-11
12	620	44.0	324	3	US-08-801-563-11
13	620	44.0	329	2	US-08-475-427-13
14	620	44.0	329	2	US-07-842-165-13
15	602.5	42.8	314	1	US-07-704-288C-7
16	602.5	42.8	314	1	US-08-379-259-7
17	592	42.0	336	1	US-07-704-288C-3
18	592	42.0	336	1	US-08-093-372-2
19	592	42.0	336	1	US-08-379-259-3
20	588	41.8	319	4	US-09-534-229C-3
21	581	41.3	302	2	US-08-475-427-6
22	581	41.3	302	2	US-07-842-165-6
23	563	40.6	328	3	US-07-791-931-7
24	557.5	39.6	318	1	US-07-704-288C-9
25	557.5	39.6	318	1	US-08-379-259-9
26	552.5	39.2	323	4	US-09-534-229C-2
27	535.5	38.0	328	4	US-09-125-891-2

28	535.5	38.0	328	4	US-09-125-891-4	Sequence 4, Appli
29	504.5	35.8	254	2	US-08-475-427-1	Sequence 1, Appli
30	504.5	35.8	254	2	US-07-842-165-1	Sequence 1, Appli
31	504.5	35.8	254	3	US-08-448-398-3	Sequence 3, Appli
32	498	35.4	316	3	US-07-791-931-8	Sequence 8, Appli
33	490	34.8	284	4	US-09-522-714-24	Sequence 24, Appli
34	477	33.9	266	1	US-08-812-025-10	Sequence 10, Appli
35	477	33.9	266	1	US-07-791-931-10	Sequence 10, Appli
36	477	33.9	266	3	US-09-138-873A-10	Sequence 10, Appli
37	462	32.8	405	4	US-09-902-540-11954	Sequence 11954, A
38	456.5	32.4	271	4	US-09-266-965-141	Sequence 141, App
39	392	27.8	372	3	US-07-791-931-4	Sequence 4, Appli
40	384.5	27.3	252	4	US-09-522-714-20	Sequence 20, Appli
41	378.5	26.9	256	4	US-09-534-229C-1	Sequence 1, Appli
42	377	26.8	259	4	US-09-522-714-18	Sequence 18, Appli
43	371.5	26.4	253	3	US-07-791-931-9	Sequence 9, Appli
44	367.5	26.1	250	1	US-08-162-475A-4	Sequence 4, Appli
45	366.5	26.0	253	1	US-08-162-475A-5	Sequence 5, Appli

#### ALIGNMENTS

RESULT 1  
US-09-522-714-2  
; Sequence 2, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522.714  
; EARLIER FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-522-714-2

Query Match	96.0%	Score 1351;	DB 4;	Length 281;
Best Local Similarity	96.0%	Pred. No. 4.6e-113;		
Matches 238;	Conservative	6;	Mismatches 4;	Indels 0; Gaps 0;
Qy	3	QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSPFNGI	62	
Db	34	QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSPFNGI	93	
Qy	63	KNQAGSCCKNFYTRSAPLSAVKAYPGFAGGSOVQKREIAAFPAHATHETGHFCVIS	122	
Db	94	KSQAGSCCKNFYTRSAPLSAVKAYPGFAGGSOVQKREIAAFPAHATHETGHFCVIS	153	
Qy	123	EISKSNAYCDPTKQWPCAAQKYYGRGLQISWNNYNYGPAGRDIGFDGLDGPGRVADA	182	
Db	154	EINKSNAYCDPTKQWPCAAQKYYGRGLQISWNNYNYGPAGRDIGFDGLDGPGRVADA	213	
Qy	183	VVAFKAALWFMNWNVRVMPQGFATRAINGALECGNNPAQNNARIQYKQYCRQLGV	242	
Db	214	VVAFKAALWFMNWNVRVMPQGFATRAINGALECGNNPAQNNARIQYKQYCRQLGV	273	
Qy	243	DPGNLTC 250		
Db	274	DPGNLTC 281		

RESULT 2  
US-09-522-714-22  
; Sequence 22, Application US/09522714









Db 64 IISSEMFQMLKHNDRNACQKGFYSYNAFINAAARSPFGTSGDTTARKKEIAAFPAQT 123  
Qy 112 THET-----GHFCYISEISKSNAICDPTKRWPCAAQKQYGRGPLOISWNY 158  
Db 124 SHETGGWATAPDGPYAWGYCWLREQSPGDYCTPS-GQWPCAPGRKYFGRGPLOISHNY 182  
Qy 159 NYGPAGRIDGFDGLDGRVARDVAFKALWFMNN-----VHRVMPQ----- 203  
Db 183 NYGFCGRAIGVDLNNPDVATPVISFKSALWFMWMTQSPKPSCHDVIGRWQPSADR 242  
Qy 204 -----GFGATIRAINGALECDGNPNQAMNARIGYKQYCRQLGVDGPNLTC 250  
Db 243 AANRLPGFVITNIINGLEGCRGTDNRVQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 10  
US-08-047-413-11  
; Sequence 11, Application US/08047413  
; Patent No. 5670706  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/047,413  
; FILING DATE: 19-APR-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-047-413-11

Query Match 44.0%; Score 620; DB 1; Length 324;  
Best Local Similarity 42.0%; Pred. No. 1.3e-47;  
Matches 123; Conservative 43; Mismatches 79; Indels 48; Gaps 9;

Qy 1 SMQNGC-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSKGGSGGGGANVAS 52

Db 22 SASQCGSQAGARCASGLCCSKFGWCGNTINDYCGPNCQS-QC-----PGPTPPGGGDLGS 77  
Qy 53 VVTGSGFENG-INKQAGSGCGKQFYTRSAFLSAVKAYPGFAHGGSOVQGRKRIIAAFPAHA 111  
Db 78 IISSEMFQMLKHNDRNACQKGFYSYNAFINAAARSPFGTSGDTTARKKEIAAFPAQT 137  
Qy 112 THET-----GHFCYISEISKSNAICDPTKRWPCAAQKQYGRGPLOISWNY 158  
Db 138 SHETGGWATAPDGPYAWGYCWLREQSPGDYCTPS-GQWPCAPGRKYFGRGPLOISHNY 196  
Qy 159 NYGPAGRIDGFDGLDGRVARDVAFKALWFMNN-----VHRVMPQ----- 203  
Db 197 NYGFCGRAIGVDLNNPDVATPVISFKSALWFMWMTQSPKPSCHDVIGRWQPSADR 256  
Qy 204 -----GFGATIRAINGALECDGNPNQAMNARIGYKQYCRQLGVDGPNLTC 250  
Db 257 AANRLPGFVITNIINGLEGCRGTDNRVQDRIGFYRRYCSILGVSFGDNLDC 309

RESULT 11  
US-08-229-050-11  
; Sequence 11, Application US/08229050  
; Patent No. 6066491  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,050  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-229-050-11

Query Match 44.0%; Score 620; DB 3; Length 324;  
Best Local Similarity 42.0%; Pred. No. 1.3e-47;  
Matches 123; Conservative 43; Mismatches 79; Indels 48; Gaps 9;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-563-11

1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSGGGGANVAS 52  
22 SAEQCSGAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC---PGGPTPPGGDLGS 77  
53 VVTGSPFNG-IKNQAGSGCEGKNYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAFHA 111  
78 IISSMFQDLKHRNDNACQCKGFYSYNAFINAARSFFGFTSGDTTARKREIAAFQAOT 137  
112 THET-----GHFCYISEISKSNAICDPTKROWPCAAGQKYGRGPIQISWNY 158  
138 SHETGGWATAPDGPYANGYCWLEQCSGPDYCTPS-GQWPCAPGRKYFGRGPIQISHNY 196  
159 NYGPAGRIDGDLGDPGRVARDVAVFAKALWFMMNN-----VHRVMPQ---- 203  
197 NYGPCGGAIGVDLLNNDLVATDPVISFKSALWFMMTPQSPKPSCHDVIIIGRWQPSADR 256  
204 -----GFGATIRAINGALECDGNPAQMNARIGYKQYCRQLGVDGPNLTC 250  
257 AANRLPGFVITNIINGLEGCGRTDSRVQDRIGFYRYCYSLGVSPGDNLDC 309

RESULT 12  
US-08-801-563-11  
Sequence 11, Application US/08801563  
Patent No. 6087560  
GENERAL INFORMATION:  
APPLICANT: Cornelissen, Bernardus J.C.  
APPLICANT: Melchers, Leo S.  
APPLICANT: Meulenhoff, Elisabeth J.S.  
APPLICANT: van Roekel, Jeroen S.C.  
APPLICANT: Sela-Buurlage, Marianne B.  
APPLICANT: Vloemans, Alexandra A.  
APPLICANT: Woloshuk, Charles P.  
APPLICANT: Bol, John F.  
APPLICANT: Linthorst, Hubertus J.M.  
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,563  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/047,413  
FILING DATE: 19-APR-1993  
APPLICATION NUMBER: US 07/647,831  
FILING DATE: 29-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20022.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 11:

1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSGGGGANVAS 52  
22 SAEQCSGAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC---PGGPTPPGGDLGS 77  
53 VVTGSPFNG-IKNQAGSGCEGKNYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAFHA 111  
78 IISSMFQDLKHRNDNACQCKGFYSYNAFINAARSFFGFTSGDTTARKREIAAFQAOT 137  
112 THET-----GHFCYISEISKSNAICDPTKROWPCAAGQKYGRGPIQISWNY 158  
138 SHETGGWATAPDGPYANGYCWLEQCSGPDYCTPS-GQWPCAPGRKYFGRGPIQISHNY 196  
159 NYGPAGRIDGDLGDPGRVARDVAVFAKALWFMMNN-----VHRVMPQ---- 203  
197 NYGPCGGAIGVDLLNNDLVATDPVISFKSALWFMMTPQSPKPSCHDVIIIGRWQPSADR 256  
204 -----GFGATIRAINGALECDGNPAQMNARIGYKQYCRQLGVDGPNLTC 250  
257 AANRLPGFVITNIINGLEGCGRTDSRVQDRIGFYRYCYSLGVSPGDNLDC 309

Query Match 44.0%; Score 620; DB 3; Length 324;  
Best Local Similarity 42.0%; Pred. No. 1.3e-47;  
Matches 123; Conservative 43; Mismatches 79; Indels 48; Gaps 9;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-563-11

1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSGGGGANVAS 52  
22 SAEQCSGAGGARCASGLCCSKFGWCGTNDYCGPNCQS-QC---PGGPTPPGGDLGS 77  
53 VVTGSPFNG-IKNQAGSGCEGKNYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAFHA 111  
78 IISSMFQDLKHRNDNACQCKGFYSYNAFINAARSFFGFTSGDTTARKREIAAFQAOT 137  
112 THET-----GHFCYISEISKSNAICDPTKROWPCAAGQKYGRGPIQISWNY 158  
138 SHETGGWATAPDGPYANGYCWLEQCSGPDYCTPS-GQWPCAPGRKYFGRGPIQISHNY 196  
159 NYGPAGRIDGDLGDPGRVARDVAVFAKALWFMMNN-----VHRVMPQ---- 203  
197 NYGPCGGAIGVDLLNNDLVATDPVISFKSALWFMMTPQSPKPSCHDVIIIGRWQPSADR 256  
204 -----GFGATIRAINGALECDGNPAQMNARIGYKQYCRQLGVDGPNLTC 250  
257 AANRLPGFVITNIINGLEGCGRTDSRVQDRIGFYRYCYSLGVSPGDNLDC 309

RESULT 13  
US-08-475-427-13  
Sequence 13, Application US/08475427  
Patent No. 5859340  
GENERAL INFORMATION:  
APPLICANT: DUBOIS, Michel  
APPLICANT: GRISON, Rene  
APPLICANT: LEGUAY, Jean-Jacques  
APPLICANT: PIGNARD, Annie  
APPLICANT: TOPPAN, Alain  
TITLE OF INVENTION: Recombinant gene coding for a protein  
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,427  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/842,165  
FILING DATE: 01-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR91/00607  
FILING DATE: 21-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 90 09460  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16781/564/BEDL  
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-475-427-13

Query Match          44.0%; Score 620; DB 2; Length 329;
Best Local Similarity 43.8%; Pred. No. 1.3e-47;
Matches 128; Conservative 39; Mismatches 79; Indels 46; Gaps 11;

Qy 3 QNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSSGGGGANVASV 54
Db 25 QNCGSQGGKVCASGQCCSKFGMCGNTNDHCGSGNCQS-QCPGGGPGPVPVTGGDLGSI 83
Qy 55 TGSFFNG-INKQAGSGCEGK-NFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFAHAT 112
Db 84 SNSMFDQMLKHNENSQCGKNNFYNAFTAAKSPFGFTSGDINARKREIAAFAHAT 143
Qy 113 HET-----GHF-----CVISISKSNAVCPTKQWPCAAAGKYVGRPLQISWNYN 159
Db 144 HETGWPSPADPGPFANGYCFLEERGNPDYCSFSS-QWPCAPGRKYFGRGPIQISHNYN 202
Qy 160 YGPAGRIDGPDGDPGRVARDVAVPAKALWFMN-----NVHRVM-----PQ----- 203
Db 203 YGPCRAIGVLLNNPDLVATPVISPKTAIFWMTQSPKPSCHDVIGRWNPASGDRS 262
Qy 204 -----GFGATRAINGALECDGNPAQNNARIGYKQYCRQLGVDPGPNLTC 250
Db 263 ANRLPGFVITNIINGLECGRGNDRVQDRIGFYRYCYGILGVSPGDNLDC 314

RESULT 14
US-07-842-165-13
; Sequence 13, Application US/07842165
; Patent No. 5932698
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: FIGNARD, Alain
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/842.165
; FILING DATE: 19920501
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
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; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-842-165-13

Query Match          44.0%; Score 620; DB 2; Length 329;
Best Local Similarity 43.8%; Pred. No. 1.3e-47;
Matches 128; Conservative 39; Mismatches 79; Indels 46; Gaps 11;

Qy 3 QNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSSGGGGANVASV 54
Db 25 QNCGSQGGKVCASGQCCSKFGMCGNTNDHCGSGNCQS-QCPGGGPGPVPVTGGDLGSI 83
Qy 55 TGSFFNG-INKQAGSGCEGK-NFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFAHAT 112
Db 84 SNSMFDQMLKHNENSQCGKNNFYNAFTAAKSPFGFTSGDINARKREIAAFAHAT 143
Qy 113 HET-----GHF-----CYISISKSNAVCPTKQWPCAAAGKYVGRPLQISWNYN 159
Db 144 HETGWPSPADPGPFANGYCFLEERGNPDYCSFSS-QWPCAPGRKYFGRGPIQISHNYN 202
Qy 160 YGPAGRIDGPDGDPGRVARDVAVPAKALWFMN-----NVHRVM-----PQ----- 203
Db 203 YGPCRAIGVLLNNPDLVATPVISPKTAIFWMTQSPKPSCHDVIGRWNPASGDRS 262
Qy 204 -----GFGATRAINGALECDGNPAQNNARIGYKQYCRQLGVDPGPNLTC 250
Db 263 ANRLPGFVITNIINGLECGRGNDRVQDRIGFYRYCYGILGVSPGDNLDC 314

RESULT 15
US-07-704-288C-7
; Sequence 7, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-7

Query Match 42.8%; Score 602.5; DB 1; Length 314;
Best Local Similarity 43.6%; Pred. No. 4.7e-46;
Matches 122; Conservative 38; Mismatches 77; Indels 43; Gaps 9;

Qy 7 QPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGSGGGGAGANVASVVTGSPFNGIKNQ 65
Db 27 CAPGLCCSKFGWCNTNDYCGPGNCQS-QCPGGPGPSGDLGG-----VISNSMPDQMLNH 80

Qy 66 AG-SGCEGK-NFYTRSAPLSAVKAYPGFAHGGSOVQKREIAAPFAHATHET----- 115
Db 81 RNDNACQGNFYSYNAFISNAGSFPFGTGTITARKREIAAFLAQTSHETTCGWPSAP 140

Qy 116 -----GHFCYISEISKSNAYCDPTKROWPCAAGQKYYGRGPLQISWNNYNGPAGRDIGFD 170
Db 141 DGPVAMGYCFLREQSGPDYCTPSS-QWPCAPGRKYFGRGPIQISHNNYNGPCGRAIGVD 199

Qy 171 GLGDPGRVARDVAVAFKAALWFNN-----NVHRVMP-----QGFGATIR 210
Db 200 LLNPNDLVATDSVTSFKSAIWFMTPOSXPSPSCHDVITGRWPSCADQAAANRVPGFVITN 259

Qy 211 AINGALECDGNNPAQMNAIGYKQYCRQLGVDPGNLTC 250
Db 260 IINGLECGHGSRSRVQDRIGFYRYCGILGVSPGDNLDC 299

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Search completed: May 24, 2005, 12:56:21  
Job time : 31.572 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 24, 2005, 12:54:28 ; Search time 89.2505 Seconds  
(without alignments)  
936.991 Million cell updates/sec

US-10-692-367-70

Title:

Perfect score: 1408

Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYKQYCRQLGVDGPNLTC 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/FCCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/FCCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1408	100.0	250	17	US-10-692-367-70
2	1377	97.8	250	17	US-10-692-367-52
3	1372	97.4	250	17	US-10-692-367-82
4	1366	97.0	254	17	US-10-692-367-68
5	1363	96.8	250	17	US-10-692-367-78
6	1360	96.6	250	17	US-10-692-367-56
7	1358	96.4	250	17	US-10-692-367-44
8	1357.5	96.4	257	17	US-10-692-367-72
9	1351	96.0	248	17	US-10-692-367-2
10	1351	96.0	250	17	US-10-692-367-50
11	1351	96.0	281	14	US-10-304-928-2
12	1350	95.9	250	17	US-10-692-367-54
13	1349	95.8	256	17	US-10-692-367-74
14	1348	95.7	250	17	US-10-692-367-22
15	1348	95.7	256	17	US-10-692-367-48
16	1344	95.5	256	17	US-10-692-367-60
17	1342	95.3	256	17	US-10-692-367-62
18	1341	95.2	250	17	US-10-692-367-36
19	1336.5	94.9	249	17	US-10-692-367-80
20	1335.5	94.9	257	17	US-10-692-367-66
21	1335	94.8	256	17	US-10-692-367-84
22	1328.5	94.4	257	17	US-10-692-367-30
23	1328.5	94.4	257	17	US-10-692-367-34
24	1325.5	94.1	259	17	US-10-692-367-40
25	1324.5	94.1	259	17	US-10-692-367-76
26	1323	94.0	250	17	US-10-692-367-58
27	1322.5	93.9	257	17	US-10-692-367-46
28	1321.5	93.9	257	17	US-10-692-367-64
29	1319	93.7	250	17	US-10-692-367-32
30	1318.5	93.6	257	17	US-10-692-367-12
31	1314.5	93.4	269	17	US-10-692-367-18
32	1312	93.2	250	17	US-10-692-367-28
33	1309.5	93.0	257	17	US-10-692-367-38
34	1303	92.5	270	17	US-10-692-367-20
35	1300.5	92.4	257	17	US-10-692-367-24
36	1285	91.3	256	17	US-10-692-367-42
37	1283.5	91.2	257	17	US-10-692-367-8
38	1271.5	90.3	255	17	US-10-692-367-1
39	1271.5	90.3	303	15	US-10-425-114-57156
40	1269	90.1	301	15	US-10-425-114-63860
41	1269	90.1	302	15	US-10-425-114-71741
42	1265.5	89.9	280	17	US-10-692-367-19
43	1264	89.8	293	15	US-10-425-114-64209
44	1264	89.8	288	15	US-10-425-114-52906
45	1258.5	89.4	280	17	US-10-692-367-17

## ALIGNMENTS

## RESULT 1

US-10-692-367-70  
; Sequence 70, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Salpanti, Nasser  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-70

Query Match 100.0%; Score 1408; DB 17; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5,2e-110;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTGSFFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 2
US-10-692-367-52
; Sequence 52, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-52

Query Match 97.8%; Score 1377; DB 17; Length 250;
Best Local Similarity 97.2%; Pred. No. 2.1e-107;
Matches 243; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTGSFFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240
```

```
Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 3
US-10-692-367-82
; Sequence 82, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-82

Query Match 97.4%; Score 1372; DB 17; Length 250;
Best Local Similarity 97.2%; Pred. No. 5.4e-107;
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSRGGSGGGGSGGGANVASVVTDAFFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPAQMNARIYYKYQYCRQL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 4
US-10-692-367-68
; Sequence 68, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68
```



```
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 254
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68

Query Match      97.0%; Score 1366; DB 17; Length 254;
Best Local Similarity 95.7%; Pred. No. 1.7e-106;
Matches 243; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

Qy 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGG-----GGANVASVVTG 56
Db 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVASVVTG 60

Qy 57 SFFNGIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETG 116
Db 61 SFFNGIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETG 120

Qy 117 HFCYSEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYPAGRDIGFDGLGDPG 176
Db 121 HFCYSEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYPAGRAIGFDGLGDPN 180

Qy 177 RVADAVVAFKAALWFMMNNVHRVMPQFGATIRAINGALCEDGNNPAQMNARIQYKQY 236
Db 181 RVADAVVAFKAALWFMMNNVHRVMPQFGATIRAINGALCEDGNNPAQMNARIGYKQY 240

Qy 237 CRQLGVDGPNLTC 250
Db 241 CRQLGVDGPNLTC 254

RESULT 5
US-10-692-367-78
; Sequence 78, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 250
; TYPE: PR1

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-56

Query Match      96.8%; Score 1363; DB 17; Length 250;
Best Local Similarity 96.0%; Pred. No. 3.1e-106;
Matches 240; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGANVASVVTGSPFN 60
Db 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANVASVVTGSPFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120

Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYPAGRAIGFDGLGDPNVAR 180

Qy 181 DAVVAFKAALWFMMNNVHRVMPQFGATIRAINGALCEDGNNPAQMNARIQYKQYCRQL 240
Db 181 DAVVAFKAALWFMMNNVHRVMPQFGATIRAINGALCEDGNNPAQMNARIGYKQYCRQL 240

Qy 241 GVDGPNLTC 250
Db 241 GVDGPNLTC 250

RESULT 6
US-10-692-367-56
; Sequence 56, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 250
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-56

Query Match      96.6%; Score 1360; DB 17; Length 250;
Best Local Similarity 96.0%; Pred. No. 5.5e-106;
Matches 240; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGANVASVVTGSPFN 60
Db 1 SMQNCGQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGANVASVVTGSPFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
```

Qy 121 ISEISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Db 121 ISEISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Qy 181 DAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Db 181 DAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Qy 241 GVDGPNLTC 250  
Db 241 GVDGPNLTC 250

## RESULT 7

US-10-692-367-44  
; Sequence 44, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-44

Query Match 96.4%; Score 1358; DB 17; Length 250;  
Best Local Similarity 95.6%; Pred. No. 8e-106;  
Matches 239; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SMQNCQCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSPFN 60  
Db 1 SMQNCQCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTDAFFN 60  
Qy 61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATHETGHFCY 120  
Db 61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSSEVERKREIAAFPAHATHETGHFCY 120  
Qy 121 ISEISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Db 121 ISEISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Qy 181 DAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Db 181 DAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARVGYKYQYCRQL 240  
Qy 241 GVDGPNLTC 250  
Db 241 GVDGPNLTC 250

## RESULT 8

US-10-692-367-72

; Sequence 72, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 10/389,432  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-72

Query Match 96.4%; Score 1357.5; DB 17; Length 257;  
Best Local Similarity 94.2%; Pred. No. 9.1e-106;  
Matches 242; Conservative 4; Mismatches 4; Indels 7; Gaps 1;  
Qy 1 SMQNCQCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASV 53  
Db 1 SMQNCQCPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASV 60  
Qy 54 VTGSFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATH 113  
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATH 120  
Qy 114 ETGHFCYISISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLG 173  
Db 121 ETGHFCYISISKSAYCDPTKRWPCAGQKYYGRGLOISWNNYGPAGRDIGFDGLG 180  
Qy 174 DPGRVARDVAVFAKALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYY 233  
Db 181 DPGRVARDVAVFAKALWFMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYY 240  
Qy 234 KOYCRQLGVDGPNLTC 250  
Db 241 KOYCRQLGVDGPNLTC 257

## RESULT 9

US-10-692-367-2  
; Sequence 2, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 10/389,432  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06

; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-692-367-2

Query Match 96.0%; Score 1351; DB 17; Length 248;  
Best Local Similarity 96.0%; Pred. No. 3.1e-105;  
Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFNGI 62  
DB 1 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFNGI 60  
QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 122  
DB 61 KSOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 120  
QY 123 EISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRDIGFDGLDGPGRVARDA 182  
DB 121 EINKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRDIGFDGLDGPGRVARDA 180  
QY 183 VVAFKAALWFWMNNVHRVMPQFGATIRAINGALCECDGNPAQMNARIGYTKQYCRQLGV 242  
DB 181 VVAFKAALWFWMNSVHGVVPGFGATTIRAINGALCECGNNPAQMNARVGYTRYQYCRQLGV 240  
QY 243 DPGPNLTC 250  
DB 241 DPGPNLTC 248

RESULT 10  
US-10-692-367-50  
; Sequence 50, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 50  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-50

Query Match 96.0%; Score 1351; DB 17; Length 250;  
Best Local Similarity 94.8%; Pred. No. 3.1e-105;  
Matches 237; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 SMQNCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFN 60  
DB 1 SMQNCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFN 60  
QY 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCY 120  
DB 61 GIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGTEVEGKREIAAPFAHATHETGHFCY 120  
QY 121 EISEKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRDIGFDGLDGPGRVAR 180  
DB 121 EISEKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLDGPGRVAR 180  
QY 181 DAVVAFKAALWFWMNNVHRVMPQFGATIRAINGALCECDGNPAQMNARIGYTKQYCRQL 240  
DB 181 DAVVAFKAALWFWMNSVHGVVPGFGATTIRAINGALCECGNNPAQMNARVGYTRYQYCRQL 240  
QY 241 GVDPGPNLTC 250  
DB 241 GVDPGPNLTC 250

RESULT 11  
US-10-304-928-2  
; Sequence 2, Application US/10304928  
; Publication No. US20030101484A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100D  
; CURRENT APPLICATION NUMBER: US/10/304,928  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/522,714  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/125,915  
; PRIOR FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-304-928-2

Query Match 96.0%; Score 1351; DB 14; Length 281;  
Best Local Similarity 96.0%; Pred. No. 3.5e-105;  
Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFNGI 62  
DB 34 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFNGI 93  
QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 122  
DB 94 KSOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 153  
QY 123 EISEKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRDIGFDGLDGPGRVARDA 182  
DB 154 EINKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLDGPGRVARDA 213  
QY 183 VVAFKAALWFWMNNVHRVMPQFGATIRAINGALCECDGNPAQMNARIGYTKQYCRQLGV 242  
DB 214 VVAFKAALWFWMNSVHGVVPGFGATTIRAINGALCECGNNPAQMNARVGYTRYQYCRQLGV 273  
QY 243 DPGPNLTC 250  
DB 274 DPGPNLTC 281

RESULT 12  
US-10-367-54  
; Sequence 54, Application US/10692367

```
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-54

Query Match          95.9%; Score 1350; DB 17; Length 250;
Best Local Similarity 94.4%; Pred. No. 3.8e-105;
Matches 236; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGANNVASVVTGSPFN 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGANNVASVVTGSPFN 60

Qy 61 GIKNOAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHTGHFCY 120
Db 61 GIKNOAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHTGHFCY 120

Qy 121 ISEISKSNAICDPTKRWPCAAAGQKYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAICDPTKRWPCAAAGQKYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVAFKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYKQYCKROL 240
Db 181 DAVAFKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYKQYCKROL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 13
US-10-692-367-74
; Sequence 74, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-74

Query Match          95.7%; Score 1348; DB 17; Length 250;
Best Local Similarity 95.2%; Pred. No. 5.5e-105;
Matches 238; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-74

Query Match          95.8%; Score 1349; DB 17; Length 256;
Best Local Similarity 93.8%; Pred. No. 4.7e-105;
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGANNVASV 54
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGANNVASV 60

Qy 55 TGSFFNGIKNOAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHE 114
Db 61 TDSFFNGIKNOAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVOGKREIAAPFAHATHE 120

Qy 115 TGHFCYISEISKSNAICDPTKRWPCAAAGQKYGRGPLQISWNYNYGPAGRDIGFDGLGD 174
Db 121 TGHFCYINEISKSNAICDPTKRWPCAAAGQKYGRGPLQISWNYNYGPAGRDIGFDGLGD 180

Qy 175 PGRVARDVAVFAKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYK 234
Db 181 PGRVARDVAVFAKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYK 240

Qy 235 QYCRQLGVDPGPNLTC 250
Db 241 QYCRQLGVDPGPNLTC 256

RESULT 14
US-10-692-367-22
; Sequence 22, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-22

Query Match          95.7%; Score 1348; DB 17; Length 250;
Best Local Similarity 95.2%; Pred. No. 5.5e-105;
Matches 238; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSSGGGANVASVVTGSPFN 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 SMQCGCGASGLCCSRFGYCGTTDBYCGDGCOSGCRSGGGSSGGGANVASVVTGSPFN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GIKKQAGSGCEGKNFYTRSFLSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETHGFCY 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 GIKQAGSGCEGKNFYTRSFLSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHETHGFCY 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 ISEISKSNAYCDPTKRWPCAAAGQKYYGRGFLQISWNNYGPAGRIDGFDGLDPRVAR 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 ISEINKSNAYCDPTKRWPCAAAGQKYYGRGFLQISWNNYGPAGRAIGFDGLDPRVAR 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 181 DAVVAFKAALWFMNNVHRVMPQGFATIRAINGALCEDGNNPAOMNARIYYKQYCRQL 240
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 DAVVAFKAALWFMNNVHRVMPQGFATIRAINGALCEDGNNPAOMNARIYYKQYCRQL 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 241 GVDPGPNLTC 250
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 RVDPGPNLTC 250
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 15

```
US-10-692-367-48
; Sequence 48, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-48
```

```
Query Match 95.7%; Score 1348; DB 17; Length 256;
Best Local Similarity 93.8%; Pred. No. 5.7e-105;
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSSGGGANVASV 54
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 SMQCGCPNVCCSKFGYCGTTDBYCGDGCOSGCRSGGGSSGGGANVASV 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 55 TGSFNGIKKQAGSGCEGKNFYTRSFLSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHE 114
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 TGSFNGIKKQAGSGCEGKNFYTRSFLSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHE 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 115 TGHCYI SEISKSNAYCDPTKRWPCAAAGQKYYGRGFLQISWNNYGPAGRIDGFDGLD 174
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 TGHPRIYI SEVKNKNAYCDPTKRWPCAAAGQKYYGRGFLQISWNNYGPAGRAIGFDGLD 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 175 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALCEDGNNPAOMNARIYYK 234
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALCEDGNNPAOMNARIYYK 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Qy 235 QYCRQLGVDPGPNLTC 250
Db 241 QYCRQLGVDPGPNLTC 256
```

Search completed: May 24, 2005, 13:12:28  
Job time : 90.2505 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:39:31 ; Search time 24.6548 Seconds  
(without alignment)  
975.638 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYKQYCRQLGVDPGNLTC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314.5	93.4	268	B42424	chitinase (EC 3.2.2)
2	1265.5	89.9	280	A42424	chitinase (EC 3.2.2)
3	873	62.0	268	S25311	chitinase (EC 3.2.2)
4	859	61.0	261	S51678	chitinase (EC 3.2.2)
5	834.5	59.3	273	T47601	class IV chitinase
6	829.5	58.9	288	S46536	chitinase (EC 3.2.2)
7	829	58.9	264	A84868	probable endochitini
8	823.5	58.5	270	S16579	chitinase (EC 3.2.2)
9	805	57.2	249	S57476	chitinase class 4
10	802.5	57.0	229	T03405	probable chitinase
11	788.5	56.0	265	H84867	probable endochitini
12	783	55.6	276	T09131	chitinase (EC 3.2.2)
13	768	54.5	266	T14345	chitinase (EC 3.2.2)
14	767	54.5	266	T14348	probable chitinase
15	762	54.1	268	T14341	probable chitinase
16	754	53.6	268	T14344	chitinase (EC 3.2.2)
17	744	52.8	250	A44039	chitinase (EC 3.2.2)
18	733.5	52.1	208	J80125	chitinase (EC 3.2.2)
19	717	50.9	277	G84867	probable endochitini
20	712.5	50.6	281	C84868	probable endochitini
21	693.5	49.3	283	D84868	probable endochitini
22	691.5	49.1	247	S15645	chitinase (EC 3.2.2)
23	682.5	48.5	266	S55778	chitinase class IV
24	639	45.4	327	T09687	chitinase (EC 3.2.2)
25	627.5	44.6	328	S05426	chitinase (EC 3.2.2)
26	621	44.1	324	S20981	chitinase (EC 3.2.2)
27	619.5	44.0	324	S56694	chitinase (EC 3.2.2)
28	611.5	43.4	323	T03614	chitinase (EC 3.2.2)
29	611.5	43.4	329	S08627	chitinase (EC 3.2.2)

30	608.5	43.2	302	2	JC2071	chitinase (EC 3.2.2)
31	608.5	43.2	318	2	S43317	chitinase (EC 3.2.2)
32	605.5	43.0	316	2	S65020	chitinase (EC 3.2.2)
33	605.5	43.0	318	2	S65019	chitinase (EC 3.2.2)
34	602	42.8	334	2	S20982	chitinase (EC 3.2.2)
35	597.5	42.4	322	1	S37344	chitinase (EC 3.2.2)
36	594.5	42.2	320	2	S38670	chitinase (EC 3.2.2)
37	592	42.0	336	2	S15997	chitinase (EC 3.2.2)
38	583.5	41.4	335	2	B45511	probable chitinase
39	583	41.4	318	2	T04403	chitinase (EC 3.2.2)
40	580.5	41.2	322	2	S59953	chitinase (EC 3.2.2)
41	580.5	41.2	329	2	T06999	chitinase (EC 3.2.2)
42	577.5	41.0	329	2	T07000	chitinase (EC 3.2.2)
43	577	41.0	311	2	T07838	chitinase (EC 3.2.2)
44	569	40.4	321	2	S57482	chitinase class 1
45	566	40.2	332	2	T04484	probable chitinase

#### ALIGNMENTS

##### RESULT 1

B42424  
chitinase (EC 3.2.1.14) precursor - maize (fragment)  
C;Species: Zea mays (maize)  
C;Date: 12-Mar-1993 #sequence\_revision 03-Feb-1994 #text\_change 10-Jul-1998  
C;Accession: B42424  
R;Huyth, O.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.  
J. Biol. Chem. 267, 6635-6640, 1992  
A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifungal activity.  
A;Reference number: A42424; MUID:92202208; PMID:1551872  
A;Accession: B42424  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-268 <HUY>  
A;Cross-references: DB:M84165  
A;Note: The authors translated the codon AAG for residue 104 as Asn, GGC for residue 105  
0 as Ile, CAA for residue 231 as Asn and CGC for residue 232 as Gly  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;20-55/Domain: hevein chitin-binding domain homology <HCB>  
P;70-268/Domain: plant chitinase homology <PCH>

Query Match 93.4%; Score 1314.5; DB 2; Length 268;

Best Local Similarity 93.6%; Pred. No. 1.4e-95;

Matches 233; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTDTDEYCGDCQSGPCRSQ-GGGSSGGGANVASVVTGSPFNG 61

Db 20 QNCQCPNVCCSKFGYCGTDTDEYCGDCQSGPCRSQGGGGGGGANVASVVTSSPFNG 79

QY 62 IKNOAGSGCEGKNFYTRSAFLSAVKYPGFAHGGSQVQKREIAAFAFAHATHETGHFCYI 121

Db 80 IKNOAGSGCEGKNFYTRSAFLSAVKYPGFAHGGSQVQKREIAAFAFAHATHETGHFCYI 139

QY 122 SEISKSNAYCDPTKQWPCAAQKYRGPIQISWNTNYGPAGRDIGPDGLDGPGRVARD 181

Db 140 SEINKSNAYCDPTKQWPCAAQKYRGPIQISWNTNYGPAGRAIGPDGLDGPGRVARD 199

QY 182 AVVAFKALWFMNVRHVRMPQGFATITNGALECDGNPAQWNRARIGYKQYCRQLG 241

Db 200 AVVAFKALWFMNVRHVRMPQGFATITNGALECDGNPAQWNRARIGYKQYCRQLG 259

QY 242 VDPGNLTC 250

Db 260 VDPGNLTC 268

##### RESULT 2

A42424

chitinase (EC 3.2.1.14) A - maize

C;Species: Zea mays (maize)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Mar-1999





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class IV chitinase (CHIV) - Arabidopsis thaliana
N:Alternate names: protein T12E18.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47601
R:Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M. Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224469
A:Accession: T47601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <BL0>
A:Cross-references: UNIPROT:Q9M2U5; EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Genetics:
A:Map position: 3
A:Introns: 139/1
A:Note: T12E18.110
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 59.3%; Score 834.5; DB 2; Length 273;
Best Local Similarity 60.2%; Pred. No. 4.4e-58;
Matches 150; Conservative 23; Mismatches 71; Indels 5; Gaps 2;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGSPCRSGGGSGGGGANVASVVTGSPFNGI 62
Db 29 QNCGSSBLCCSFQFGCNTSDYCGVCGQGPCFA-----PPANGSVSAEIVTQEFFNGI 84

Qy 63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFHATHETGHFCVIS 122
Db 85 ISQAASSCAGNRFYSRGAFLEALDSYSRFRGVSTDDSRREIAAFHATHETGHFCYIE 144

Qy 123 EI-SKSNAYCDPTKRWPCAAQKQYGRGPIQLISWNNYGPAGRDIGFDGLDGPGRVARD 181
Db 145 EIDGASKDYCDENATQYPCNENKGYGRGPIQLSNFNYGAGTAIGFDGLNAPETVATD 204

Qy 182 AVAFKAAALWFMWNNHVRVMPQGGATIRANGALECDGNPAQMNARIGYKQYCRQLG 241
Db 205 PVISPKTALWYTNRVQPVISQFGATIRANGALECDGANTATVQARVRYTTCRQLG 264

Qy 242 VDPGNLTC 250
Db 265 VDPGNLTC 273

RESULT 6
S46536
chitinase (EC 3.2.1.14) - beet
C:Species: Beta vulgaris (beet)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46536
R:Nielsen, K.K.; Bojlsen, K.; Roepstorff, P.; Mikkelsen, J.D.
Plant Mol. Biol. 25, 241-257, 1994
A:Title: A hydroxyproline-containing class IV chitinase of sugar beet is glycosylated w
A:Reference number: S46536; MUID:94289648; PMID:8018873
A:Accession: S46536
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-288 <N1E>
A:Cross-references: UNIPROT:P42820; EMBL:L25826; NID:G510277; PID:AAA32916.1; PID:G5102
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
P:28-64/Domain: hevein chitin-binding domain homology <HCB>
P:89-288/Domain: plant chitinase homology <PCH>

Query Match 58.9%; Score 829.5; DB 2; Length 288;
Best Local Similarity 59.3%; Pred. No. 1.1e-57;
Matches 156; Conservative 30; Mismatches 60; Indels 17; Gaps 5;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDCG-CQSGPCRSGGGS-----SGGGGANV 50
Db 28 QNCGCAPNLCCSNFQFCGTGTGYCGVGNQCQSGPCBGGTPTTPTTPTTPTTGTGGGSSV 87
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Qy 51 ASVVTGSPFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFH 110
Db 88 SDIVSQAFFDGIICQAAASCPEKKNFYTRAAPFLSVD--PKFNEGSSDDNKRETAAPFAH 145

Qy 111 ATHTGHFCYISET--SKSNAYCDPTK-RQWPCAAQKQYGRGPIQLISWNNYGPAGRDI 167
Db 146 ISHTTTLCHIEERDGDVGDAYCDQDKAAQYPCAAKGYGRGPLQLSLWNNYALAGAI 205

Qy 168 GFDGLDGPGRVARDVAVFAALWFMWNNHVRVMPQGGATIRANGALECDGNPAQMN 227
Db 206 GFDGLGNPEKATDVNTSFKAAWFMWNTVHSVMNQGFGATTKAINGALECNGQDOAN 265

Qy 228 ARIGYKQYCRQLGVDGPNLTC 250
Db 266 DRIOFYKKYCADFGVAPGDNLTC 288

RESULT 7
A84868
probable endochitinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84868
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84868
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:O24658; GB:AR002093; NID:G2281111; PID:AAB64047.1; GSPDB:GN
C:Genetics:
A:Gene: At2G43590
A:Map position: 2
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 58.9%; Score 829; DB 2; Length 264;
Best Local Similarity 59.4%; Pred. No. 1.2e-57;
Matches 148; Conservative 33; Mismatches 58; Indels 10; Gaps 5;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGSPCRSGGGSGGGGANVASVVTGSPFNGI 62
Db 25 QNCGCAPNLCCSFQYCGTDDAYCGVGCRCSPCR--GSGTPTGG--SVGSIIVTQGFNNI 80

Qy 63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFHATHETGHFCVIS 122
Db 81 INQAGNCGAKRFYTRDSFVNAANTFNFANSVT----RREIATWFAHTHETGHFCYIE 136

Qy 123 EIS-KSNAYCDPTKRWPCAAQKQYGRGPIQLISWNNYGPAGRDIGFDGLDGPGRVARD 181
Db 137 EINGATRNYSOSSNTQYPCAPGKGYGRGPIQLSNWNNYGCACGSLGLDLRLQPELVGSN 196

Qy 182 AVAFKAAALWFMWNNHVRVMPQGGATIRANGALECDGNPAQMNARIGYKQYCRQLG 241
Db 197 PTVAFTGLWFMWNSVRPVLNQGGATIRANG-MECNGNSGAVNARIGYRDYCGQLG 255

Qy 242 VDPGNLTC 250
Db 256 VDPGNLUSC 264

RESULT 8
S16579
chitinase (EC 3.2.1.14) precursor - kidney bean
C:Species: Phaseolus vulgaris (kidney bean)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S16579
R:Margis-Pinheiro, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.; Burkard
Plant Mol. Biol. 17, 243-253, 1991
A:Title: Isolation of a complementary DNA encoding the bean PR4 chitinase: an acidic en
```

A;Reference number: S16579; MUID:91322521; PMID:1863776

A;Accession: S16579

A;Molecule type: mRNA

A;Residues: 1-270 <MAP>

A;Cross-references: UNIPROT:P27054; EMBL:X57187

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase class 4 - cowpea (fract)

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;24-59/Domain: hevein chitin-binding domain homology <HCB>

F;70-270/Domain: plant chitinase homology <PCH>

Query Match 58.5%; Score 823.5; DB 2; Length 270;

Best Local Similarity 59.7%; Pred. No. 3.2e-56;

Matches 151; Conservative 28; Mismatches 67; Indels 7; Gaps 4;

1 SMQNGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANV-ASVVTGSFF 59

22 SAQNGCGAEGJCCSGYCGTGEDYCGTGCGQCGPCTTASPPPSN----NVNADILTADFL 77

60 NGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIIAFAFHAHATHGHFC 119

78 NGIIDQADSGCAGKKNFYTRDAFLSALNSYTDGFRVGSDDSKRIIAAFAHFTTHGHFC 137

120 YISEI-SKSNAYCDPTK-RQWPCAGQKYGRGPIQISWNNYNYGPAGRDIGFDGLGPGR 177

138 YIEIDGASKDYCDDEESIAQYPCSSSKYHGGRGPIQLSNFNYGPGANNFDGLGAPET 197

178 VARDAAVAFKAALWFMNNVHRVMPQGFATIRANGALECDGNPAQMNARIQYKQYC 237

198 VSDVVVSGFKTALWYMQHVRPVINOQGFATIRANGALECDGANPTTVQARVNYTTCR 257

238 RQLGVDPGPNLTC 250

258 RQLGVATGDNLTC 270

#### RESULT 9

S57476

chitinase class 4 - cowpea (fract)

C;Species: Vigna unguiculata (cowpea)

C;Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S57476

R;Vivo, L.F.T.; Broughton, W.; Krause, A.

A;Reference number: S57468

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-249 <VOL>

A;Cross-references: UNIPROT:Q43686; EMBL:X88803; NID:9871767; PIDN:CAA61281.1; PID:98717

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase class 4 - cowpea (fract)

F;4-39/Domain: hevein chitin-binding domain homology <HCB>

F;50-249/Domain: plant chitinase homology <PCH>

Query Match 57.2%; Score 805; DB 2; Length 249;

Best Local Similarity 59.5%; Pred. No. 8.2e-56;

Matches 150; Conservative 27; Mismatches 69; Indels 6; Gaps 4;

1 SMQNGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANV-ASVVTGSFF 60

2 SAQNGCGAEGJCCSGYCGTGEEYCGTGCGQCGPCTTASPPPSN----SSLSNNVNVADIIVTDAFFN 58

61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIIAFAFHAHATHGHFCY 120

59 GIIDQADSGCVGSFYARDAFLSALDSYTDGFRVGSDDSKRIIAAFAHFTTHGHFCY 118

121 ISEI-SKSNAYCDPTK-RQWPCAGQKYGRGPIQISWNNYNYGPAGRDIGFDGLGPGRV 178

119 IEEIDGASKDYCDDEESIAQYPCSS-SRGYTVVPVQLSNFNYGPGANNFDGLGPETV 177

179 ARDAVAFKAALWFMNNVHRVMPQGFATIRANGALECDGNPAQMNARIQYKQYCR 238

178 SNDVVVSGFKTALWYMQHVRPVINOQGFATIRANGALECDGANPTTVQARVNYTTCR 237

Qy 239 QLGVDGPNLTC 250

Db 238 QLGVDGDNLTC 249

#### RESULT 10

T03405

probable chitinase (BC 3.2.1.14) IIB - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C;Accession: T03405

R;Truong, N.; Itoh, Y.

A;Description: Nucleotide sequence of rice class II chitinase cDNA.

A;Reference number: Z14936

A;Accession: T03405

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-229 <TRU>

A;Cross-references: UNIPROT:O04138; EMBL:AB003194

A;Experimental source: cv. Nipponbare

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase class II chitinase

C;Keywords: Glycosidase; hydrolase; polysaccharide degradation

F;30-229/Domain: plant chitinase homology <PCH>

Query Match 57.0%; Score 802.5; DB 2; Length 229;

Best Local Similarity 58.3%; Pred. No. 1.2e-55;

Matches 140; Conservative 27; Mismatches 37; Indels 1; Gaps 1;

47 GANVASVVTGSFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIIA 106

25 GVSVESVVTGAFFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIIA 84

107 FEAHATHGHFCYISEISKSNA-YCDPTKRWPCAAGQKYGRGPIQISWNNYNYGPAGR 165

85 FFHVTHETHGMCYINEINGANNMDYCDKSNKQPCQPKKYYGRGPIQISWNNYNYGPAGK 144

166 DIGFDGLGDPGRVARDAAVAFKAALWFMNNVHRVMPQGFATIRANGALECDGNPPAQ 225

145 NIGFDGLRDPDKAQDPTISFKTALWFMNNVHRVMPQGFATIRANGALECDGNPPAQ 204

226 MNARIGYKQYCRQLGVDPGPNLTC 250

205 VNARVNYKYDCRQFGVSPGNNLYC 229

#### RESULT 11

H84867

probable endochitinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: H84867

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-265 <STO>

A;Cross-references: UNIPROT:O24598; GB:AB002093; NID:g2281112; PIDN:AB64048.1; GSPDB:GN

C;Genetics:

A;Gene: At2g43580

A;Map position: 2

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase class II chitinase

Query Match 56.0%; Score 788.5; DB 2; Length 265;

Best Local Similarity 57.0%; Pred. No. 1.7e-54;

Matches 142; Conservative 34; Mismatches 64; Indels 9; Gaps 4;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSFPNGI 62

Db 25 QNCDCAPNLCSPQGYCGTADYCGSTCQSGPCRVRGGPPT---GAGLVGNIVTQIFNNI 81  
Qy 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAPFAHATHETHGFCYIS 122  
Db 82 INOAGNGCAGKSFYTRDSFINATNTPPSFAN---TVTRRIATWFAHFTVETGHFCYIE 137  
Qy 123 EIS-KSNAYCDPTKQWPCACQKYGGRPLQISWNNYNGPAGRDIGFDGLDGPGRVARD 181  
Db 138 EINGASRVNCDQNNRQYPCAPAKSYHGRGPLLLSNFNYGACGQSLGLDLRLRQPELVSN 197  
Qy 182 AVAFKAALWFNNVHVRVMPQFGATIRAINGALECDGNNPAQNNARIGYKQYCRQLG 241  
Db 198 PVAFTALFWKSVRPLVQGFATIRAISSG-FDCGRNLGGVNAIGYRDYCGQLG 256  
Qy 242 QGVDPGNLTC 250  
Db 257 LDPGANITC 265

RESULT 12.  
T09131  
chitinase (BC 3.2.1.14) - white spruce  
C:Species: Picea glauca (white spruce)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09131  
R: Dong, J.Z.; Dunstan, D.I.  
A: Description: Developmental regulation of a gene encoding chitinase during somatic embryo  
A: Reference number: Z16579  
A: Accession: T09131  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: mRNA  
A: Residues: 1-276 <DQNA>  
A: Cross-references: UNIPROT: Q40838; EMBL: L42467; NID: g1161164; PID: g1161165  
C: Geneticks:  
A: Gene: chi  
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C: Keywords: glycosidase; hydrolase; polysaccharide degradation  
F: 27-62/Domain: hevein chitin-binding domain homology <HCB>

Query Match 55.6%; Score 783; DB 2; Length 276;  
Best Local Similarity 53.6%; Pred. No. 4.7e-54;  
Matches 135; Conservative 40; Mismatches 71; Indels 6; Gaps 4;  
Qy 3 QNCQCPNVCCSKFGYCGTDTDEYCGDQCGQSPCRSGGGGGGGGGANVASVVTGSPFNGI 62  
Db 27 QNCQCSAGVCCSQYGYCGTTSAYCGKCKSGPCYSSGGSPSAGSGSVGGIISQSFNGL 86  
Qy 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAPFAHATHETHGFCYIS 122  
Db 87 AGGAGSSCEGKGFYTYNAFAAANAFSGFTTGSNDVKRELAAPFANVWHTGGLCYIN 146  
Qy 123 EISKSNAYCDPTKQWPCACQKYGGRPLQISWNNYNGPAGRDIGFDGLDGPGRVARD 182  
Db 147 EKNPMMKYCQ--SSSTWCTSGKSHYGRGPLQLSWNNYNGAVKSGISGFDGLNPNPKVGKDP 205  
Qy 183 VVAFKAALWFNNV--NNVHRVMP--QGFGATIRAINGALECDGNNPAQNNARIGYKQYCR 238  
Db 206 TTSSKTAWFNNKRNCHSAITSGKLGGLTIKAIN-SNECNGNSGSEVNSRVNYKKICS 264  
Qy 239 QGVDPGNLTC 250  
Db 265 QLVGDPGANVSC 276

RESULT 13  
T14345  
chitinase (BC 3.2.1.14) BP3-3/E7, class IV - carrot  
C:Species: Daucus carota (carrot)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14345  
R: Kragh, K.; De Vries, S.C.

submitted to the EMBL Data Library, March 1996  
A: Reference number: Z17995  
A: Accession: T14345  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: mRNA  
A: Residues: 1-266 <KRA>  
A: Cross-references: UNIPROT: Q96410; EMBL: U52847; NID: g1549332; PID: g1549333  
A: Experimental source: strain sg766 trophy  
C: Geneticks:  
A: Gene: EP3  
C: Function:  
A: Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosamin  
A: Pathway: polysaccharide degradation  
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C: Keywords: glycosidase; hydrolase; polysaccharide degradation  
F: 21-56/Domain: hevein chitin-binding domain homology <HCB>  
F: 69-266/Domain: plant chitinase homology <PCH>

Query Match 54.5%; Score 768; DB 2; Length 266;  
Best Local Similarity 55.4%; Pred. No. 6.8e-53;  
Matches 139; Conservative 38; Mismatches 70; Indels 4; Gaps 4;  
Qy 1 SMQNCQCPNVCCSKFGYCGTDTDEYCGDQCGQSPCRSGGGGGGGGGANVASVVTGSPFN 60  
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYCGEGCQAGFC-TWTATPGGNGVSVADIVTDDFFN 77  
Qy 61 GIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAPFAHATHETHGFCY 120  
Db 78 GIISQATGDCDCKNFYTRSAFLNALQYSVSSFGTSGSADDSKREIAAPFAHATHETHGFC 137  
Qy 121 EISIS-KSNAYCDPTKQWPCACQKYGGRPLQISWNNYNGPAGRDIGFDGLDGPGRVA 179  
Db 138 KBETNGRDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYVIDAGKSNFDFGLNPNPDI 196  
Qy 180 RDVAFKAALWFNNVHVRVMPQFGATIRAINGALECDGNNPAQNNARIGYKQYCRQ 239  
Db 197 SDAVSFRTALWVKVQSVTTQGFATIRAIN-SIECNGGSPDANVSRVSLNSYCSK 255  
Qy 240 LGVDPGNLTC 250  
Db 256 FGVAFGDNQRC 266

RESULT 14  
T14348  
probable chitinase (BC 3.2.1.14) BP3B/E6, class IV - carrot  
C:Species: Daucus carota (carrot)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14348  
R: Kragh, K.; De Vries, S.C.  
A: Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosamin  
A: Pathway: polysaccharide degradation  
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C: Keywords: glycosidase; hydrolase; polysaccharide degradation  
F: 21-56/Domain: hevein chitin-binding domain homology <HCB>  
F: 69-266/Domain: plant chitinase homology <PCH>  
Query Match 54.5%; Score 767; DB 2; Length 266;  
Best Local Similarity 55.8%; Pred. No. 8.1e-53;  
Matches 140; Conservative 35; Mismatches 72; Indels 4; Gaps 4;  
Qy 1 SMQNCQCPNVCCSKFGYCGTDTDEYCGDQCGQSPCRSGGGGGGGGGANVASVVTGSPFN 60

Db	19	SAQNCNCTAGLCCSKHGYCGTTSDYCGEGCQAGPC-TNTAPTGGGNGVSVADIVTDDFFN	77
Qy	61	GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVQGKREIAAPFAHATHETHGFCY	120
Db	78	GIISQATGDCDGNFYTRSAFLNALQSYSSFGTSGSADDSKREIAAPFAHATHETHGYFCH	137
Qy	121	ISETIS-KSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPACRDIGFDGLGDPGRVA	179
Db	138	KEETNGRDKNYCE-SKAGYPCNVNVKRYFGRGFLQLTWNVNYIDAGNSNDFDGLNPDIVA	196
Qy	180	RDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMVARIGYYKQYCRQ	239
Db	197	SDAVVSFKTALWYWKVKVQSVTSQGFATIRAIN-SIECNGGSPDAVNSRVSLNSYCSK	255
Qy	240	LGVDPGPNLTC	250
Db	256	FGVAPGDNQRC	266
RESULT 15			
TI14341			
probable chitinase (EC 3.2.1.14) EP3-1/H5, class IV - carrot (fragment)			
C;Species: Daucus carota (carrot)			
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
C;Accession: TI14341			
R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, P.; Hendriks, T.; Meijer, E.A.; K			
Plant Mol. Biol. 31, 631-645, 1996			
A;Title: Characterization of carrot chitinases able to rescue the temperature-sensitive			
A;Reference number: Z17992; MUID:96382431; PMID:8790295			
A;Accession: TI14341			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: mRNA			
A;Residues: 1-268 <KRA>			
A;Cross-references: UNIPROT:Q96408; EMBL:U52845; NID:gl549328; PIDN:AAC49435.1; PID:gl54			
A;Experimental source: strain sg766 trophy			
C;Genetics:			
A;Note: EP3			
C;Function:			
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami			
A;Pathway: polysaccharide degradation			
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl			
C;Keywords: glycosidase; hydrolase; polysaccharide degradation			
Query Match 54.1%; Score 762; DB 2; Length 268;			
Best Local Similarity 55.4%; Pred. No. 2e-52;			
Matches 139; Conservative 33; Mismatches 75; Indels 4; Gaps 4;			
Qy	1	SMQNCGQPNVCCSKFYCGTTDEYCGDGCGPCRCGGSGGGGANVASVVTGSPFN	60
Db	21	SAQNCNCAAGLCCSKHYCGTTSDYCGEGCQAGPC-TNSAPSGGNAVSVADIVTDDFFN	79
Qy	61	GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSGVQGKREIAAPFAHATHETHGFCY	120
Db	80	GIISQATGDCDGNFYTRSAFLNALQSYSSFGTSGSADDSKREIAAPFAHATHETHGYFCH	139
Qy	121	ISETIS-KSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPACRDIGFDGLGDPGRVA	179
Db	140	KEETSGRDHNYCQST-AEYPCNPVNVKRYFGRGFLQLTWNVNYIDAGNSNDFDGLNPDIVA	198
Qy	180	RDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMVARIGYYKQYCRQ	239
Db	199	SDAVVSFKTALWYWKVKVQSVTSQGFATIRAIN-SIECNGGSPDAVNSRVSLNSYCSK	257
Qy	240	LGVDPGPNLTC	250
Db	258	FGVAPGDNQRC	268

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:21:21 ; Search time 112.919 Seconds  
(without alignments)  
1133.730 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYKQYKQLGVDPGNLTC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1351	96.0	279	2 Q6JBP8	Q6jbp8 zea mays (s
2	1345.5	95.6	280	2 Q6JBQ0	Q6jbp0 zea mays (s
3	1345.5	95.6	286	2 Q6JBQ4	Q6jbp4 zea mays (s
4	1338.5	95.1	286	2 Q6JBP3	Q6jbp3 zea diplope
5	1336.5	94.9	278	2 Q6JBP7	Q6jbp7 zea diplope
6	1336.5	94.9	284	2 Q6JBQ9	Q6jbp9 zea mays (s
7	1335.5	94.9	278	2 Q6JBP2	Q6jbp2 zea diplope
8	1335.5	94.9	278	2 Q6JBP5	Q6jbp5 zea diplope
9	1335.5	94.9	280	2 Q6JBP9	Q6jbp9 zea mays (s
10	1335.5	94.9	280	2 Q6JBQ2	Q6jbp2 zea mays (s
11	1335.5	94.9	280	2 Q6JBQ8	Q6jbp8 zea mays (s
12	1332.5	94.6	282	2 Q6JBQ6	Q6jbp6 zea mays (s
13	1331.5	94.6	280	2 Q6JBQ7	Q6jbp7 zea mays (s
14	1329.5	94.4	282	2 Q6JBQ3	Q6jbp3 zea mays (s
15	1329	94.1	281	2 Q6JBQ1	Q6jbp1 zea mays (s
16	1325	94.1	281	2 Q6JBQ5	Q6jbp5 zea mays (s
17	1323	94.0	279	2 Q6JBQ5	Q6jbp5 zea mays (s
18	1314.5	93.4	269	1 CH1B_MAIZE	P29023 zea mays (m
19	1301	92.4	282	2 Q6JBR2	Q6jbr2 tripsacum d
20	1279	90.8	277	2 Q6JBK3	Q6jbk3 zea mays (s
21	1278	90.8	274	2 Q6JBK1	Q6jbk1 zea diplope
22	1277	90.7	276	2 Q6JBK0	Q6jbk0 zea diplope
23	1273.5	90.4	276	2 Q6JBK2	Q6jbk2 zea mays (s
24	1272.5	90.4	280	2 Q6JBK9	Q6jbk9 zea mays (s
25	1271	90.3	278	2 Q6JBK4	Q6jbk4 zea mays (s
26	1270.5	90.2	276	2 Q6JBL1	Q6jbl1 zea mays (s
27	1269	90.1	277	2 Q6JBK6	Q6jbk6 zea mays (s
28	1268.5	90.1	274	2 Q6JBL4	Q6jbl4 zea mays (s
29	1266.5	90.0	278	2 Q6JBL5	Q6jbl5 zea mays (s
30	1265.5	89.9	280	2 Q6JBK8	Q6jbk8 zea mays (s
31	1264	89.8	279	2 Q6JBL0	Q6jbl0 zea mays (s

32	1263.5	89.7	276	2 Q6JBK7	Q6jbk7 zea mays (s
33	1263.5	89.7	278	2 Q6JBL3	Q6jbl3 zea mays (s
34	1258.5	89.4	280	1 CH1A_MAIZE	P29022 zea mays (m
35	1224	86.9	261	2 Q94EL5	Q94el5 saccharum d
36	1211	86.0	277	2 Q6JBL6	Q6jbl6 tripsacum d
37	1175.5	83.5	261	2 Q94EL3	Q94el3 sorghum bal
38	1135	80.6	262	2 Q93WT2	Q93wt2 sorghum bic
39	1130	80.3	262	2 Q94LL5	Q94ll5 sorghum bic
40	1129	80.2	272	2 Q93WT1	Q93wt1 sorghum bic
41	1127	80.0	262	2 Q94ELA	Q94el4 sorghum aru
42	1011.5	71.8	288	2 Q7Y120	Q7y120 oryza sativ
43	974	69.2	285	2 Q7XU64	Q7xu64 oryza sativ
44	942	66.9	264	2 Q7XAU6	Q7xau6 vitis vinif
45	926	65.8	264	2 Q24531	Q24531 vitis vinif

ALIGNMENTS

RESULT 1  
Q6JBP8 PRELIMINARY; PRT; 279 AA.  
AC Q6JBP8; 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Chitinase.  
GN Name=chiB;  
OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=76912;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
RA Tiffin P.;  
RT "Comparative evolutionary histories of chitinase genes in the genus  
ze and family poaceae.";  
RL Genetics 167:1331-1340(2004).  
DR EMBL; AY532735; AAT40004.1; -.  
DR EMBL; AY532723; AAT39992.1; -.  
DR HSSP; P10969; 1KTV.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0004568; F:chitinase activity; IEA.  
DR GO; GO:0016998; P:cell wall catabolism; IEA.  
DR GO; GO:0006032; P:chitin catabolism; IEA.  
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
DR InterPro; IPR002086; Aldehyd dehydrog.  
DR InterPro; IPR001002; Chitin binding\_1.  
DR InterPro; IPR000726; Glyco\_hydro\_19.  
DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
DR PRINTS; PR00451; CHITINBINDING.  
DR ProDom; PD000609; Chitin binding\_1; 1.  
DR ProDom; PD354900; Glyco\_hydro\_19; 1.  
DR SMART; SM00270; ChtdB1; 1.  
DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
DR PROSITE; PS00026; CHIT\_BIND\_1; 1.  
DR PROSITE; PS50941; CHIT\_BIND\_2; 1.  
KW Chitin-binding.  
SQ SEQUENCE 279 AA; 28925 MW; 8F38B91DE3B48BE6 CRC64;

Query Match 96.0%; Score 1351; DB 2; Length 279;  
Best Local Similarity 96.0%; Pred. No. 4.7e-102;  
Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 QNCQCPNVCCSKFGYCGTTDEYCGDQCQSGGSGGGGANVASVVTGSFFNGI 62  
Db 32 QNCQCPNVCCSKFGYCGTTDEYCGDQCQSGGSGGGGANVASVVTGSFFNGI 91  
Qy 63 KNQAGSCGCKNFTYRSNFLSAVKAYPGFANGSGVQVKREIAAFPAHATHETGHFCYIS 122

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Db 92 KSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGHFCYIS 151
Qy 123 ELSKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 182
Db 152 EINKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211
Qy 183 VVAFKAALWFWMNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIQYKYQYCRQLGV 242
Db 212 VVAFKAALWFWMNSVHGVVPPQGFATIRAINGALECGGNNPAQMNARVGYRYQYCRQLGV 271
Qy 243 DPGPNLTC 250
Db 272 DPGPNLTC 279

RESULT 2
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AC Q6JBQ0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Baleas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532733; AAT40002.1; -.
DR HSSP; P10369; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0006098; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00026; CHIT_BIND_1_2; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 28993 MW; 7B6E2DA395C32FDB CRC64;

Query Match 95.6%; Score 1345.5; DB 2; Length 280;
Best Local Similarity 96.0%; Pred. No. 1.3e-101;
Matches 239; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGSGGGANVASVVTGSPFNG 61
Db 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGSGGGANVASVVTGSPFNG 91
Qy 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGHFCYI 121
Db 92 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGHFCYI 151
Qy 122 SEISKSNAAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
Qy 122 SEISKSNAAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181

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Db 152 SEISKSNAAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211
Qy 182 AVAFKAALWFWMNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIQYKYQYCRQLG 241
Db 212 AVAFKAALWFWMNSVHGVVPPQGFATIRAINGALECGGNNPAQMNARVGYRYQYCRQLG 271
Qy 242 VDPGNLTC 250
Db 272 VDPGNLTC 280

RESULT 3
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AC Q6JBQ4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Baleas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532729; AAT39998.1; -.
DR HSSP; P10369; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0006098; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00026; CHIT_BIND_1_2; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 283 AA; 29405 MW; 551581B126791A58 CRC64;

Query Match 95.6%; Score 1345.5; DB 2; Length 283;
Best Local Similarity 96.0%; Pred. No. 1.3e-101;
Matches 239; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGSGGGANVASVVTGSPFNG 61
Db 35 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGSGGGANVASVVTGSPFNG 94
Qy 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGHFCYI 121
Db 95 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGHFCYI 154
Qy 122 SEISKSNAAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
Db 155 SEISKSNAAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 214
Qy 182 AVAFKAALWFWMNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIQYKYQYCRQLG 241

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||||| 215 AVAFKALWFMWNSVHGVPQFGATTAINGALECCGNPAQNNARVYTRQCRQUG 274
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AC Q6JBP3;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532740; AAT40009.1; -.
DR HSP; P10969; IK7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 286 AA; 29352 MW; 7577FEE94C0773A CRC64;

Query Match 95.1%; Score 1338.5; DB 2; Length 286;
Best Local Similarity 93.3%; Pred. No. 5e-101;
Matches 238; Conservative 6; Mismatches 4; Indels 7; Gaps 1;

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QY 56 GSPFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAFAFAHATHET 115
DB 92 GSFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAFAFAHATHET 151

QY 116 GHFCYISISKSNAYCDPTKQWPCAAQKYYGRGFLQISWNYNGPAGRDIGPDLGDP 175
DB 152 GHFCYISINKSNAYCDPSKQWPCAAQKYYGRGFLQISWNYNGPAGRAIGPDLGDP 211

QY 176 GRVARDVAVPAKALWFMWNNVHRVMPQGFATIRAINGALECCGNPAQNNARIGYYKQ 235
DB 212 GRVARDVAVPAKALWFMWNSVHGVPQFGATTAINGALECCGNPAQNNARVYTRQ 271

QY 236 YCRQLGVDPGNLTC 250
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AC Q6JBP7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532736; AAT40005.1; -.
DR HSP; P10969; IK7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 278 AA; 28838 MW; 8D65AB2FCE9D1585 CRC64;

Query Match 94.9%; Score 1336.5; DB 2; Length 278;
Best Local Similarity 95.6%; Pred. No. 7e-101;
Matches 237; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGSSGGGANVASVVTGSFFNGI 62
DB 32 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGSSGGGANVASVVTGSFFNGI 90

QY 63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAFAFAHATHETGHFCYIS 122
DB 91 KSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAFAFAHATHETGHFCYIS 150

QY 123 EISKSNAYCDPTKQWPCAAQKYYGRGFLQISWNYNGPAGRDIGPDLGDPGRVARD 182
DB 151 EINKSNAYCDPTKQWPCAAQKYYGRGFLQISWNYNGPAGRAIGPDLGDPGRVARD 210

QY 183 VVAFKALWFMWNNVHRVMPQGFATIRAINGALECCGNPAQNNARIGYYKQYCRQLGV 242
DB 211 VVAFKALWFMWNSVHGVPQFGATTAINGALECCGNPAQNNARVYTRQYCRQLGV 270

QY 243 DPGNLTC 250
DB 271 DPGNLTC 278
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RESULT 6
Q6JBQ9 ID Q6JBQ9 PRELIMINARY; PRT; 284 AA.
AC Q6JBQ9
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532724; AAT39993.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 284 AA; 29256 MW; B210BB7C204A6567 CRC64;

Query Match 94.9%; Score 1336.5; DB 2; Length 284;
Best Local Similarity 93.7%; Pred. No. 7.2e-101;
Matches 237; Conservative 7; Mismatches 4; Indels 5; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGG-----SSGGGGANVASVVTGS 57
Db 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSSSGGGGANVASVVTGS 91

QY 58 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 117
Db 92 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 151

QY 118 FCIYSEISKSNAYCDPTKRWPCAAQKQYGRGPIQISWNNYGPAGRDIGFDGLGDPGR 177
Db 152 FCIYSEINKSNAYCDPSKRWPCAAQKQYGRGPIQISWNNYGPAGKAIGFDGLGDPGR 211

QY 178 VARDAAVAFKAALWFMMNVHRVMPQGFATIRANGALECDGNPNPQMNARIIGYKQYC 237
Db 212 VARDAAVAFKAALWFMMNVHRVMPQGFATIRANGALECDGNPNPQMNARVGYRQYC 271

QY 238 RQLGVDPGNLTC 250
Db 272 RQLGVDPGNLTC 284

RESULT 7
Q6JB2 ID Q6JB2 PRELIMINARY; PRT; 278 AA.
AC Q6JB2

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGG-----SSGGGGANVASVVTGS 57
Db 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGSSSSGGGGANVASVVTGS 91

QY 58 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 117
Db 92 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 151

QY 118 FCIYSEISKSNAYCDPTKRWPCAAQKQYGRGPIQISWNNYGPAGRDIGFDGLGDPGR 177
Db 152 FCIYSEINKSNAYCDPSKRWPCAAQKQYGRGPIQISWNNYGPAGKAIGFDGLGDPGR 211

QY 178 VARDAAVAFKAALWFMMNVHRVMPQGFATIRANGALECDGNPNPQMNARIIGYKQYC 237
Db 212 VARDAAVAFKAALWFMMNVHRVMPQGFATIRANGALECDGNPNPQMNARVGYRQYC 271

QY 238 RQLGVDPGNLTC 250
Db 272 RQLGVDPGNLTC 284

RESULT 8
Q6JB5 ID Q6JB5 PRELIMINARY; PRT; 278 AA.
AC Q6JB5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 26, Last annotation update)
DE Chitinase.

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GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT Zea and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532738; AAT40007.1; -.
DR EMBL; AY532739; AAT40008.1; -.
DR EMBL; AY532742; AAT40011.1; -.
DR EMBL; AY532737; AAT40006.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0004698; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR PRINTS; PR00182; Chitin binding_1.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000609; Glyco_hydro_19; 1.
DR SMART; SM00270; Chitinase.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE 19_1; 1.
DR PROSITE; PS00774; CHITINASE 19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 278 AA; 29024 MW; 6DDA23E340CA0610 CRC64;

Query Match 94.9%; Score 1335.5; DB 2; Length 278;
Best Local Similarity 95.6%; Pred. No. 8.5e-101;
Matches 237; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 3 QNCCQPNVCCSKFYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNGI 62
DB 32 QNCCQPNVCCSKFYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNGI 90

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYIS 122
DB 91 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYIS 150

QY 123 EISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYNGPAGRDIGFDGLGDPGRVARD 182
DB 151 EINKSNAYCDPSKRWPCAAQKYYGRGPLQISWNNYNGPAGRAIGFDGLGDPGRVARD 210

QY 183 VVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNPAQNNARIYYKYQYCRQLGV 242
DB 211 VVAFKAALWFWMNSVHGVVPGFGATIRAINGALECGGNNPAQNNARVGYTRYQYCRQLGV 270

QY 243 DPGPNLTC 250
DB 271 DPGPNLTC 278

RESULT 9
Q6JBP9 PRELIMINARY; PRT; 280 AA.
AC Q6JBP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
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OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT Zea and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532734; AAT40003.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0004698; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR SMART; SM00270; Chitinase.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE 19_1; 1.
DR PROSITE; PS00774; CHITINASE 19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 29009 MW; 64BB647946D9F05F CRC64;

Query Match 94.9%; Score 1335.5; DB 2; Length 280;
Best Local Similarity 95.2%; Pred. No. 8.5e-101;
Matches 237; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 3 QNCCQPNVCCSKFYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNG 61
DB 32 QNCCQPNVCCSKFYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNG 91

QY 62 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYI 121
DB 92 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYI 151

QY 122 SEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNNYNGPAGRDIGFDGLGDPGRVARD 181
DB 152 SEINKSNAYCDPSKRWPCAAQKYYGRGPLQISWNNYNGPAGRAIGFDGLGDPGRVARD 211

QY 182 AVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNPAQNNARIYYKYQYCRQLG 241
DB 212 AVAFKAALWFWMNSVHGVVPGFGATIRAINGALECGGNNPAQNNARVGYTRYQYCRQLG 271

QY 242 VDPGNLTC 250
DB 272 VDPGNLTC 280

RESULT 10
Q6JBQ2 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
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OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RL zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532731; AAT4000.1; -.  
 DR HSSP; P10969; 1KTV.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; P:chitinase activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR001002; Chitin binding\_1.  
 DR Pfam; PF00182; Glyco\_hydro\_19.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR ProDom; PD034900; Glyco\_hydro\_19; 1.  
 DR SMART; SM00270; ChtBD1; 1.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN\_1.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE; PS00026; CHIT\_BIND\_1\_1; 1.  
 DR PROSITE; PS50941; CHIT\_BIND\_1\_2; 1.  
 KW Chitin-binding.  
 SQ SEQUENCE 280 AA; 28963 MW; 60FA61748883998 CRC64;  
  
 Query Match 94.9%; Score 1335.5; DB 2; Length 280;  
 Best Local Similarity 95.2%; Pred. No. 8.5e-101;  
 Matches 237; Conservative 5; Mismatches 6; Indels 1; Gaps 1;  
  
 QY 3 QNCCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61  
 DB |||||  
 QY 32 QNCCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 91  
 DB |||||  
 QY 62 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFAHATHETGHFCYI 121  
 DB |||||  
 QY 92 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFAHATHETGHFCYI 151  
 DB |||||  
 QY 122 SEISKSNAVCPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181  
 DB |||||  
 QY 152 SEISKSNAVCPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211  
 DB |||||  
 QY 182 AVAFAKALWFMMNVRHVPQGFATIRAINGALECDGNPAQNNARIQYKQYCRQLG 241  
 DB |||||  
 QY 212 AVAFAKALWFMMNVRHVPQGFATIRAINGALECDGNPAQNNARIQYKQYCRQLG 271  
 DB |||||  
 QY 242 VDPGNLTC 250  
 DB |||||  
 QY 272 VDPGNLTC 280  
 DB |||||  
  
 RESULT 11  
 Q6JB08 PRELIMINARY; PRT; 280 AA.  
 ID Q6JB08  
 AC Q6JB08; 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DE Chitinase.  
 GN Name=chiB;  
 OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;

RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RL zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532725; AAT39994.1; -.  
 DR HSSP; P10969; 1KTV.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; P:chitinase activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR001002; Chitin binding\_1.  
 DR Pfam; PF00182; Glyco\_hydro\_19.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR ProDom; PD034900; Glyco\_hydro\_19; 1.  
 DR SMART; SM00270; ChtBD1; 1.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN\_1.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE; PS00026; CHIT\_BIND\_1\_1; 1.  
 DR PROSITE; PS50941; CHIT\_BIND\_1\_2; 1.  
 KW Chitin-binding.  
 SQ SEQUENCE 280 AA; 28922 MW; 7FCE9A0996867FCA CRC64;  
  
 Query Match 94.9%; Score 1335.5; DB 2; Length 280;  
 Best Local Similarity 95.2%; Pred. No. 8.5e-101;  
 Matches 237; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
  
 QY 3 QNCCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61  
 DB |||||  
 QY 32 QNCCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 91  
 DB |||||  
 QY 62 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFAHATHETGHFCYI 121  
 DB |||||  
 QY 92 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFAHATHETGHFCYI 151  
 DB |||||  
 QY 122 SEISKSNAVCPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181  
 DB |||||  
 QY 152 SEISKSNAVCPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211  
 DB |||||  
 QY 182 AVAFAKALWFMMNVRHVPQGFATIRAINGALECDGNPAQNNARIQYKQYCRQLG 241  
 DB |||||  
 QY 212 AVAFAKALWFMMNVRHVPQGFATIRAINGALECDGNPAQNNARIQYKQYCRQLG 271  
 DB |||||  
 QY 242 VDPGNLTC 250  
 DB |||||  
 QY 272 VDPGNLTC 280  
 DB |||||  
  
 RESULT 12  
 Q6JB06 PRELIMINARY; PRT; 282 AA.  
 ID Q6JB06  
 AC Q6JB06; 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DE Chitinase.  
 GN Name=chiB;  
 OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RL zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).

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DR EMBL; AY532727; AAT39996.1; -.
DR HSSP; P10969; 1KTV.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR00726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR ProDom; PD00609; Chitin binding_1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 282 AA; 29133 MW; FBB060F48CA67945 CRC64;

Query Match          94.6%; Score 1332.5; DB 2; Length 282;
Best Local Similarity 94.8%; Pred. No. 1.5e-100;
Matches 236; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61
DB 34 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 93

QY 62 IKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGGSVQVQKREIAAFPAHAHETHGHFCYI 121
DB 94 IKSQAGSGCEGKFNFTSAFLSAVKAYPGFAHGGSVQVQKREIAAFPAHAHETHGHFCYI 153

QY 122 SEIKSNAYCDPTKQWPCAGQKYGRGPIQISWNYNYPAGRDIGFDGLDGPGRVARD 181
DB 154 SEIKSNAYCDPTKQWPCAGQKYGRGPIQISWNYNYPAGRDIGFDGLDGPGRVARD 213

QY 182 AVAFKALWFMNNVHVRMPQGFATIRANGALECDGNNPAQNNARIGYKYKQCRQLG 241
DB 214 AVAFKALWFMNNVHVRMPQGFATIRANGALECDGNNPAQNNARIGYKYKQCRQLG 273

QY 242 VDPGNLTC 250
DB 274 VDPGNLTC 282

RESULT 13
Q6JBQ7 ID Q6JBQ7 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532726; AAT39995.1; -.
DR HSSP; P10969; 1KTV.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.

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DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR00726; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 28965 MW; 47102378A9B6799D CRC64;

Query Match          94.6%; Score 1331.5; DB 2; Length 280;
Best Local Similarity 94.8%; Pred. No. 1.8e-100;
Matches 236; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61
DB 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 91

QY 62 IKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGGSVQVQKREIAAFPAHAHETHGHFCYI 121
DB 92 IKNQAGSGCEGKFNFTSAFLSAVKAYPGFAHGGSVQVQKREIAAFPAHAHETHGHFCYI 151

QY 122 SEIKSNAYCDPTKQWPCAGQKYGRGPIQISWNYNYPAGRDIGFDGLDGPGRVARD 181
DB 152 SEIKSNAYCDPTKQWPCAGQKYGRGPIQISWNYNYPAGRDIGFDGLDGPGRVARD 211

QY 182 AVAFKALWFMNNVHVRMPQGFATIRANGALECDGNNPAQNNARIGYKYKQCRQLG 241
DB 212 AVAFKALWFMNNVHVRMPQGFATIRANGALECDGNNPAQNNARIGYKYKQCRQLG 271

QY 242 VDPGNLTC 250
DB 272 VDPGNLTC 280

RESULT 14
Q6JBQ3 ID Q6JBQ3 PRELIMINARY; PRT; 282 AA.
AC Q6JBQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532730; AAT39999.1; -.
DR HSSP; P10969; 1KTV.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.

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DR InterPro; IPR001002; Chitin binding_1.
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DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00026; CHIT_BIND_I_2; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 282 AA; 29147 MW; 4E10632A4F979D20 CRC64;

Query Match          94.4%; Score 1329.5; DB 2; Length 282;
Best Local Similarity 94.8%; Pred. No. 2.6e-100;
Matches 236; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

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DB 34 QNCGCQPNVCCSKFGYCGTTDEYCGDCGCGSQGSPCRSGGGGGGGGGANVASVVTSSPFNG 93

QY 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETHGFCYI 121
DB 94 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETHGFCYI 153

QY 122 SEISKSNAVCDDPTKQWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
DB 154 SEISKSNAVCDDPTKQWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 213

QY 182 AVVAFAKALWFMMNHNVRVMPQGFATIRAINGALCECDGNPAQMNARIGYYKQYCRQLG 241
DB 214 AVVAFAKALWFMMNHNVRVMPQGFATIRAINGALCECDGNPAQMNARIGYYKQYCRQLG 273

QY 242 VDPGPNLTC 250
DB 274 VDPGPNLTC 282

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## RESULT 15

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chIB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532722; AAT39991.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; F:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.

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DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00026; CHIT_BIND_I_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 281 AA; 28979 MW; C23523FE12D986A6 CRC64;

Query Match          94.4%; Score 1329; DB 2; Length 281;
Best Local Similarity 94.4%; Pred. No. 2.9e-100;
Matches 236; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

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DB 32 QNCGCQPNVCCSKFGYCGTTDEYCGDCGCGSQGSPCRSGGGGGGGGGANVASVVTGSPFN 91

QY 61 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETHGFCY 120
DB 92 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETHGFCY 151

QY 121 SEISKSNAVCDDPTKQWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
DB 152 SEISKSNAVCDDPTKQWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVAR 211

QY 181 DAVVAFAKALWFMMNHNVRVMPQGFATIRAINGALCECDGNPAQMNARIGYYKQYCRQL 240
DB 212 DAVVAFAKALWFMMNHNVRVMPQGFATIRAINGALCECDGNPAQMNARIGYYKQYCRQL 271

QY 241 GVDPGPNLTC 250
DB 272 GVDPGPNLTC 281

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Search completed: May 24, 2005, 12:54:17  
Job time : 113.919 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:37:22 ; Search time 2973.37 Seconds  
(without alignments)  
4074.095 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFYCG.....GYKQYCRQLGVDPGNLTC 250

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
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2: gb.htg.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.ey.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1351	96.0 1094 6	AR321624 Sequence
2	1314.5	93.4 810 8	M84165 Zea mays ch
3	1312.5	93.2 1121 8	AY532735 Zea mays
4	1306.5	92.8 1127 8	AY532733 Zea mays

5	1299	92.3	1081	8	AY532737	AY532737 Zea diplo
6	1299	92.3	1081	8	AY532738	AY532738 Zea diplo
7	1299	92.3	1081	8	AY532742	AY532742 Zea diplo
8	1299	92.3	1127	8	AY532723	AY532723 Zea mays
9	1298	92.2	1114	8	AY532725	AY532725 Zea mays
10	1294	91.9	1123	8	AY532729	AY532729 Zea mays
11	1293.5	91.9	1133	8	AY532727	AY532727 Zea mays
12	1292.5	91.8	1123	8	AY532726	AY532726 Zea mays
13	1287.5	91.4	1128	8	AY532740	AY532740 Zea diplo
14	1286	91.3	1126	8	AY532732	AY532732 Zea mays
15	1285	91.3	1138	8	AY532724	AY532724 Zea mays
16	1284.5	91.2	1122	8	AY532736	AY532736 Zea diplo
17	1281.5	91.0	1140	8	AY532731	AY532731 Zea mays
18	1279.5	90.9	1080	8	AY532739	AY532739 Zea diplo
19	1278	90.8	1134	8	AY532734	AY532734 Zea mays
20	1277.5	90.7	1111	8	AY532741	AY532741 Zea diplo
21	1271	90.3	1127	8	AY532730	AY532730 Zea mays
22	1270.5	90.2	1130	8	AY532722	AY532722 Zea mays
23	1262	89.6	1138	8	AY532728	AY532728 Zea mays
24	1258.5	89.4	843	8	MZBCHITA	M84164 Zea mays ch
25	1243.5	88.3	1104	8	AY532782	AY532782 Zea diplo
26	1242.5	88.2	985	8	AY532721	AY532721 Tripsacum
27	1242.5	88.2	1107	8	AY532781	AY532781 Zea diplo
28	1242.5	88.2	1110	8	AY532783	AY532783 Zea diplo
29	1242.5	88.2	1110	8	AY532784	AY532784 Zea diplo
30	1242.5	88.2	1110	8	AY532785	AY532785 Zea diplo
31	1242.5	88.2	1110	8	AY532786	AY532786 Zea diplo
32	1242.5	88.2	1110	8	AY532787	AY532787 Zea diplo
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34	1242.5	88.2	1131	8	AY532780	AY532780 Zea mays
35	1237	87.9	1122	8	AY532771	AY532771 Zea mays
36	1234	87.6	1104	8	AY532772	AY532772 Zea mays
37	1233	87.6	1115	8	AY532768	AY532768 Zea mays
38	1232	87.5	1120	8	AY532769	AY532769 Zea mays
39	1230	87.4	1101	8	AY532770	AY532770 Zea mays
40	1227	87.1	1127	8	AY532776	AY532776 Zea mays
41	1217.5	86.5	1094	8	AY532778	AY532778 Zea mays
42	1217.5	86.5	1094	8	AY532779	AY532779 Zea mays
43	1216.5	86.4	1132	8	AY532774	AY532774 Zea mays
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ALIGNMENTS

RESULT 1  
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LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6563020.  
ACCESSION AR321624  
VERSION AR321624.1 GI:33706864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1. (bases 1 to 1094)  
AUTHORS Simmons,C.R. and Yalpani,N.  
TITLE Maize chitinases and their use in enhancing disease resistance in crop plants  
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .1094  
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Score:	98.39%	Conservative:	6
Percent Similarity:	95.97%	Mismatches:	4
Best Local Similarity:	95.95%	Indels:	0
Query Match:	6	Gaps:	0
DB:			

US-10-692-367-70 (1-250) x AR321624 (1-1094)		MEDLINE 92202208 PUBMED 1551872 COMMENT Original source text: Zea mays (library: Lamda GT 10 corn seed (imbibed)) seed DNA. FEATURES source 1. .810 /organism="Zea mays" /mol_type="genomic DNA" /db_xref="taxon:4577" /tissue_type="seed" /tissue_lib="Lamda GT 10 corn seed (imbibed)" 1. .810 /gene="seed chitinase" 1. .810 /gene="seed chitinase" /codon_start=1 /evidence=experimental /product="chitinase B" /protein_id="AAA33445.1" /db_xref="GI:168443" /translation="POLVALGLALLCAVAGPAAQNGCOPNVCCSKFGYCGTTDEYCGDCQSGPCBSRGSGSGGGANVASVVTSSPENGKNOAGSGCEKNFVTRSAFLS AVAGYPPGPHGGSQVKRIEIAAPFAHAHETHGFCYISINKSNAYCDTQKQWPCA AGQKYYGRGPLEQISWNYNYGPAGRAIGFDGLDGPGRVADAVAFKAALWFMNWSVHG VVPQGFATTRAMQRALECGGNPNPAQWNAFVGYRYOYCRQLGVDPPGNLTC"
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Qy	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGly----GlyGlyGly 41
Db	121	GACGAGTACTGTGCGCAGCGGTGCGAGTCCGGCGCCGTCGCGCTCGGGCCGGCGGGCGGC 180
Qy	42	SerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGly 61
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Qy	62	IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe 81
Db	241	ATCAAGAACCAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCGAGCGCGTTC 300
Qy	82	LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyLys 101
Db	301	CTGAGCGCGTCAAGGGCTACCCAGGGCTTCGCCCATGCGGGTCGCAAGTGCGAGGGCAAG 360
Qy	102	ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIle 121
Db	361	CGCGAGATCGCGCTTCTTCGGCGCACGCCACGACGAGACCGGGGCATTTCTGTACTATC 420
Qy	122	SerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141
Db	421	AGCGAGATCAACAAGCAACGCTACTGCGACCCGACCAAGAGGCGAGTGGCGCGTGGCC 480
Qy	142	AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161
Db	481	GCGGGGCAGAAGTACTACGGGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGGG 540
Qy	162	ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
Db	541	CCCCCGGGAGGGCCATCGGCTTCGACGGGCTCGGGGACCCCGGACGGGTGGCGGGGAC 600
RESULT 2		
MZCHITB		
LOCUS		810 bp DNA linear PLN 27-APR-1993
DEFINITION		Zea mays chitinase B (seed chitinase) gene, 3' end.
ACCESSION		M84165
VERSION		M84165.1 GI:168442
KEYWORDS		chitinase B.
SOURCE		Zea mays
ORGANISM		Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
1 (bases 1 to 810)		
Huynh, Q.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.		
Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed		
J. Biol. Chem. 267 (10), 6635-6640 (1992)		

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Qy 182 AlaValValAlaPheLysAlaAlaLeuTTPheTTPMetAenValHisArgValMet 201
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Db 661 CCGCAGGGGTTCCGGCGCCACCACCGAGGCCATGCAACCGGCCCTCGAGTGGCGGGGAC 720
Qy 222 AsnProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 721 AACCCCGCCAGATGAACCGCGCTCGGTCTACTACAGGAGTACTGCCCGCAGCTCGGC 780
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 781 GTCGACCCCGGGCCCAACCTCACCTGC 807

RESULT 3
AY532735
LOCUS
DEFINITION
Zea mays subsp. parviglumis isolate p15 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532735
VERSION
AY532735.1 GI:48093251
KEYWORDS
Zea mays subsp. parviglumis
SOURCE
Zea mays subsp. parviglumis
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1121)
AUTHORS
Tiffin, P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1121)
AUTHORS
Tiffin, P.
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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LTC"

ORIGIN
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Score: 1312.50 Matches: 237
Percent Similarity: 84.08% Conservative: 6
Best Local Similarity: 82.01% Mismatches: 5
Query Match: 93.22% Indels: 41

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DB:
US-10-692-367-70 (1-250) x AY532735 (1-1121)
Gaps: 1

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 107 CAGNACTGGGCTGCCAGCCAAACGATATGTCAGCANGTTTGGCTACTGGGCGACGACC 166
Qy 23 AspGlnTyrCysGlyAseGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 167 GACGAGTACTTCGCGCGACGCGGTCCAGTCCGGGCGCGTCCGGCGCGCGCGCAGC 226
Qy 43 SerGlyGlyGlyGlyAlaAenValAlaSerValValThrGlySerPheAenGlyIle 62
Db 227 AGTGGCGCGGTGGTGGAAACGGCTAGCGTGTCAACCGGCTCTCTTCTTCAACGGGATC 286
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 287 AAGAGCCAGCGCGGAGCGGTCCGAGGCGCAAGAACTTCTACACCGGAGCGCTTCTGTG 346
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 347 AGCGCGCTCAAGGCGTACCAGCGCTTCGCCCATCGCGGTCCGAGGTGCAGGGCAAGCGC 406
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis 117
Db 407 GAGATCGCGCCTTCTTCGCGCACGCCACGACGAGACCGGGCGTAAGTTGGCTCGCTCT 466
Qy 117 ----- 117
Db 467 TCAGCGCGCGCAGGTCTTTGATTTTAAATTGACCCATCATGCTCATCAATTTATTT 526
Qy 118 -----PheCysTyrIle 121
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Qy 122 SerGluIleSerLysSerAenAlaTyrCysAseProThrLysArgGlnTTPProCysAla 141
Db 587 AGCGAGATCAACAAAGAGCAACGCGCTACTGCGACCGGACCAAGAGGAGTGGCGCGCGCC 646
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTTPAenTyrAsnTyrGly 161
Db 647 CGCGGCGCAGAGTACTACGGCGCGCGCCGCTGCAGATCTCTGGAACTACACTACGGG 706
Qy 162 ProAlaGlyArgAsePheGlyPheAseGlyLeuGlyAseProGlyArgValAlaAArgAse 181
Db 707 CCGCGCGGAGGCGCATCGGCTTCGACGGCTCGGGGACCCCGCAGGCGTGGCGCGGAC 766
Qy 182 AlaValValAlaPheLysAlaAlaLeuTTPheTTPMetAenValHisArgValMet 201
Db 767 GCGTGGTGGCGTTCAAGCGCGCGCTCTGGTTCTGGATGAACAGCGTGCACGGGTGGTG 826
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAseGlyAse 221
Db 827 CCGCAGGGGTTCCGGCGCCACCACCGAGGCCATCAACGGCGCCCTCGAGTGGCGGGGAC 886
Qy 222 AsnProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 887 AACCCCGCCAGATGAACCGCGCTCGGTCTACTACAGGAGTACTGCCCGCAGCTCGCGC 946
Qy 242 ValAspProGlyProAenLeuThrCys 250
Db 947 GTCGACCCCGGGCCCAACCTCACCTGC 973

RESULT 4
AY532733
LOCUS
DEFINITION
Zea mays subsp. parviglumis isolate p12 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532733
VERSION
AY532733.1 GI:48093247
KEYWORDS
Zea mays subsp. parviglumis
SOURCE

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CDS
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TC"

ORIGIN
Alignment Scores:
Pred. No.: 6,51e-91 Length: 1081
Score: 1299.00 Matches: 236
Percent Similarity: 84.91% Conservative: 6
Best Local Similarity: 82.81% Mismatches: 5
Query Match: 92.26% Indels: 38
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532737 (1-1081)

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Db 107 CAGAACTCGCGCTGCCAGCCAAACGCTGCTGTCAGCAAGTTCCGCTACTCGCGCACGACC 166
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 167 GACGAGTACTCGCGGACGCGGTGTCAGTTCGGGCCCGTCCGCTCG---GGCGCGGCGAGC 223
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyIle 62
Db 224 AGTGGCGCGGTGTCGGAACGTGGCTAGCTGCTGCTCACCAGCTCTCTTCTTCAACGGCATC 283
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyIysAsnPheTyrThrArgSerAlaPheLeu 82
Db 284 AAGAACCAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGCGGAGCGGCTTCCTG 343
Qy 83 SerAlaValIysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 344 AGCCCGTCAAGCGTACCAGGCTTCGCCATGCGCGGTGCGCAGGTGCGAGGCAAGCGC 403
Qy 103 GluIleAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117
Db 404 GAGATCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCGTAAAGTTGGCTCGGTCT 463
Qy 117 ----- 117
Db 464 TCCGCGCGCGCAGGTTCTTTGATTTTGTACCCATCATGCTGATCAATTTTTTTTTTTT 523
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Db 524 TTGMAAATTCGCTGCTGTGTGTCAGCGGCGAGATTCTGCTACATCAGCGAGATCAAC 583
Qy 126 LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLys 145
Db 584 AAGACCAACGCTTACTCGGACCCCAAGCAAGAGGCGAGTGGCGCGCGCGGCGGCGAG 643
Qy 146 TyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArg 165
Db 644 TACTACGGGCGCGCGCTGTCAGATCTCGTGGAACTTACAACTACGCGGCGCGCGGAGG 703
Qy 166 AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAla 185
Db 704 GCCATCGGCTTCGACGGGCTCGGGACCCCGCGAGGTGGCGCGGACGCGGTGGCG 763
Qy 186 PheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPhe 205
Db 764 TTCAAGCGCGGCTCTCGTTCTGATGAACAGCGTGCACGGGTGGTGGCGCGAGGGGTTTC 823
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Qy 206 GlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCysAspGlyAsnAsnProAlaGln 225
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Qy 226 MetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
Db 884 ATGACGCGCGCTCGGCTACTACAGGCATACCTGCGCCAGCTCGGCGTCGACCCCGG 943
Qy 246 ProAsnLeuThrCys 250
Db 944 CCCAACCTCACTGC 958

RESULT 6
LOCUS AY532738 1081 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea diploperennis isolate d4 chitinase (chiB) gene, complete cds.
ACCESSION AY532738
VERSION AY532738.1 GI:48093257
KEYWORDS
SOURCE Zea diploperennis
ORGANISM Zea diploperennis
REFERENCE 1. (bases 1 to 1081)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
Zealand family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2. (bases 1 to 1081)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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TC"

ORIGIN
Alignment Scores:
Pred. No.: 6,51e-91 Length: 1081
Score: 1299.00 Matches: 236
Percent Similarity: 84.91% Conservative: 6
Best Local Similarity: 82.81% Mismatches: 5
Query Match: 92.26% Indels: 38
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532738 (1-1081)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerIysPheGlyTyrCysGlyThrThr 22
Db 107 CAGAACTCGCGCTGCCAGCCAAACGCTGCTGTCAGCAAGTTCCGCTACTCGCGCACGACC 166
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 167 GACGAGTACTCGCGGACGCGGTGTCAGTTCGGGCCCGTCCGCTCG---GGCGCGGCGAGC 223
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyIle 62
Db 224 AGTGGCGCGGTGTCGGAACGTGGCTAGCTGCTGCTCACCAGCTCTCTTCTTCAACGGCATC 283
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyIysAsnPheTyrThrArgSerAlaPheLeu 82
Db 284 AAGAACCAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGCGGAGCGGCTTCCTG 343
Qy 83 SerAlaValIysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 344 AGCCCGTCAAGCGTACCAGGCTTCGCCATGCGCGGTGCGCAGGTGCGAGGCAAGCGC 403
Qy 103 GluIleAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117
Db 404 GAGATCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCGTAAAGTTGGCTCGGTCT 463
Qy 117 ----- 117
Db 464 TCCGCGCGCGCAGGTTCTTTGATTTTGTACCCATCATGCTGATCAATTTTTTTTTTTT 523
Qy 118 -----PheCysTyrIleSerGluIleSer 125
Db 524 TTGMAAATTCGCTGCTGTGTGTCAGCGGCGAGATTCTGCTACATCAGCGAGATCAAC 583
Qy 126 LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLys 145
Db 584 AAGACCAACGCTTACTCGGACCCCAAGCAAGAGGCGAGTGGCGCGCGCGGCGGCGAG 643
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Qy 166 AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAla 185
Db 704 GCCATCGGCTTCGACGGGCTCGGGACCCCGCGAGGTGGCGCGGACGCGGTGGCG 763
Qy 186 PheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPhe 205
Db 764 TTCAAGCGCGGCTCTCGTTCTGATGAACAGCGTGCACGGGTGGTGGCGCGAGGGGTTTC 823
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Db      524  TTGGAAATTCGGCTGCTGTGTGTCACCGGCAGATTTCGTCTACATCAGCGCATCAAC 583
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Db      584  AAGAGCAACGCTACTTGCACCAAGCAAGAGGAGTGGCGGTGCGCGCGGCGCAGAAG 643
Qy      146  TyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyProAlaGlyArg 165
Db      644  TACTACGGCGCGCGCGCTGCAGATCTCTGGGAACATACAACTACGGGCGCGCGGGAGG 703
Qy      166  AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAla 185
Db      704  GCCATCGGCTTCGACGGGCTCGGGACCCCGCAGGGTGGCGGCGGCGGTGGCG 763
Qy      186  PheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMetProGlnGlyPhe 205
Db      764  TTCAAGCGCGCGCTCTGGTCTTGATGAACAGCGTGCACGGGGTGGTGGCGCGAGGTTTC 823
Qy      206  GlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGlyAenAenProAlaGln 225
Db      824  GGCCGCCACCCAGGGGCTCATCAAGCGGCGCTTCAGAGTGGCGGCGCAACACCCGCGCAG 883
Qy      226  MetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
Db      884  ATGAACGGCGGTGGCTACTACAGGATACTTGGCGGCGAGTCTGGGCTCGACCCCGGG 943
Qy      246  ProAenLeuThrCys 250
Db      944  CCCAACCTCACCTGC 958

RESULT 8
LOCUS   AY532723
DEFINITION
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complete cds.
ACCESSION
AY532723
VERSION
AY532723.1 GI:48093227
KEYWORDS
Zea mays subsp. parviglumis
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1127)
REFERENCE
AUTHORS
Tiffin,P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
AUTHORS
Tiffin,P.
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Alignment Scores:
Pred. No.:      6.8e-91      Length:      1127
Score:          1299.00      Matches:    237
Percent Similarity: 83.51%      Conservative: 6
Best Local Similarity: 81.44%      Mismatches: 5
Query Match:     92.26%      Indels:    43
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US-10-692-367-70 (1-250) x AY532723 (1-1127)

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Db      107 CAGAACTGCGGCTGCCAGGCCAAGCATATGCTGCAGCAAGTTTGGCTACTCGCGGCACGACC 166
Qy      23  AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db      167 GACGAGTACTCGCGGACGCGGTGCCAGTCCGGCCCGTCCGCTCGGGCGGCGGCGGAGC 226
Qy      43  SerGlyGlyGlyGlyAlaAenValAaSerValValThrGlySerPheAenGlyIle 62
Db      227 AGTGGCGGCGTGGTGCAGACGTGGCTAGCGTGCACCGGCTCTTCTTCAACGGCATC 286
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Db      287 AAGAGCAGCGCCGGGAGCGGCTGCGAGGGCAAGAACTTCTACACCGGAGCGGCTTCTGTG 346
Qy      83  SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
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Qy      103 GluIleAlaAlaPhePheAlaHisAlaThrHisGlu----- 114
Db      407 GAGATCGCGCCCTTCTTGGCGCACGCCACGACGAGACCGGGCGTAAGCTGGCTCTATCT 466
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Qy      115 -----ThrGlyHis-PheCysTy 120
Db      527 ATTTTTCGAAAAATTTTCGGCTGCTGTGTGTGTCACCGGCGAGATTTCGCTA 586
Qy      120 rIleSerGluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCy 140
Db      587 CATCAGCGAGATCAACAAGAGCAACGCCTACTCGGACCCCGACCAAGAGGAGTGGCGGTG 646
Qy      140 sAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTy 160
Db      647 CGCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 706
Qy      160 rGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAr 180
Db      707 CGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 766
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Qy      200 lMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGl 220
Db      827 GGTGCGCGAGGGTTCGGCGCCACACAGGGCGCATCAACGGGCGGCTTCGAGTGGCGCGG 886
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Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
US-10-692-367-70 (1-250) x AY532725 (1-1114)			
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Db	107	CAGAACTGGGCTCCAGCCAAACGTTCTGTCGACGAGTTCGGCTACTCGGCGACGACC 166	
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Db	167	GACGAGTACTGCGCGCAGCGGTGCCAGTCCGGGCCCGCTCGCGCTCGGGCGCGCGCGGC 226	
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Db	227	AGCAGTGGCGCGGTGGTGGGAACGTGGGTAGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 286	
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Db	287	ATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCCGCGAGCGCTTC 346	
Qy	82	LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101	
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Qy	102	ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117	
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Qy	117	----- 117	
Db	467	TCCTCCGCGCGCGCAGGTCTTTGTGATTTTGTGACCCATCATGCTGATCAATTTCTTTT 526	
Qy	118	-----PheCysTyrLleSer 122	
Db	527	TTTTTTTGGAAATTCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 586	
Qy	123	GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142	
Db	587	GAGATCAACAGAGCAACCGCTACTCGACCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 646	
Qy	143	GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro 162	
Db	647	GGCGAGAGTACTACGGCGCGCGCGCTGCGATCTCGTGGAACTACAACTACGCGGCC 706	
Qy	163	AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182	
Db	707	GCGGGAGGCGCCATCGGCTTCGACGCGCTCGGGGACCCCGCGAGGGTGGCGGGAGCGCC 766	
Qy	183	ValValAlaPheLysAlaAlaLeuTyrTrpMetAsnValHisArgValMetPro 202	
Db	767	GTGTTGGCTTCAAGGGCGCGCTCTGGTTCGTGATGAACAGCGTGCACGGGGTGGTCCG 826	
Qy	203	GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsn 222	
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Qy	243	AspProGlyProAsnLeuThrCys 250	
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AUTHORS			
TITLE			
JOURNAL			
PUBMED			

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REFERENCE
AUTHORS Tiffin, P.
TITLE Direct Submission
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1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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ORIGIN
Alignment Scores:
Pred. No.: 1.64e-90 Length: 1123
Score: 1294.00 Matches: 238
Percent Similarity: 83.51% Conservative: 5
Best Local Similarity: 81.79% Mismatches: 5
Query Match: 91.90% Indels: 43
DB: 8 Gaps: 2
US-10-692-367-70 (1-250) x AY532729 (1-1123)
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Db 110 CAGAACTCGCGCTGCCAGCCAAAGCTCTGCTGCAGCAAGTTCCGCTACTCGCGCAGCAC 169
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 41
Db 170 GACGAGTACTCGCGGACGGTGCAGTCGGGCCCGCTGCCGCTCGGGCGCGCGGCGAGC 229
Qy 42 SerSerGlyGlyGlyAlaAasnValAlaSerValThrGlySerPhePheAasnGly 61
Db 230 AGCAGTGGCGCGCTGCTGCAGACGTGCTAGCGTCCGCTCGCGCTCGCGCGCGCGGCG 289
Qy 62 IleLysAenGlnAlaGlySerGlyCysGlnLysAenPheTyrThrArgSerAlaPhe 81
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Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db 350 CTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATCGCGGTGCGAGTGCAGGGCGAG 409
Qy 102 ArgGluLeuAlaAlaPhePheAlaHisAlaThrHisGlu 114
Db 410 CGCGAGATCGCGCTTCTTCGCGCAGCCACGACGAGACCGGGCGCTAAGTTGGCTCGG 469
Qy 114 ----- 114
Db 470 TCTTCGCGCGCGCAGAGTTCTTTGATTTTAAATTTGACCCATCATGCTGATCAATTTT 529
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220 YasnAasnProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLe 240
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950 CGGCGTGCACCCCGGGCCCAACCTCACCTGC 980
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LOCUS AY532727 1133 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea mays subsp. parviglumis isolate p5 chitinase (chIB) gene,
complete cda.
ACCESSION AY532727
VERSION AY532727.1 GI:48093235
KEYWORDS
SOURCE Zea mays subsp. parviglumis
ORGANISM Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Tiffin, P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1133)
AUTHORS Tiffin, P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Best Local Similarity: 80.76% Mismatches: 6
Query Match: 91.87% Indels: 43
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532727 (1-1133)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGly 41
Db 173 GAGCAGTACTCGCGGACGCGGTGCAGTCGGCGCGCGCTCGCGCGCGCGCGCGCG 232
Qy 42 SerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGly 61
Db 233 GGCAGTGGTGGCGGTGGTGGAGCTGGCTAGCGTGGCTACCGGCTCTCTTCAACGGC 292
Qy 62 IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe 81
Db 293 ATCAAGACCGAGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACACCGCGAGCGGTC 352
Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db 353 CTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATCGCGGGTGCAGAGTGCAGGGCAAG 412
Qy 102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117
Db 413 CGCGAGATCGCGCGCTTCTTCGCGCACGCCACGACGAGACCGCGCGCGTAAGTTGGCTCCG 472
Qy 117 ----- 117
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LOCUS Zea mays subsp. parviglumis isolate p4 chitinase (chiB) gene,
DEFINITION complete cds.
ACCESSION AY532726
VERSION AY532726.1 GI:48093233
KEYWORDS
SOURCE Zea mays subsp. parviglumis
ORGANISM Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1123)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
Zealand family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1123)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Query Match: 91.80% Indels: 43
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532726 (1-1123)

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QY 62 IleIysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe 81  
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QY 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101  
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VERSION AY532740.1 GI:48093261  
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SOURCE Zea diploperennis  
ORGANISM Zea diploperennis  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1128)  
Tiffin, P.  
Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
Genetics 167 (3), 1331-1340 (2004)  
15280246  
PUBMED  
2 (bases 1 to 1128)  
Tiffin, P.  
AUTHORS  
TITLE Direct Submission

JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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Query Match: 91.44% Indels: 48  
DB: 8 Gaps: 2

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ACCESSION
  AY532724
VERSION
  AY532724.1
KEYWORDS
  GI:48093229
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  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 1138)
REFERENCE
  AUTHORS
  TITLE
  Comparative evolutionary histories of chitinase genes in the genus
  Zea and family poaceae
  JOURNAL
  Genetics 167 (3), 1331-1340 (2004)
  PUBMED
  15280246
  REFERENCE
  2 (bases 1 to 1138)
  AUTHORS
  Tiffin, P.
  TITLE
  Direct Submission
  JOURNAL
  Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
  1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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  Query Match: 91.26% Indels: 47
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QY 78 ArgSerAlaPheLeuSerAlaValIysAlaTyrProGlyPheAlaHisGlyGlySerGln 97
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QY 117 His-PheCysTyrIleSerGluIleSerIysSerAsnAlaTyrCysAspProThrLysAr 136
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QY 136 gGlnTTPProCysAlaAlaGlyGlnIlystYrTyrGlyArgGlyProIleuGlnIleSerTr 156
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QY 156 pAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProG1 176
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:33:17 ; Search time 370.316 Seconds

(without alignment)  
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Title: US-10-692-367-70

Perfect score: 1408

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US10692367/runat\_20052005\_172254\_19994/app\_query.fasta\_1.846  
-DB=N Geneseq\_16Dec04 -OPMT=fastcap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pfco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10692367 @CGN 1.1 468 @runat\_20052005\_172254\_19994 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:\*

1:	Geneseqn1980s:*
2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004as:*
13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1408	100.0	753	13 ADS92685	Ads92685 Chitinase
2	1377	97.8	753	13 ADS92667	Ads92667 Chitinase
3	1372	97.4	753	13 ADS92697	Ads92697 Chitinase
4	1366	97.0	753	13 ADS92683	Ads92683 Chitinase
5	1363	96.8	753	13 ADS92693	Ads92693 Chitinase

6	1360	96.6	753	13	ADS92671	Ads92671 Chitinase
7	1358	96.4	753	13	ADS92659	Ads92659 Chitinase
8	1357.5	96.4	774	13	ADS92687	Ads92687 Chitinase
9	1351	96.0	753	13	ADS92665	Ads92665 Chitinase
10	1351	96.0	1094	3	AAA96222	AAA96222 cDNA enco
11	1350	95.9	753	13	ADS92669	Ads92669 Chitinase
12	1348	95.7	753	13	ADS92637	Ads92637 Chitinase
13	1348	95.7	771	13	ADS92663	Ads92663 Chitinase
14	1345	95.5	771	13	ADS92689	Ads92689 Chitinase
15	1344	95.5	771	13	ADS92675	Ads92675 Chitinase
16	1342	95.3	771	13	ADS92677	Ads92677 Chitinase
17	1341	95.2	753	13	ADS92651	Ads92651 Chitinase
18	1336.5	94.9	750	13	ADS92695	Ads92695 Chitinase
19	1335.5	94.9	774	13	ADS92681	Ads92681 Chitinase
20	1335	94.8	771	13	ADS92699	Ads92699 Chitinase
21	1328.5	94.4	774	13	ADS92645	Ads92645 Chitinase
22	1328.5	94.4	774	13	ADS92649	Ads92649 Chitinase
23	1325.5	94.1	780	13	ADS92655	Ads92655 Chitinase
24	1324.5	94.1	780	13	ADS92691	Ads92691 Chitinase
25	1323	94.0	753	13	ADS92673	Ads92673 Chitinase
26	1322.5	93.9	774	13	ADS92661	Ads92661 Chitinase
27	1321.5	93.9	774	13	ADS92679	Ads92679 Chitinase
28	1319	93.7	753	13	ADS92647	Ads92647 Chitinase
29	1318.5	93.6	774	13	ADS92627	Ads92627 Chitinase
30	1312	93.2	753	13	ADS92643	Ads92643 Chitinase
31	1309.5	93.0	774	13	ADS92653	Ads92653 Chitinase
32	1300.5	92.4	774	13	ADS92639	Ads92639 Chitinase
33	1285	91.3	771	13	ADS92657	Ads92657 Chitinase
34	1283.5	91.2	774	13	ADS92623	Ads92623 Chitinase
35	1271.5	90.3	840	11	ADJ12126	Adj12126 Maize cDN
36	1255	89.1	765	13	ADS92641	Ads92641 Chitinase
37	1253	89.0	777	13	ADS92631	Ads92631 Chitinase
38	1245	88.4	777	13	ADS92619	Ads92619 Chitinase
39	1244.5	88.4	756	13	ADS92629	Ads92629 Chitinase
40	1242.5	88.2	756	13	ADS92621	Ads92621 Chitinase
41	1236.5	87.8	756	13	ADS92625	Ads92625 Chitinase
42	1011.5	71.8	843	8	ADA70140	Ada70140 Rice gene
43	1011.5	71.8	843	11	ADJ11575	Adj11575 Rice DNA
c 44	1011.5	71.8	906	11	ADJ11773	Adj11773 Rice cDNA
c 45	1011.5	71.8	909	11	ADJ11435	Adj11435 Rice DNA

#### ALIGNMENTS

RESULT 1  
ADS92685  
ID ADS92685 standard; DNA; 753 BP.  
XX  
XX  
AC ADS92685;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
Chitinase variant polynucleotide #32.  
XX  
Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
PI Muller ML, True T, Simmons CR, Yalpani N;

```
XX WPI; 2004-365417/34.
DR P-PSDB; ADS92666.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 69; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC polynucleotide is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 141 A; 245 C; 261 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,31e-117 Length: 753
Score: 1408.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92685 (1-753)

QY 1 SerMetGlnAsnCySGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGGCGTGCAGCAAAAGTATCTGTCAGCAAGTTTCGGTACTGCGGC 60

QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACAACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGCGCCGCTCGCGCGCGGC 120

QY 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60
DB 121 GGCACGAGTGGCGGGGTGGTGCAGAACGTGGTACGGTCCGTCACCGGCTCTCTTCAAC 180

QY 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
DB 181 GCATCAGAACACGCGCGGAGCGGTGCGAGGSCAAGACTTCTACACCGGAGCGG 240

QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
DB 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGGCGGTACAGGTGCGGCG 300

QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
DB 301 AAGCCGAGATCGCCGCTTCTTCGCGCAGCGCAGCAGACCGCGGCAATTCGTGTAC 360

QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
DB 361 ATCAGCGAGATCAGCAAGACGAAACGCTTCTGCGACCGCGACCAAGAGCGATGCGGTG 420

QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyr 160
DB 421 GCGCGGCGGCGAGAGTACTACGGGCGCGCGCTGTCAGATCTCGTGAACCTACAACTAC 480

QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
DB 481 GGGCCCGCGGGGAGGAGCATCGGCTTCACAGCGGCTTCGGGACCCCGCGGCGGCGG 540

QY 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
DB 541 GACGCGGTGGTGGCTTCAAGCGCGGCTCTGGTTCGTGATGAACAACGTCACCGTGTG 600

QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
DB 1 TCGATGCAGAACTCGCGGTGCCAGCAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60
```

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DB 601 ATGCCCGCAGGCTTCGGCGCCACCACCATCAGGCGCCATCAACGCGCGCTCGAGTGCACGGG 660
QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
DB 661 AACAAACCCCGCCAGATGACGCGCATCGGCTACTACAAGCAGTACTGCGCGCAGCTC 720
QY 241 GlyValAspProGlyProAsnLeuThrCys 250
DB 721 GCGCTGACCCAGGCGCCCAACCTCCTTGC 750

RESULT 2
ADS92667
ID ADS92667 standard; DNA; 753 BP.
XX
AC ADS92667;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #23.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
WPI; 2004-365417/34.
DR P-PSDB; ADS92668.
XX
New chitinase polynucleotides and polypeptides, useful in producing
plants with enhanced resistance against a fungus or a nematode.
XX
Claim 4; SEQ ID NO 51; 197pp; English.
XX
The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 135 A; 245 C; 265 G; 108 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,2e-114 Length: 753
Score: 1377.00 Matches: 243
Percent Similarity: 98.80% Conservative: 4
Best Local Similarity: 97.20% Mismatches: 3
Query Match: 97.80% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92667 (1-753)

QY 1 SerMetGlnAsnCySGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGGTGCCAGCAACGATGCTGCAGCAAGTTTGGCTACTGCGGC 60
```

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACGACCGACGAGTACTCGCGCGACGGGTGCGAGTCCGGCCCGTCCGCTCGCGCGCGGC 120  
Qy 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAen 60  
Db 121 GCGACGAGTGGCGCGGTGGTGGCAACGTGTGCTAGCTGCTGACCGGTCTCTTCTTCAAC 180  
Qy 61 GlyTleAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
Db 181 GGCATCAAGACCGAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240  
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
Db 241 TTCTCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTGCGAGTGCAGGCG 300  
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
Db 301 AAGCGCGAGATCGCGCCTTCTTCGCGCATGTGACGACGAGACCGGGCATTTCTGCTAC 360  
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
Db 361 ATCAGCGAGATCAACAGACGACCGCTTCTGCGCATGTGACGACGAGACCGGGCATTTCTGCTAC 420  
Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160  
Db 421 GCGCGCGGCGCAAGTACTACGGCGCGCGCGCTGCTGCGATCTGCTGGAACCTACAACTAC 480  
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180  
Db 481 GGGCGCGCGGAGGGCGCATCGCTTTCACCGCGCTCGGGGACCGCGCGGCGGTGGCGCGG 540  
Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200  
Db 541 GACCGCGTGTGGCGTTCAAGCGCGCGCTCTGTGTTCTGATGACACAGTGCACCGTGTG 600  
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
Db 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGGCGCCTCGAGTGGCGCGG 660  
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
Db 661 AACAAACCGCGCGAGATGAACGCGCGCTCGCTGCTACTACAGGCGAGTACTGCGCGCGAGCTC 720  
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250  
Db 721 GCGGTGCGACCGCGCGCGCACTCACTTGC 750

## RESULT 3

ADS92697

ID ADS92697 standard; DNA; 753 BP.

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX AC ADS92697;

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92698.

XX New chitinase polynucleotides and polypeptides, useful in producing

XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 81; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides

XX encoding them. A method of enhancing plant resistance to a fungus or

XX nematode comprising introducing into a plant a recombinant expression

XX cassette comprising a promoter operably linked to a chitinase

XX polynucleotide of the invention. The plant is maize or soybean. The

XX fungus is from the genus Fusarium. The nematode is from the genus

XX Heterodera. The polynucleotides and polypeptides are useful in enhancing

XX plant resistance to a fungus or nematode. This sequence represents a

XX chitinase variant polynucleotide of the invention.

XX SQ Sequence 753 BP; 140 A; 240 C; 263 G; 110 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 8.98e-114 Length: 753

XX Score: 1372.00 Matches: 243

XX Percent Similarity: 98.40% Conservative: 3

XX Best Local Similarity: 97.20% Mismatches: 4

XX Query Match: 97.44% Indels: 0

XX DB: 13 Gaps: 0

XX US-10-692-367-70 (1-250) x ADS92697 (1-753)

XX Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20

XX Db 1 TCGATGACAGAACTCGCGCTGCCAGCAACGATATGTGTCAGCAAGATTTGGCTACTGCGGC 60

XX Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40

XX Db 61 ACGACCGACGAGTACTCGCGCGACGGGTGCGAGTCCGGCCCGTCCACTCGCGCGCGGC 120

XX Qy 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAen 60

XX Db 121 GGCAGCAGTGGCGCGGTGGTGGCAATGTGCTAATGTGGTCCACGACGCGTTCTTCAAC 180

XX Qy 61 GlyTleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80

XX Db 181 GGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240

XX Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100

XX Db 241 TTCTCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTGCGAGTGCAGGCG 300

XX Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120

XX Db 301 AAGCGCGAGATTCGCGCCTTCTTCGCGCATGCCACGACGACGAGACCGGCAATTTCTGCTAC 360

XX Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140

XX Db 361 ATCAGCGAGATCAACAGACGACCGCTTCTGCGCATGCCAGCGCGCGCGCGAGTGCAGGCG 420

XX Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160

XX Db 421 GCGCGCGGCGCAAGTACTACGGCGCGCGCGCTGCGAGTCTCTGCTGGAACCTACAACTAC 480

XX Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180

XX Db 481 GGGCGCGCGGAGGGCGCATCGCTTTCACCGCGCTCGGGGACCGCGCGGCGGTGGCGCGG 540

XX Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200

Db 541 GACGCGGTGGTCTTCAAGCGCGCTCTGGTTCTGGATGAACAACGTCACCGCTGTG 600  
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGly 220  
Db 601 ATGCCGCAAGGGTTCCGTGCGCACCATCCGGGCGCATCAACGGCGCCTCGAGTGGCGCGGG 660  
Qy 221 AenAenProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
Db 661 AACAAACCCCGCCAGATGACGCGCGCATCGCTACTACAGCAGTACTCGCGCCAGCTC 720  
Qy 241 GlyValAspProGlyProAenLeuThrCys 250  
Db 721 GCGTCGACCCAGGGCCCAACCTCACTTGC 750

## RESULT 4

ADSS92683  
ID ADSS92683 standard; DNA; 765 BP.

AC  
XX

ADSS92683;

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #31.

DE Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

OS

XX

PN WO2004037194-A2.

XX

PD 06-MAY-2004.

XX

PF 22-OCT-2003; 2003WO-US033588.

XX

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX

PA (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX

XX Muller ML, True T, Simmons CR, Yalpani N;

PI P-PSDB; ADSS92684.

XX

DR WPI; 2004-365417/34.

XX

XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.

XX

PS Claim 4; SEQ ID NO 67; 197pp; English.

XX

CC The invention relates to chitinase polypeptides and the polynucleotides

CC encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression

CC cassette comprising a promoter operably linked to a chitinase

CC polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genus

CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing

CC plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polynucleotide of the invention.

XX

SQ Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 3.16e-113 Length: 765

Score: 1366.00 Matches: 243

Percent Similarity: 96.85% Conservative: 3

Best Local Similarity: 95.67% Mismatches: 4

Query Match: 97.02% Indels: 4

DB: 13 Gaps: 1

US-10-692-367-70 (1-250) x ADSS92683 (1-765)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGACAGAACTCGGCTGCCAGCAAACTATGCTGCAGCAAGTTCCGCTACTCGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACAACCGACGAGTACTCGCGCACGGGTGCCAGTCGGGCGCGCTCGCTCGCGCGCGGC 120  
Qy 41 GlySerSerGlyGly-----GlyGlyAlaAenValAlaSerValValThrGly 56  
Db 121 GCGCGCGCGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
Qy 57 SerPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyr 76  
Db 181 TCCTTCTTCAACGGCATCAGAACGAGCGCGGAGCGGGTGCAGAGGCAAGAACTTCTAC 240  
Qy 77 ThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySer 96  
Db 241 ACCCGAGCGCGTTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTCA 300  
Qy 97 GlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGly 116  
Db 301 CAGGTGACAGGCAAGCGGAGATTGCCGCTTCTTCGCGCACGCCACGACGACGACGCGG 360  
Qy 117 HisPheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThrLysArg 136  
Db 361 CATTTCTGTACATCAGCGGAGATCAACAGNGCAACGCCCTACTCGGACCCGACCAAGAG 420  
Qy 137 GlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrp 156  
Db 421 CAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGCGGCGCGCGCTCGAGATCTCGTGG 480  
Qy 157 AsnTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGly 176  
Db 481 AACTACAACTACGCGCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540  
Qy 177 ArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsn 196  
Db 541 AGGTTGGCGCAGGACGCGGTGGTGGCTTCAAGGGGGGCGCTCTGGTTCTGGATGAACA 600  
Qy 197 ValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeu 216  
Db 601 GTGCACCGTGTGATGCGCGCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGCTC 660  
Qy 217 GluCysAspGlyAenAenProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyr 236  
Db 661 GAGTGCAGCGGAGAAACACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
Qy 237 CysArgGlnLeuGlyValAspProGlyProAenLeuThrCys 250  
Db 721 TGCGCGCAGCTCGGCGTGCAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 762

## RESULT 5

ADSS92693

ID ADSS92693 standard; DNA; 753 BP.

XX

AC ADSS92693;

XX

DT 02-DEC-2004 (first entry)

XX

DE Chitinase variant polynucleotide #36.

XX

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

KW Heterodera.

XX

OS Synthetic.

XX

PN WO2004037194-A2.

XX

PD 06-MAY-2004.

XX

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PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92671.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 77; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 142 A; 244 C; 262 G; 105 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,76e-113 Length: 753
Score: 1363.00 Matches: 240
Percent Similarity: 98.00% Conservative: 5
Best Local Similarity: 96.00% Mismatches: 5
Query Match: 96.80% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92693 (1-753)

QY 1 SerMetGlnAsnGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAAGAACTGGCGGTGCGAGCAACAGTATGCTGCAGCAAGTTTCGGTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCCCGCTGCCACTCGGCGGCGGC 120
QY 41 GlySerSerGlyGlyGlyAlaAsnValLaserValThrGlySerPhePheAsn 60
DB 121 GCGACGACGTGGCGGCGGTGGTGTGAACGTGGCCAGCATCGTGACCGGCTCTCTTCAAC 180
QY 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
DB 181 GGCATCAAGAACCGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACCCCGGAGCGCG 240
QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
DB 241 TTCTGTAGCGCGTCAAGCGGTACCCAGCGTTGCGCCATGCGCGGACGAGGTGGAGGCG 300
QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
DB 301 AAGCGGAGATGGCGGCTTCTTCGCGACGCCAGCAGCAGAGCGGCGCATTTCTGTCTAC 360
QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCys 140
DB 361 ATCAGCGAGATCAGCAGAGCAACGCCCTACTTGGACCCGACACAGAGCGAGTGGCGGTGC 420
QY 141 AlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyr 160
DB 421 GCCGCGGCGCAGAACTACTACGAGCGCGCGCTGCGAGATCTCGTGGAACTACAACCTAC 480

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QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
DB 481 GGGCCCCGGGGAGGCCATCGGCTTCGACGGGTTCGGGGACCCCAACAGGGTGGCGGG 540
QY 181 AspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgVal 200
DB 541 GACGCGGTGGTGGGTTCAAGGCGCGCTCTGGTCTTGGATGAACAGCGTGCACCGTGTG 600
QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
DB 601 ATGCGCGAGGGCTTCGGCGCCACCATCAGGCGCCATCAACGGCGCCCTCGAGTGGCGGG 660
QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
DB 661 AACAAACCGCGCCAGATGAAGCGCGCATCGGTACTACAAAGCAGTACTGCCCGCAGCTC 720
QY 241 GlyValAspProGlyProAsnLeuThrCys 250
DB 721 GGCCTGACCCAGCGGCGCCACCTCACTTGC 750

RESULT 6
ADS92671
ID ADS92671 standard; DNA; 753 BP.
XX
AC ADS92671;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #25.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92672.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 55; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 144 A; 245 C; 255 G; 109 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.07e-112 Length: 753
Score: 1360.00 Matches: 240

```

Percent Similarity: 97.20% Conservatives: 3  
 Best Local Similarity: 96.00% Mismatches: 7  
 Query Match: 96.55% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92671 (1-753)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGCGGCTGCAGCAACATATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 Db 61 ACAACGACGAGTACTGCGGCGACGGGTGCCAGTCCGCGCTGCCTCCACTCGCGGCGCGT 120

Qy 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60  
 Db 121 GCGCGCGTGGCGGCGGTGGTGCAGAACGTGCTAGCTGCACCGGCTCTCTTTCAAC 180

Qy 61 GlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
 Db 181 GGCATCAGAACCCAGCGCGGAGCGGTGCGAGGCGAAGACTTCTACCCGCGAGCGCG 240

Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
 Db 241 TTCTCTAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTACAGGTCGAGGC 300

Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
 Db 301 AAGCGCGAGATGCGCGCTCTTTCGCGCATGTACGACGAGACCGGCGCATTTCTGTAC 360

Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
 Db 361 ATCAGGAGATCAACAAGAGCAACGCTTCTGCGACCCGACCAAGAGCGAGTGGCGGTG 420

Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160  
 Db 421 GCGCGCGGCGAGAGTACTACGCGCGCGCGCTGTCAGATCTCGTGAACACTACAACCTAC 480

Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180  
 Db 481 GGGCGCGCGGAGGAGCATCGCTTCAACGGGCTCGCCGACCCCAACAGGGTGGCGGAG 540

Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200  
 Db 541 GACGCGGTGTGGCTTCAAGCGCGGCTCTGTCTGTGATGAACAACGTGCACCGTGTG 600

Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
 Db 601 ATGCGCGAGGCTTGGCGCGCACCATCATCAGGCGCATCAACGCGCGCTCGAGTGGCGGG 660

Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
 Db 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTCAAGAGTACTGCGCGCGAGCTC 720

Qy 241 GlyValAspProGlyProAsnLeuThrCys 250  
 Db 721 GCGGTGAGCCAGGCGCCCACTCTTTC 750

RESULT 7  
 ADS92659  
 ID ADS92659 standard; DNA; 753 BP.  
 XX  
 AC ADS92659;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polynucleotide #19.  
 XX  
 KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 XX  
 OS Synthetic.

WO2004037194-A2.  
 06-MAY-2004.  
 22-OCT-2003; 2003WO-US033588.  
 22-OCT-2002; 2002US-0420666P.  
 06-NOV-2002; 2002US-00290086.  
 14-MAR-2003; 2003US-00389432.  
 (VERD-) VERDIA INC.  
 (PTON-) PIONEER HI-BRED INT INC.  
 Muller ML, True T, Simmons CR, Yalpani N;  
 WPI; 2004-365417/34.  
 P-PSDB; ADS92660.

New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.  
 Claim 4; SEQ ID NO 43; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus *Fusarium*. The nematode is from the genus *Heterodera*. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.

Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.62e-112 Length: 753  
 Score: 1358.00 Matches: 239  
 Percent Similarity: 98.00% Conservative: 6  
 Best Local Similarity: 95.60% Mismatches: 5  
 Query Match: 96.45% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92659 (1-753)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGCGGCTGCAGCAACATATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 Db 61 ACGACCGACGAGTACTGCGGCGAGCGGTGCGAGTCCGCGCGCTGCGGCGCGCGC 120

Qy 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60  
 Db 121 GGCAGCAGTGGCGGCGGTGGTGCAGAACGTGCTAATGTGTGTCACCGAGCGGCTTCTCAAC 180

Qy 61 GlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
 Db 181 GGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGAAGACTTCTACCCGCGAGCGCG 240

Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
 Db 241 TTCTCTAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTCCGAGTCCGAGCGC 300

Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
 Db 301 AAGCGCGAGATGCGCGCTCTTTCGCGCATGTACGACGAGACCGGCGCATTTCTGTAC 360

Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
 Db 361 ATCAGGAGATCAACAAGAGCAACGCTTCTGCGACCCGACCAAGAGCGAGTGGCGGTG 420



QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyr 160  
 DB 421 GCCGGGGGAGAGTACTACGGGGCGCGCGCTGCAGATCTCGTGGAACTACAACTAC 480  
 QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180  
 DB 481 GGGCCCGGGGGAGGCCATCGCTTCAGCGGGCTCGGGGACCCCGGCGAGGTGGCGGG 540  
 QY 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnValHisArgVal 200  
 DB 541 GACCGCGTGGTGGCTTCAAGCGCGCTCTGGTTCTGGATCAACAACTGCACCGTGTG 600  
 QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
 DB 601 ATGCGCAGGGCTTCGGGCGCCACCATCAGGGCCATCAACGGCGCTCGAGTGGCGGG 660  
 QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
 DB 661 AACAAACCGCGCCAGATGACCGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
 QY 241 GlyValAspProGlyProAsnLeuThrCys 250  
 DB 721 GCGGTGAGCCAGGGGCCCAACCTCACTTGC 750

## RESULT 8

ADS92687  
 ID ADS92687 standard; DNA; 774 BP.  
 AC ADS92687;

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #33.

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-P5DB; ADS92688.

XX New chitinase polynucleotides and polypeptides, useful in producing

XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 71; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus Fusarium. The nematode is from the genus  
 CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.85e-112 Length: 774  
 Score: 1357.50 Matches: 242  
 Percent Similarity: 95.72% Conservative: 4  
 Best Local Similarity: 94.16% Mismatches: 4  
 Query Match: 96.41% Indels: 7  
 DB: 13 Gaps: 1

US-10-692-367-70 (1-250) x ADS92687 (1-774)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGCAGAACTCGGCTGCCAGCAAACTATGCTGCAGCAAGTTCCGGCTACTGCCGC 60  
 QY 21 ThrThrAspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 DB 61 ACGACCGACGAGTACTCGGGCGACGGGTGCCAGTCCGGCCGCTCGCGTCCGGCGCGGT 120  
 QY 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerVal 53  
 DB 121 GCGCGCGCGCGCGCGCGAGCGCGGAGGCAGTGGCGGTGGCAACGTGGCTAATGTG 180  
 QY 54 ValThrGlySerPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 73  
 DB 181 GTCACCGACGCGCTTCTTCAACGGCATCAAGAGCAGCGCGGAGCGGGTGGAGGGCAAG 240  
 QY 74 AsnPheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHis 93  
 DB 241 AACTTCTACACCGGAGCGGCTTCTGAGCGCGCTCAAGGGGTACCCAGGGTTCGCCCAT 300  
 QY 94 GlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 113  
 DB 301 GCGCGGTCAACAGTGCAGGGCAAGCGGAGATCGCGCTTCTTCCGCGCACGCCACGCAC 360  
 QY 114 GluThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspPro 133  
 DB 361 GAGACCGGGCATTTCTGTCTATCAGCGAGATCAACAGAGCAACGCCCTACTGCCAGCCG 420  
 QY 134 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 153  
 DB 421 ACCAAGAGGAGTGGCGCTGCGCGCGGGGAGAGTACTACGGGGCGGGCCGCTGCAG 480  
 QY 154 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGly 173  
 DB 481 ATCTCGTGGAACTACAACTACGGCGCGCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 540  
 QY 174 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 193  
 DB 541 GACCCCGGCGGGTGGCGGGGACGCCGTGGTGGGTTCAGAGGGCGCGCTCTGGTTCGG 600  
 QY 194 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 213  
 DB 601 ATGAACAACGTGCACCGTGTGATCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660  
 QY 214 GlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyr 233  
 DB 661 GCGCGCTCGAGTGCAGCGGAAACAACCCCGCCAGATGAACGGCGCATCGGCTACTAC 720  
 QY 234 LysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250  
 DB 721 AAGCAGTACTGCCGCCAGCTCGCGTGCAGCCAGGGGCCCAACCTCACTTGC 771

## RESULT 9

ADS92665  
 ID ADS92665 standard; DNA; 753 BP.

XX ADS92665;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #22.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
XX Synthetic.  
XX  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
XX  
XX 06-NOV-2002; 2002US-00290086.  
XX  
XX 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
XX  
XX (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
XX P-PSDB; ADS92666.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 4; SEQ ID NO 49; 197pp; English.  
XX  
XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.  
XX  
XX SQ Sequence 753 BP; 138 A; 238 C; 270 G; 107 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 6.86e-112 Length: 753  
XX Score: 1351.00 Matches: 237  
XX Percent Similarity: 97.20% Conservative: 6  
XX Best Local Similarity: 94.80% Mismatches: 7  
XX Query Match: 95.95% Indels: 0  
XX DB: 13 Gaps: 0  
XX  
XX US-10-692-367-70 (1-250) x ADS92665 (1-753)  
XX  
XX QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20  
XX  
XX Db 1 TCGATGCGAAGTCTGGGCTGCGGCGGAGCCAAACATGCTGCGAGCAAGTTGGCTACTGCGGC 60  
XX  
XX QY 21 ThrThrAepGluTyrCysGlyAepGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
XX  
XX Db 61 ACGACCGACGAGTACTGGGCGGACGGGTGCGAGTGGGCGGCGGCGGCTGCGGCGGCGGC 120  
XX  
XX QY 41 GlySerSerGlyGlyGlyGlyAlaAenValAlaSerValValThrGlySerPheAen 60  
XX  
XX Db 121 GGCAGCAGTGGCGGCGGTGTGAACGTGGCCAGCATCGTGACCGGCTCTTCTTCAAC 180  
XX  
XX QY 61 GlyTleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAla 80  
XX  
XX Db 181 GGCATCAGAACACCGGCGGAGCGGTGCGAGGCGAAGACTTCTACCCCGGAGCGCG 240  
XX  
XX QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
XX  
XX Db 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGACCGAGGTGGAGGC 300  
XX  
XX QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
XX  
XX

Db 301 AAGCGCAGATCGCGCGCTTCTTCGCGCATGTCCAGCATGAGACCGGCGCATTTCTGCTAC 360  
QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAepProThrLysArgGlnTyrProCys 140  
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTTGCACCCGACCAAGAGCAGTGGCGGTC 420  
QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyr 160  
Db 421 GCCGGGGGCGAAGTACTACGGGGCGGCGCGCTCGCAGATCTCGTGGAACTACAACTAC 480  
QY 161 GlyProAlaGlyArgAepIleGlyPheAepGlyLeuGlyAepProGlyArgValAlaArg 180  
Db 481 GGGCCCGCGGAGGCCATCGGCTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGGG 540  
QY 181 AspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValIleArgVal 200  
Db 541 GACGCTGTGGTGGGCTTCAAGGGCGGCGCTCTGGTTCGGATGAACAGCGTGCACGGGTG 600  
QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAepGly 220  
Db 601 GCGCGCGAGGGGTTGCGGGCCACCATCAGGGCCATCAACGGCGACTCGAGTGGCGGG 660  
QY 221 AsnAenProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
Db 661 AACCAACCGCGCCAGATGAACGCGGCGTGGCTACTACAGCAGTACTGCCACAGCTC 720  
QY 241 GlyValAepProGlyProAenLeuThrCys 250  
Db 721 GCGCTCGACCGAGGGCCCAACCTCACTTGC 750  
XX  
XX RESULT 10  
XX AAA96222  
XX ID AAA96222 standard; cDNA; 1094 BP.  
XX AC AAA96222;  
XX DT 08-FEB-2001 (first entry)  
XX DE cDNA encoding a maize chitinase polypeptide designated ZmCh2.  
XX KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;  
XX pathogen control; disease resistance; molecular marker; ss.  
XX OS Zea mays.  
XX FH Key Location/Qualifiers  
XX FT CDS 51..896  
XX FT /\*tag= a  
XX FT /product= "chitinase"  
XX PN WO200056908-A2.  
XX XX  
XX PD 28-SEP-2000.  
XX XX  
XX PF 09-MAR-2000; 2000WO-US006121.  
XX XX  
XX PR 24-MAR-1999; 99US-0125915P.  
XX XX  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX XX  
XX PI Simmons CR, Yalpani N;  
XX XX  
XX P-PSDB; AAB18894.  
XX DR WPI; 2000-628269/60.  
XX DR P-PSDB; AAB18894.  
XX XX  
XX FT New maize chitinase genes encoding seven chitinases of glucosyl hydrolase  
XX family 19 are useful for enhancing disease resistance in crop plants by  
XX modulating its expression in plants.  
XX XX  
XX PS Claim 1; Page 64-65; 96pp; English.  
XX XX  
XX CC The present sequence encodes a chitinase polypeptide. The specification  
XX describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896,

CC AAB18939, and AAB18902-05), and glucosyl hydrolase family 18 chitinases  
CC (AAB18955, AAB1897-98 and AAB18900-01). The level of chitinase in plants  
CC can be modulated to enhance disease resistance in crop plants and for  
CC control of pathogens. The chitinase polynucleotides are also useful as  
CC molecular markers for genotype in a plant, and for sequence shuffling.  
XX  
SQ Sequence 1094 BP; 226 A; 339 C; 368 G; 161 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.08e-111 Length: 1094  
Score: 1351.00 Matches: 238  
Percent Similarity: 98.39% Conservative: 6  
Best Local Similarity: 95.97% Mismatches: 4  
Query Match: 95.95% Indels: 0  
DB: 3 Gaps: 0

US-10-692-367-70 (1-250) x AAA96222 (1-1094)

QY 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
DB 150 CAGAACTCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTCGGCGCACGACC 209  
QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
DB 210 GACGAGTACTCGGCGCAGCGGTGCCAGTCGGCCCGTCCGCTCGGGCGGCGGCGCAGC 269  
QY 43 SerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle 62  
DB 270 AGTGGCGCGGTGGTGGCAAGCTGCTAGCGTCGTACCGGCTCTCTTCTTCAACGGCATC 329  
QY 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82  
DB 330 AAGACCGAGCGCGGAGCGGTGGCGAGGCGAAGAACTTCTACCCCGGAGCGGCTTCCTG 389  
QY 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
DB 390 AGCGCGCTCAGGCGTACCCAGGCTTCGCCCATGCGCGGTCCAGTGCAGGCCAAGCGC 449  
QY 103 GlulleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
DB 450 GAGATCGCGCGCTTCTCGCGCAGCCACGCCAGCAGACCGGCGCATTTCTGCTACATCAGC 509  
QY 123 GlulleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrrProCysAlaAla 142  
DB 510 GAGATCAACAGAGCAACGCCCTACTGCGACCGCACCAAGAGCGAGTGGCGCGCGCG 569  
QY 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro 162  
DB 570 GGGCAGAGTACTACGGCGCGCGCGCTCGATCTGCTGGAACTACAACTACGGGCGC 629  
QY 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182  
DB 630 CGGGGAGGGGCATCGGCTTCAGCGGCTCGGGACCCCGCGCAGGTCGGCGGCGCGCC 689  
QY 183 ValValAlaPheLysAlaAlaLeuTrrPheTrpMetAsnAsnValHisArgValMetPro 202  
DB 690 GTGGTGGCGGTTCAGAGCGCGCGCTCGGTCTCGAATGAACAGCGTGCACGGGTGGTGGCG 749  
QY 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsn 222  
DB 750 CAGGGGTTCGGCGCACCAACAGGGCCATCAACGGCGCTTCGATGTCGGCGGAGCAAC 809  
QY 223 ProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTrrCysArgGlnLeuGlyVal 242  
DB 810 CCGCGCCAGATGAACCGCGGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTCGGCGCTC 869  
QY 243 AspProGlyProAsnLeuThrCys 250  
DB 870 GACCCCGGCGCCCACTCCTCCTGC 893

RESULT 11

ADS92669

ID ADS92669 standard; DNA; 753 BP.

XX ADS92669;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #24.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
PA  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
DR WPI; 2004-365417/34.  
DR P-PSDB; ADS92670.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 53; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 753 BP; 141 A; 248 C; 254 G; 110 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.44e-112 Length: 753  
Score: 1350.00 Matches: 236  
Percent Similarity: 97.60% Conservative: 8  
Best Local Similarity: 94.40% Mismatches: 6  
Query Match: 95.88% Indels: 0  
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92669 (1-753)

QY 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
DB 1 TCGATGCAGAACTCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
DB 61 ACAGCCAGCAGTACTCGGCGCGCGGTGGCGAGTCGGGCGGTCCTCGGCGGCGCGC 120  
QY 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60  
DB 121 GCGAGCAGTGGCGCGGTGGTGGCAACGTGCTAGCGTCGTCACCGGCTCTTCTTCAAC 180  
QY 61 GlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAla 80  
DB 181 GGCATCAAGAACAGCGCGGCGGAGCGGTCGCGAGGCGCAAGAACTTCTACCCCGGCGCGC 240

```
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGly 100
Db 241 TTCTCTAGCGCGCTCAAGCGGTACCCAGGCTTGGCCCATGGCGGTGCGAGGTGCGAGGC 300
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCATGTCAAGCATGAGACCGGGCATTTCTGCTAC 360
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCys 140
Db 361 ATCAGCGAGATCAACAGAGCAACCGCTTCTGCGACCCGACCAAGAGGCAAGTGGCGTGC 420
Qy 141 AlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 421 GCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGCGAGTGTCTGTGAACCTACAACTAC 480
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 481 GGGCGCGCGGAGGAGCATCGGCTTCAACGGGCTCGCGGACCCCAACAGAGGTGGCGGAG 540
Qy 181 AspAlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 541 GAGCGGTGATCGCGGTTCAAGTCGGCGCTCTGTGTTCTGGATGAACAGCTGCACGCTG 600
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
Db 601 ATGCGCGAGGCTTTCGGCGCCACCATCAGGCGCATCAACGGCGGCTCGAGTGGCGGG 660
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeu 240
Db 661 AACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTC 720
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250
Db 721 GCGGTGACCCAGGCGCCCACTCACTTGC 750
```

## RESULT 12

AD92637  
ID AD92637 standard; DNA; 753 BP.

XX AC AD92637;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #8.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-0303588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR P-PSDB; AD92638.

XX PT New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 21; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX SQ Sequence 753 BP; 132 A; 247 C; 269 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.28e-111 Length: 753  
Score: 1348.00 Matches: 238  
Percent Similarity: 98.00% Conservatives: 7  
Best Local Similarity: 95.20% Mismatches: 5  
Query Match: 95.74% Indels: 0  
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x AD92637 (1-753)

```
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCCAGCAGTACTCGCGCGAGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 120
Qy 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60
Db 121 GGCAGCAGTGGCGGCGGTGGTGGCAACGTGGTAGCGTGTACCGGCTCTCTTCTTCAAC 180
Qy 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
Db 181 GGCATCAAGACCCAGGCGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 240
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
Db 241 TTCTCTAGCGCGCTCAAGCGGTACCCAGGCTTCCCGCATGGCGGTGCGAGGTGCGAGGC 300
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCATGTCAGCACCGCACCGAGACCGGGCATTTCTGCTAC 360
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCys 140
Db 361 ATCAGCGAGATCAACAGAGCAACCGCTTCTGCGACCCGACCAAGAGGCAAGTGGCGTGC 420
Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 421 GCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGCGAGTGTCTGTGAACCTACAACTAC 480
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 481 GGGCGCGCGGAGGCGCATCGGCTTCAAGCGGCTCGGCGACCCCGCGAGGTTGGCGGG 540
Qy 181 AspAlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 541 GAGCGGTGATCGCGGTTCAAGTCGGCGCTCTGTGTTCTGGATGAACAGCTGCACGCTG 600
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
Db 601 ATGCGCGAGGCTTTCGGCGCCACCATCAGGCGCATCAACGGCGGCTCGAGTGGCGGG 660
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeu 240
Db 661 AACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTC 720
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250
Db 721 GCGGTGACCCAGGCGCCCACTCACTTGC 750
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Db      721 CGCGTCGACCCAGGGCCCAACTACCTGTC 750
RESULT 13
ADSR2663
ID      ADS92663 standard; DNA; 771 BP.
XX      AC
XX      ADS92663;
XX      02-DEC-2004 (first entry)
XX      Chitinase variant polynucleotide #21.
XX      Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX      Heterodera.
XX      Synthetic.
XX      WO2004037194-A2.
XX      06-MAY-2004.
XX      22-OCT-2003; 2003WO-US033588.
XX      22-OCT-2002; 2002US-0420666P.
XX      06-NOV-2002; 2002US-00290086.
XX      14-MAR-2003; 2003US-00389432.
XX      (VERD-) VERDIA INC.
XX      (PION-) PIONEER HI-BRED INT INC.
XX      Muller ML, True T, Simmons CR, Yalpani N;
XX      WPI; 2004-365417/34.
XX      P-FSDB; ADS92664.
XX      New chitinase polynucleotides and polypeptides, useful in producing
XX      plants with enhanced resistance against a fungus or a nematode.
XX      Claim 4; SEQ ID NO 47; 197pp; English.
XX      The invention relates to chitinase polypeptides and the polynucleotides
XX      encoding them. A method of enhancing plant resistance to a fungus or
XX      nematode comprises introducing into a plant a recombinant expression
XX      cassette comprising a promoter operably linked to a chitinase
XX      polynucleotide of the invention. The plant is maize or soybean. The
XX      fungus is from the genus Fusarium. The nematode is from the genus
XX      Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX      plant resistance to a fungus or nematode. This sequence represents a
XX      chitinase variant polynucleotide of the invention.
XX      SQ Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,31e-111      Length:      771
Score:          1348.00      Matches:      240
Percent Similarity: 95.31%      Conservative: 4
Best Local Similarity: 93.75%      Mismatches: 6
Query Match:     95.74%      Indels:      6
DB:              13      Gaps:        1

US-10-692-367-70 (1-250) x ADS92663 (1-771)

Qy      1 SerMetGlnAanCysGlyCysGlnProAenValCysSerLysPheGlyTyrCysGly 20
Db      1 TCGATGCAGAACTGGCGGTGCGAGCAACATGATGTCGACGAAATTCGGCTACTCGGCG 60
Qy      21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db      61 ACGACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGCCGCTGCGCGCGCGCGCG 120
Qy      41 GlySerSerGlyGly-----GlyGlyAlaAenValAlaSerValVal 54
Db      121 GCGCGCGCGCGCGCGAGGGCGGAGGCGGAGTGGCGGTGCGAACGTGGCTAGCGTCTC 180

Qy      55 ThrGlySerPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAen 74
Db      181 ACCGGCTCCTTTCAACGGCATCAAGAACCGAGCCCGGAGCGGTGCGAGGGCAAGAAC 240
Qy      75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94
Db      241 TTCTACACCCGGAGCGGTTCCTGAGCGCGCTCAAGGGGTACCCAGGGCTTCGCCATGGC 300
Qy      95 GlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThHisGlu 114
Db      301 GGGTCACAGGTGCGAGGCAAGCGAGATCGCCCTTCTTCGGGCGATGTCAAGCAGAG 360
Qy      115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThr 134
Db      361 ACCGGCATTTTCGCTACATCAGCGAGGTCAACAGAGCAACGCTTACTGCGACCCGACC 420
Qy      135 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154
Db      421 AAGAGCGAGTGGCGCTGCGCGCGGGGCGAGTACTACGGCGCGGCGCGCTGCGAGATC 480
Qy      155 SerTrpAenTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174
Db      481 TCGTGAACACTACAACTACGGGCCCGCGGGAGGGCCATCGGCTTTGACGGGCTCGGGAC 540
Qy      175 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 194
Db      541 CCGCGAGGGTGGCGCGGAGCGCGCTGGTGGCGTTCAGGCGCGGCGCTCGGTTCTGGATG 600
Qy      195 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGly 214
Db      601 AACAACTGACACCGTGTGATGCGCGAGGGTTCGCGCGCCACCATCAGGGCCATCAAGCGC 660
Qy      215 AlaLeuGluCysAspGlyAenAenProAlaGlnMetAenAlaArgIleGlyTyrTrpLys 234
Db      661 GCGCTCGAGTGGCGCGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGG 720
Qy      235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAenLeuThrCys 250
Db      721 CAGTACTGCGCGAGCTCGCGCTGACCCAGCGGCGCCCAACCTCACTTGC 768

RESULT 14
ADSR2689
ID      ADS92689 standard; DNA; 771 BP.
XX      AC
XX      ADS92689;
XX      02-DEC-2004 (first entry)
XX      Chitinase variant polynucleotide #34.
XX      Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX      Heterodera.
XX      Synthetic.
XX      WO2004037194-A2.
XX      06-MAY-2004.
XX      22-OCT-2003; 2003WO-US033588.
XX      22-OCT-2002; 2002US-0420666P.
XX      06-NOV-2002; 2002US-00290086.
XX      14-MAR-2003; 2003US-00389432.
XX      (VERD-) VERDIA INC.
XX      (PION-) PIONEER HI-BRED INT INC.
XX      Muller ML, True T, Simmons CR, Yalpani N;
XX      WPI; 2004-365417/34.
XX      P-FSDB; ADS92690.

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XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 73; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 771 BP; 140 A; 249 C; 275 G; 107 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 2.44e-111 Length: 771  
Score: 1345.00 Matches: 239  
Percent Similarity: 94.92% Conservative: 4  
Best Local Similarity: 93.36% Mismatches: 7  
Query Match: 95.53% Indels: 6  
DB: 13 Gaps: 1  
  
US-10-692-367-70 (1-250) x ADS92689 (1-771)  
  
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAAGAACTCGCGTGCAGCAACATGATGTCAGCAAGATTCGGCTACTGCGGC 60  
  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACGACCGACGAGTACTGCGGCGACGGTGCAGTCGGCCCGCGCGCGCGCGC 120  
  
Qy 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerValVal 54  
Db 121 GCGGTGTCGCGCGCGGAGCGCGGCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 180  
  
Qy 55 ThrGlySerPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyValAsn 74  
Db 181 ACCGACTCTTCTTCAACGGCATCAAGAGCCAGCGCGGAGCGGTCGCGGCAAGAAC 240  
  
Qy 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94  
Db 241 TTCTACACCGCGAGCGCTTCTGAGCGCGTCAAGGCGTACCCAGGCTTCGCCCATGCG 300  
  
Qy 95 GlySerGlnValGlnGlyLysArgGluLeuAlaPheAlaHisAlaThrHisGlu 114  
Db 301 GGGTCGCAAGGTGCAGGCAAGCGGAGATCGCGCTTCTTCGGCGCATGTCAACGCGAG 360  
  
Qy 115 ThrGlyHisPheCysTyrLysSerGluLysSerLysSerAsnAlaTyrCysAspProThr 134  
Db 361 ACCGGGCAATTTCTGCTACATCAACAGATCAACAGAGCAACGCTTCTGCGACCCGACC 420  
  
Qy 135 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154  
Db 421 AAGAGGCGAGTGGCGTGGCGCGCGGCGAGGATACAGGCGTGGCGCGCTGCAGATC 480  
  
Qy 155 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174  
Db 481 TCGTGGAACTCAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGGGAC 540  
  
Qy 175 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 194  
Db 541 CCGGCGAGGTGGCGCGGAGCCGCTGGTGGGGTTCAGGGCGGCGCTCTGGTTCTGGATG 600  
  
Qy 195 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 214  
Db 601 AACACAGTGCACCGTGTGATCGCGCGGCTTCGGCGGCCACCATCAGGGCCATCAACGGC 660  
  
Qy 215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrIys 234

Db 661 GCCCTCGAGTGCAGCGGAACAACCGCGCCAGATGAACGCGCATCGGCTACTACAAG 720  
Qy 235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250  
Db 721 CAGTACTGCCCGCAGCTCGCGCTGACCCAGGCGCCAACTCACTTGC 768  
  
RESULT 15  
ADS92675  
ID ADS92675 standard; DNA; 771 BP.  
XX ADS92675;  
AC ADS92675;  
XX 02-DEC-2004 (first entry)  
XX Chitinase variant polynucleotide #27.  
XX Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
KW *Heterodera*.  
XX Synthetic.  
XX WO2004037194-A2.  
XX 06-MAY-2004.  
XX 22-OCT-2003; 2003WO-US033588.  
XX 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92676.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 59; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3e-111 Length: 771  
Score: 1344.00 Matches: 238  
Percent Similarity: 94.92% Conservative: 5  
Best Local Similarity: 92.97% Mismatches: 7  
Query Match: 95.45% Indels: 6  
DB: 13 Gaps: 1  
  
US-10-692-367-70 (1-250) x ADS92675 (1-771)  
  
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAAGAACTCGCGTGCAGCAACATGATGTCAGCAAGATTCGGCTACTGCGGC 60  
  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40

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Db 61 ACACCGACGCTACTCGCGGACGGGTGCCAGTCGGGCCCGCTCGCGCTCGGGCGCGGT 120
Qy 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerValVal 54
Db 121 GCGCGCGTGGCGGCGGAGCGCGGAGCGAGTGGCGGTGCCAAGCTGGCTAAATGTGTC 180
Qy 55 ThrGlySerPhePheAsnGlyIleIysAsnGlnAlaGlySerGlyCysGluGlyIysAsn 74
Db 181 ACCGACGGTCTTCAACGGCNCACGAACCCAGGCCGGAGCGGTGCGAGGGCAAGAAC 240
Qy 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94
Db 241 TTCTACACCCGAGCGGTCTCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGGC 300
Qy 95 GlySerGlnValGlnGlyIysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114
Db 301 GGGTCACAGGTGCAGGGCAAGCGGAGATTGCCGCTTCTTCGCGCATGTCAACGACGAG 360
Qy 115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThr 134
Db 361 ACCGGGCAATTTCTGTATCATACGAGATCAACAAGACAAGCCCTACTGCGACCCGACC 420
Qy 135 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154
Db 421 AAGAGGCAGTGGCGTGGCGCGCGGCGAGAGTACTACGGGCGGCGCGCTGCAGATC 480
Qy 155 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174
Db 481 TCGTGGAACTACAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGGAC 540
Qy 175 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 194
Db 541 CCCGCGAGGGTGGCGGAGCGCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCGGATG 600
Qy 195 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 214
Db 601 AACACGTGCACCGTGTATGCCGCGAGGGCTTCGGCGCCACCATCAGGGCCCATCAACGEC 660
Qy 215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLys 234
Db 661 GCCCTCGAGTGCAGCGGAACAACCCCGCCAGATGAACGGCGCGCTCGGCTACTACAGG 720
Qy 235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
Db 721 CAGTACTGCCCGCAGCTCGGCGTCGACCCAGGGCCCAACCTCACTGC 768
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Search completed: May 23, 2005, 17:44:57  
Job time : 374.316 secs

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GenCore version 5.1.6  
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Run on: May 23, 2005, 17:19:13 ; Search time 125.74 Seconds  
(without alignments)  
3253.303 Million cell updates/sec

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Perfect score: 1408  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
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3: /cgm2\_6/ptodata/1/ina/5A.COMB.seq:\*  
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5: /cgm2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1351	96.0	1094	4	US-09-522-714-1
2	861	61.2	1048	4	US-09-522-714-21
3	830	58.9	1079	1	US-08-181-271A-37
4	830	58.9	1079	1	US-08-449-315-37
5	830	58.9	1079	1	US-08-444-803-37
6	830	58.9	1079	1	US-08-449-043-37
7	830	58.9	1079	1	US-08-456-265A-37
8	830	58.9	1079	1	US-08-455-416-37
9	830	58.9	1079	1	US-08-455-244-37
10	830	58.9	1079	1	US-08-454-876-37
11	830	58.9	1079	2	US-08-457-364-37
12	830	58.9	1079	2	US-08-456-262-37

13	830	58.9	1079	2	US-08-456-240-37	Sequence 37, Appl
14	830	58.9	1079	2	US-08-455-736-37	Sequence 37, Appl
15	830	58.9	1079	2	US-08-971-217-37	Sequence 37, Appl
16	830	58.9	1079	3	US-09-350-600-37	Sequence 37, Appl
17	830	58.9	1079	4	US-09-906-234-37	Sequence 37, Appl
18	825	58.6	1116	4	US-09-522-714-31	Sequence 31, Appl
19	697.5	49.5	881	4	US-09-522-714-29	Sequence 29, Appl
20	621	44.1	943	2	US-08-475-427-15	Sequence 15, Appl
21	621	44.1	943	2	US-07-842-165-15	Sequence 15, Appl
22	620	44.0	1152	1	US-08-047-413-10	Sequence 10, Appl
23	620	44.0	1152	3	US-08-229-050-10	Sequence 10, Appl
24	620	44.0	1152	3	US-08-801-563-10	Sequence 10, Appl
25	592	42.0	1151	1	US-07-704-288C-2	Sequence 2, Appl
26	592	42.0	1151	1	US-08-093-372-1	Sequence 1, Appl
27	592	42.0	1151	1	US-08-379-259-2	Sequence 2, Appl
28	591.5	42.0	1225	1	US-08-286-020-1	Sequence 1, Appl
29	591.5	42.0	1225	1	US-08-603-919-1	Sequence 8, Appl
30	588	41.8	960	4	US-09-534-229C-8	Sequence 14, Appl
31	581	41.3	905	2	US-08-475-427-14	Sequence 14, Appl
32	581	41.3	905	2	US-07-842-165-14	Sequence 14, Appl
33	572.5	40.7	1153	2	US-08-475-427-4	Sequence 4, Appl
34	572.5	40.7	1153	2	US-07-842-165-4	Sequence 4, Appl
35	572.5	40.7	1153	3	US-08-448-398-6	Sequence 6, Appl
36	572.5	40.7	1163	2	US-08-475-427-12	Sequence 12, Appl
37	572.5	40.7	1163	2	US-07-842-165-12	Sequence 12, Appl
38	572.5	40.7	1863	1	US-08-525-507-16	Sequence 16, Appl
39	572.5	40.7	1863	2	US-08-475-427-9	Sequence 9, Appl
40	572.5	40.7	1863	2	US-07-842-165-9	Sequence 7, Appl
41	549.5	39.0	972	4	US-09-534-229C-7	Sequence 5, Appl
42	549.5	39.0	1163	4	US-09-522-714-5	Sequence 1, Appl
43	535.5	38.0	1318	3	US-09-125-891-1	Sequence 5, Appl
44	533.5	37.9	3012	2	US-08-475-427-5	Sequence 5, Appl
45	533.5	37.9	3012	2	US-07-842-165-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-522-714-1  
; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-09-522-714-1

Alignment Scores:  
Pred. No.: 5.77e-138 Length: 1094  
Score: 1351.00 Matches: 238  
Percent Similarity: 98.39% Conservative: 6  
Best Local Similarity: 95.97% Mismatches: 4  
Query Match: 95.95% Indels: 0  
DB: 4 Gaps: 0

US-10-692-367-70 (1-250) x US-09-522-714-1 (1-1094)

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210	Db		GACGAGTACTGCGCGCAGCGGTGCAGTCGGGCGCGTGGCGCTCGGGCGCGCGGCGAGC	269
43	Qy		SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyIle	62
270	Db		AGTGGCGGCGGTGGTGCGAACGTGGCTAGCGTCGTCAACCGGCTCTCTTCTTCAACGCGCATC	329
63	Qy		LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu	82
330	Db		AGAGCCAGCCCGGAGCGGGTGCAGGCGAAGAACTTCTACACCGCGAGCGGTCCTCGT	389
83	Qy		SerAlaValLysAlaLysProGlyPheAlaHisGlySerGlnValGlnGlyLysArg	102
390	Db		AGCGCCGTCAAGCGGTACCCAGGCTTCGCCCATCGCGGTTCGACGGTGCAGGGCAAGCGC	449
103	Qy		GluIleAlaAlaPhePheAlaHisAlaThrHisglnThrGlyHisPheCysTyrIleSer	122
450	Db		GAGATCGCGCGCTTCTTCGCGCAGCCACGACGAGACCCGGGCAATTTCTGCTACATCAGC	509
123	Qy		GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla	142
510	Db		GAGATCAACAGAGGCAACGCCCTACTGCGACCCGACCAAGAGGCAGTGGCGCTCGCGCGG	569
143	Qy		GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyPro	162
570	Db		GGCGAAGAAGTACTAGCGGCGGGCGCGCTGCGAGATCTCGTGAACCTACAACTACGGGCGC	629
163	Qy		AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla	182
630	Db		GGGGGAGGGCCCATCGGCTTCAGCGGCTCGGGGACCCCGGAGGGTGGCGGGAGCGCC	689
183	Qy		ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro	202
690	Db		GTGTGGCGTTCAAGCGCGGCTCTGGTTCTTGGATGAACAGCGTGCACGGGGTGGTGCGG	749
203	Qy		GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCysAspGlyAsnAsn	222
750	Db		CAGGGGTTTCGGCGCCACCCAGCGGCCATCAACGGCGCCCTCGAGTGTGGCGGGAAACAAC	809
223	Qy		ProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyVal	242
810	Db		CCGCGCCAGATGACCGCGGTGTGGCTACTACAGGCGAGTACTGCCCGCCAGCTCGCGCGTC	869
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Db	642	GCGGTGTCGCGTTCGCGTTCGGTCTGGTGTGGAGAACACGTCGACGGGGCCATC	701
Qy	200	ValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsp	219
Db	702	GTCTCCGGCCAGGGCTTCGGGGCCACCATCGGGGCCATCAACGGGGCGCTCGAGTGCAC	761
Qy	220	GlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrIysGlnTyrCysArgGln	239
Db	762	GGCAAGAACCCCACTCCGTCAACACCGGTGTCCTACTACAAGCAGTTCTGCAGGAT	821
Qy	240	LeuGlyValAspProGlyProAsnLeuThrCys	250
Db	822	TTCCGGCTCGACCCGGGCAACACCTCACCTGC	854

RESULT 3  
US-08-181-271A-37  
; Sequence 37, Application US/08181271A  
; Patent No. 5614395  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.

RESULT 3  
US-08-181-271A-37  
; Sequence 37, Application US/08181271A  
; Patent No. 5614395  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
;

APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,271A  
FILING DATE: 13-JAN-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-181-271A-37

Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-181-271A-37 (1-1079)

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Db 153 GATGCATACCTGCGGTGTGGATGCCGATCAGGTCTCTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyTyr 62  
Db 207 CCGACCGGAGGG-----TCGGTCGTAGCATGTGCACCAAGGTTCTTTAAACAATATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCCAGCTGTTAATGTTGCGCGGGGAAAGATTTACACCCGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACCTTTCCCACTTTGCCAATCTCTGTACC-----AGACGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCAGAGACCGGACATTTCTGTACATAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141  
Db 429 GAGATTAAACGAGCAACACGTAACCTACTGTCAGAGCAGCAACACATAATACCATGTCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161  
Db 489 CCGGGAAGAGGCTACTTCGGTCGTGGTCCGATCCAACTATCATGGAACATACAACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGCTCAAGCTCTCGGCTTTGACCTTCACGACGCCCGCAACTTGTGGGTAGCAAC 608  
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTCAGTTCGGGTTTGTGGTTTGGATGATAGCGTAAGCCCGGTTCTG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCysAspGlyAsn 221  
Db 669 AACCAAGGGTTTGAGGCCACCATTTAGACTATTATATGGA---ATGGAATGTAAACGGTGGT 725  
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241

Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGATATAGAGACTATTGGGACAGCTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGACCCCTGGTCTTAACCTTAGTTGC 812

## RESULT 4

US-08-449-315-37  
; Sequence 37, Application US/08449315  
; Patent No. 5650505  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,315  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/769,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-449-315-37

Alignment Scores:  
Pred. No.: 4,84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-449-315-37 (1-1079)

Qy 3 GluAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTACTGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGGTGGATGCCGATCAGTCTCTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62  
Db 207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAAGGTTTCTTTAACATATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGTAATGTTGCGCGGGAAGAATTCACCCGTAAGTCTTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyArg 102  
Db 321 AACGCGCTAATACTTTCCCACTTTGCCAATTTCTGTACC-----AGAGGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCACGAGACCGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTTPProCysAla 141  
Db 429 GAGATTAAACGAGCAACACAGTAAGTACTGTCAGAGCAGCAACACACATATCCCATGTGCA 488

Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrrAsnTyrAsnTyrGly 161  
 Db 489 CCGGAAAGGCTACTTCGGTCGTGGTCCGATCCAACTATCATGGAACCTCAACACTACCGA 548  
 Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAsp 181  
 Db 549 GCGTGTGTCAAAGTCTCGTCTTGACCTTCTACCCAGCCGGAACCTTGTGGGTAGCAAC 608  
 Qy 182 AlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201  
 Db 609 CCAACTGTAGCTTTCAGGTCGGTGTGTGGTTTGGATGAATAGCGTAAGCCGCTTCG 668  
 Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAlaGlyAlaLeuGluCysAspGlyAsn 221  
 Db 669 AACCAAGGGTTGGAGCCACCATTAAGCTATTATATGA--ATGGAATGTAAACGGTGGT 725  
 Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
 Db 726 AATCCGGTCAGTCAACGCAAGGATTGGATCTATAGACTATTTGGACAGCTTGGT 785  
 Qy 242 ValAspProGlyProAsnLeuThrCys 250  
 Db 786 GTGACCCCTGGTCTTAACCTTAGTTGC 812

## RESULT 5

US-08-444-803-37  
 ; Sequence 37, Application US/08444803  
 ; Patent No. 5654414  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ryals, John A.  
 ; APPLICANT: Alexander, Danny C.  
 ; APPLICANT: Beck, James J.  
 ; APPLICANT: Duesing, John H.  
 ; APPLICANT: Friedrich, Leslie B.  
 ; APPLICANT: Goodman, Robert M.  
 ; APPLICANT: Harms, Christian  
 ; APPLICANT: Meins, Jr., Frederick  
 ; APPLICANT: Montoya, Alice  
 ; APPLICANT: Moyer, Mary B.  
 ; APPLICANT: Neuhaus, Jean-Marc  
 ; APPLICANT: Payne, George B.  
 ; APPLICANT: Sperison, Christoph  
 ; APPLICANT: Stinson, Jeffrey R.  
 ; APPLICANT: Unnes, Scott J.  
 ; APPLICANT: Ward, Eric R.  
 ; APPLICANT: Williams, Shericca C.  
 ; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 ; NUMBER OF SEQUENCES: 106  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CIBA-GEIGY Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/444,803  
 ; FILING DATE: 19-MAY-1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/181,271  
 ; FILING DATE: 13-JAN-94  
 ; APPLICATION NUMBER: US 08/093,301  
 ; FILING DATE: 16-JUL-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/937,197  
 ; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/678,378  
 ; FILING DATE: 1-APR-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/305,566  
 ; FILING DATE: 6-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/165,667  
 ; FILING DATE: 8-MAR-1988  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/042,847  
 ; FILING DATE: 6-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/632,441  
 ; FILING DATE: 21-DEC-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/425,504  
 ; FILING DATE: 20-OCT-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/848,506  
 ; FILING DATE: 6-MAR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/768,122  
 ; FILING DATE: 27-SEP-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/580,431  
 ; FILING DATE: 7-SEP-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/368,672  
 ; FILING DATE: 20-JUN-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/329,018  
 ; FILING DATE: 24-MAR-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/045,957  
 ; FILING DATE: 12-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Elmer, James Scott  
 ; REGISTRATION NUMBER: 36,129  
 ; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8614  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1079 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-444-803-37

Alignment Scores:  
 Pred No.: 4,84e-81 Length: 1079  
 Score: 830.00 Matches: 148  
 Percent Similarity: 73.09% Conservative: 34  
 Best Local Similarity: 59.44% Mismatches: 57  
 Query Match: 58.95% Indels: 10  
 DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-444-803-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
 Db 93 CAAAACTGCGGTTCGGCTCCAAACCTCTGTTGCAGTCAGTTCCGTTACTGTGTACCGAC 152  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
 Db 153 GATGCATACCTCGCGTGTGGATGCCGATCAGGTCCCTTGTAGA-----GGTAGTGGAAAC 206  
 Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyTyr 62  
 Db 207 CCGACCCGAGGG-----TCGGTCGGTAGCATTTGTGACACAGGTTTCTTTAAACATATT 260

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QY 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
261 ATCAACCAAGCTGGTAATGGTTGGCGGGAAAGATTCTACACCGGAGCTCTTCGTT 320
QY 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
321 AACGCGCTAATACTTCTCCCAACTTTGCCAATCTCTGTACC-----AGACGT 368
QY 103 GluLeuAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 GAATATTGCTACATGTTTGGCTCATTTCACTCAGAGACCGGACATTTCTGCTACATAGAA 428
QY 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 GAGATTACGGAGCAACACGTAACCTGTCAGAGCAGCACACACATACCATGTGCA 488
QY 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrGly 161
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
489 CCGGAAAGGCTACTTCGGTCCGTCCGATCCCAACTATCATGGAACACTCAACTACGGA 548
QY 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
549 GCGTGTGTCAAAGTCTCGGCTTGCCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608
QY 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMet 201
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
609 CCAACTGTAGCTTTCAGTCCGGTTTGGTTTGGATGATAGCGTAAGCGCGGTCTG 668
QY 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGGA---ATGGAATGTAACGGTGGT 725
QY 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
726 AATTCGGTGCAGTCAACGCAAGGATTTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785
QY 242 ValAspProGlyProAsnLeuThrCys 250
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
786 GTGGACCTCGTCTCACTTAACCTTAGTTGC 812

RESULT 6
US-08-449-043-37
; Sequence 37, Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-449-043-37

Alignment Scores: 4.84e-81 Length: 1079
Pred. No.: 830.00 Matches: 148
Score: 73.09%
Percent Similarity: 73.09%
Conservative: 34
```

Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-449-043-37 (1-1079)

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QY 3 GlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
DB 93 CAATACTGGTGGCTCCAAACCTCTGTTCAGTCAGTTCGGTTACTGGTACCGAAC 152
QY 23 AspGlyTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
DB 153 GATGCATACCTGGGTGGTGGATCGCATCGCTCTGTAGA-----GGTAGTGAACC 206
QY 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62
DB 207 CCGACCGGAGGG-----TCGGTCGGTAGCATGTGTGACACAGGTTCTTTAAACAAT 260
QY 63 LysAsnGlnAlaGlySerGlyCysGlnLysAsnPheTyrThrArgSerAlaPheLeu 82
DB 261 ATCAACCAAGCTGTAATGGTTGCGCGGGGAAGAATTTACCCCGTACTCTTTCGTT 320
QY 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
DB 321 AACCGCGCTAATACTTTCCCAACTTTCGCAATTCGTGTACC-----AGAGGT 368
QY 103 GluLeuAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
DB 369 GAAATTGCTACCATGTTTGTCTCAATTCACACGAGACCGGACATTTCTGCTACATAGAA 428
QY 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
DB 429 GAGATTACGAGGACCAACGTAACCTACTGCCAGACGACCAACACCAATATCCCATGTGCA 488
QY 142 AlaGlyLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
DB 489 CCGGGAAGAGCTACTTCGGTTCGGTTCGGTCCGATCCAACTATCATGGAACCTCAACTACGA 548
QY 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
DB 549 CGGTGTGCTCAAGTCTCGGCTTGTGACCTTCTAGCCAGCCGCAACTTGTGGTAGCAAC 608
QY 182 AlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
DB 609 CCAACTGTAGCTTTTCAGTCGGTGTGGTGGTGGTGGATGATAGCGTAAGCCCGGTTCTG 668
QY 202 ProGlnGlyPheGlyValThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
DB 669 AACCAAGGTTTGGAGCCACCATTAGACTATTATAGA---ATGGAATGTAACTGGT 725
QY 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
DB 726 AATTCGGTGCAGTCAACGCAAGGATTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785
QY 242 ValAspProGlyProAsnLeuThrCys 250
DB 786 GTGACCCCTGCTCAACTTAGTTGTC 812
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## RESULT 7

US-08-456-265A-37  
; Sequence 37, Application US/08456265A  
; Patent No. 5767369  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Ryals, John A.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Stinson, Jeffrey R.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,265A  
; FILING DATE: 31-MAY-95  
; CLASSIFICATION: 435  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 08/181,271  
; FILING DATE: 13-JAN-1994  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIORITY DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-456-265A-37

## Alignment Scores:

Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-456-265A-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAACCTCGGTTGGCTTCCAAACCTCTGTTCAGTCAGTTCGTTACGTTGGTACCGAC 152  
Qy 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTCGGTTGGATGCGATCGATCGTCTTGTAGA-----GGTAGTGGAC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyLe 62  
Db 207 CCGACCGGAGG-----TCGGTCGGTAGCATTTGTGACACAAAGTTTCTTTAAACAATATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGlnGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGTAATGTTGGCGGGGAAAAAGATTCTACACCGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACCCCGCTAATCTTTCCCACTTTGCCAATCTCTGTACC-----AGACGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTCGTACCATGTTTGTCTCAITTCACCTACGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer----LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141  
Db 429 GAGATTAAACGAGCAACAGTAACTACTGCGCAGAGCAGCAACACACAATACCCATGTGCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161  
Db 489 CCGGAAGAGGCTACTTCTCGTGGTGGTCCGATCACTATCATGGAATCACTACACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGTCAGAGTCTCGTCTTGACCTTCTACGCCAGCCCGAATTTGTGGGTAGCAAC 608  
Qy 182 AlaValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTTCAGTCCGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221  
Db 669 AACCAAGGTTTGAGCCACCATTTAGACTATTATGGA---ATGGAAATGTAACGGTGGT 725  
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
Db 726 AATTCGGTGCAGTCAACGCAAGGATTTGGTACTACTAGAGACTATTGTGGACAGCTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGAGCCCTGCTCTTAACCTTAGTTGC 812

## RESULT 8

US-08-455-416-37  
Sequence 37, Application US/08455416  
Patent No. 577200

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:





FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-244-37

Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-455-244-37 (1-1079)

Qy 3 GlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyThrThr 22  
Db 93 CAAAACTCGGTTGGCTCCAAACCTCTGTCAGTCAGTTCGGTTACTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTCGGTTGGATGCGATCGATCGTCTGTGTAG- - - - -GGTAGTGGAC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyLeu 62  
Db 207 CCGACCGGAGG- - - - -TCGGTCGGTAGCATTTGTGACACAGGTTCTTTAACAATATT 260  
Qy 53 LysHsnGlnAlaGlySerGlyCysGlnGlyLysAsnPhetThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGGTGAATGGTGGCGGGGAAAGATTCTACCCGGTACTTTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLeuArg 102  
Db 321 AACGCGCTAATACTTTCCCAACTTTCGCAATCTGTGTACC- - - - -AGAGCT 368  
Qy 103 GluLeuAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCAITTCCTACGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer- - -LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141  
Db 429 GAGATTAAACGGACCAACGTAATCTACTGCGGACGAGCAGCAACACACAAATACCCATGTGCA 488

Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrGly 161  
Db 489 CCGGAAAGGCTACTTCGGTTCGGTCCGATCAACTATATCGAACTACAACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGGTCAAAAGTCTCGGCTCTTGACCTTCTACGCCAGCCCGCAACTTGTGGGTAGCAAC 608  
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTCAGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221  
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Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
Db 726 AATTCCGGTGCAGTCAACGCAAGGATTGGATCTATATAGAGACTATTGTGGACAGCTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGACCCCTGCTCTTAACCTTAGTTGC 812

RESULT 10  
US-08-454-876-37  
; Sequence 37, Application US/08454876  
; Patent No. 5804693  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,876  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA: US 07/937,197  
APPLICATION NUMBER: 06-NOV-1992

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; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
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; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/E1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-454-876-37

Alignment Scores:
Pred. No.: 4,848-81 Length: 1079
Score: 830.00 Matches: 148
Percent Similarity: 73.09% Conservative: 34
Best Local Similarity: 59.44% Mismatches: 57
Query Match: 58.95% Indels: 10
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-454-876-37 (1-1079)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 93 CAAAACTCGGTTGGCTCCAAACCTCTGTTGCAGTCAGTTGGTTACTGTTGTTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 GATGCATCTCGGTTGGTGGATCGCGATCGGTCCTTGTAGA-----GGTAGTGGAAACC 206
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62
Db 207 CCGACCGGAGGG-----TCGGTCGGTAGCATTTGTGACACAAAGGTTTCTTTAAACAATATT 260

Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82
Db 261 ATCAACCAAGCTGGTAATATGGTTGGCGGGGAAAGATTCTACACCGTGACTCTTTCTGTT 320
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 321 AACCCCGCTAATACTTTTCCCAACTTTGCCAATTTCTGTTACC-----AGACGT 368
Qy 103 GluIleAlaAlaPhePheAlaHisGlnThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 369 GAAATTGCTACCATGTTTGTCTCAITTCACACGAGACCGGACATTTCTGCTACATAGAA 428
Qy 123 GluIleSer----LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
Db 429 GAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGCAACACACATATCCCATGTGCA 488
Qy 142 AlaGlyGlnLysTyrTyrGlyValGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
Db 489 CCGGAAAGGCTACTTCGGTCTGGTCCGATCCACTATCATGGAACCTACACTACCGA 548
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
Db 549 GCGTGTGCTCAAGCTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTTGGGTAGCAAC 608
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTrpMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTTCAGTCTGGGTTTGTGGTATTAATGGA---ATGGAATGAACGGTGTG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGTTTGGAGCCACCATTAGAGCTATTATGGA---ATGGAATGAACGGTGTG 725
Qy 222 AsnProAlaGlnMetAsnAlaAargIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATTCGGGTGCGAGTCAAGCAAGGATTTGGATACTATAGAGACTATTGTGGACAGCTTGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGACCCCTGGTCTCAACCTTAGTTGTC 812

RESULT 11
US-08-457-364-37
; Sequence 37, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr. Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
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COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/457,364  
 FILING DATE: 31-MAY-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/181,271  
 FILING DATE: 13-JAN-94  
 APPLICATION NUMBER: US 08/093,301  
 FILING DATE: 16-JUL-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/937,197  
 FILING DATE: 6-NOV-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/678,378  
 FILING DATE: 1-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/305,566  
 FILING DATE: 6-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/165,667  
 FILING DATE: 8-MAR-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/042,847  
 FILING DATE: 6-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/632,441  
 FILING DATE: 21-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/425,504  
 FILING DATE: 20-OCT-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/948,506  
 FILING DATE: 6-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/768,122  
 FILING DATE: 27-SEP-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/580,431  
 FILING DATE: 7-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/368,672  
 FILING DATE: 20-JUN-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/329,018  
 FILING DATE: 24-MAR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/045,957  
 FILING DATE: 12-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elmer, James Scott  
 REGISTRATION NUMBER: 36,129  
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8614  
 TELEFAX: (919)541-8689  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1079 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-457-364-37

Alignment Scores:  
 Pred. No.: 4.84e-81 Length: 1079  
 Score: 830.00 Matches: 148  
 Percent Similarity: 73.09% Conservative: 34

Best Local Similarity: 59.44% Mismatches: 57  
 Query Match: 58.95% Indels: 10  
 DB: 2 Gaps: 5

US-10-692-367-70 (1-250) x US-08-457-364-37 (1-1079)

Qy 3 GlnAsnCySGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
 Db 93 CAAAACTCGCGTTCGGCTCCAAACCTCTGTTGTCAGTCAGTTCGGTACTGTTGGTACCGAC 152  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42  
 Db 153 GATGCATACCTCGCGTGTGGATGCCGATCCAGTCCCTTTGTAGA-----GGTAGTGGAAAC 206  
 Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62  
 Db 207 CCGACCGGAGG-----TCGGTCGTAGCATTGTGACACAGGTTTCTTTAAACAATTT 260  
 Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
 Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGAAGATTCTACACCGCTGACTCTTCGTT 320  
 Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
 Db 321 AACGCCGCTAATACTTTCCCACTTTGCCAATTTCTGTATCC-----AGACGT 368  
 Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
 Db 369 GAAATGCTACCATGTTGCTCATTTCACGACCGGACATTTCTGTCATAGAA 428  
 Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141  
 Db 429 GAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGCAACACACAATACCCATGTGCA 488  
 Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161  
 Db 489 CCGGGAAGAGGCTACTTCGGTCCGTCGATCCCACTATCATGGAACATCACTACGAACTACGGA 548  
 Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAsp 181  
 Db 549 CGGTGTGTCAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGCACTTGTGGGTAGCAAC 608  
 Qy 182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnValHisArgValMet 201  
 Db 609 CCAACTGTAGCTTTCCAGTCCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGT 668  
 Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221  
 Db 669 AACCAAGGGTTTGGAGCCCACTTTAGAGCTATTAAATGGA---ATGGAATGTAACCGTGGT 725  
 Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
 Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGATCTATAGACTATTGTTGGACACTTGGTGGTGGT 785  
 Qy 242 ValAspProGlyProAsnLeuThrCys 250  
 Db 786 GTGGACCTCGTCTCACTAACCCTTAGTTGC 812

RESULT 12  
 US-08-456-262-37  
 ; Sequence 37, Application US/08456262  
 ; Patent No. 5851766  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ryals, John A.  
 ; APPLICANT: Alexander, Danny C.  
 ; APPLICANT: Beck, James J.  
 ; APPLICANT: Duesing, John H.  
 ; APPLICANT: Friedrich, Leslie B.  
 ; APPLICANT: Goodman, Robert M.  
 ; APPLICANT: Harms, Christian  
 ; APPLICANT: Meins, Jr., Frederick  
 ; APPLICANT: Montoya, Alice  
 ; APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,262  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
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APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
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APPLICATION NUMBER: US 07/425,504  
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PRIOR APPLICATION DATA:  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
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ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
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INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-456-262-37  
Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
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Query Match: 58.95% Indels: 10  
DB: 2 Gaps: 5  
US-10-692-367-70 (1-250) x US-08-456-262-37 (1-1079)  
Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACCTGCGGTTCGCTCCAAACCTCTGTTGCGAGTCAGTTCGGTTACTGTGTACCCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGTGGATGCCGATCAGGTCTCTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAenValAenValAenValThrGlySerPheAenGlyIle 62  
Db 207 CCGACCGGAGGG-----TCGGTCGTAGTACCTGTGACACAGGTTCTTTAAACAATATT 260  
Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGTGTANTGTTGCGCGGGAAGAAAGATTTCTACACCGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACTTTCCCACTTTGCCAATCTCTGTACC-----AGAGGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGlnThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTGTCTCATTTCACTCAGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer---LysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141  
Db 429 GAGATTACGGAGCAACACGTAATACTTGCAGAGCAGCAGACACACATACCCATGTGA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAsnTyrGly 161  
Db 489 CCGGGAAGAGGCTACTTCGGTCGTGGTCCGATCAACTATCATCGAACAACATCACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGCTCAAGCTCTCGGTCCTTGACCTTTCAGCCAGCCCGAACCTTTGTGTAGTGAAC 608  
Qy 182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTTCAGTTCGGGTTTGGTTTGGATGATAGCTTAAGCCCGGTTCTG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGlyCysAspGlyAen 221  
Db 669 AACCAAGGGTTTGGAGCCACCATTAGACTATTATATGA---ATGGAATGTAACGGTGT 725  
Qy 222 AenProAlaGlnMetAenAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeuGly 241  
Db 726 AATTCCGGTGCAGTCAACGCAAGGATTGGATATATAGAGACTATTGTGGACAGCTGTGT 785  
Qy 242 ValAspProGlyProAenLeuThrCys 250  
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Db 786 GTGACCTGGTCTTAACCTAGTTGC 812  
RESULT 13.  
US-08-456-240-37  
; Sequence 37, Application US/08456240  
; Patent No. 5856154  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,240  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-456-240-37  
Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 2 Gaps: 5  
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Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTCAGTCAGTTCGGTTACTGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTCGGTGTGGTCCGATCAGGTCTTGTAGA-----GGTAGTGGAAACC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyIle 62  
Db 207 CCGACCGGAGG-----TCGGTCGGTAGCATTTGACACAAAGGTTTCTTTAACAATATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyAsnPheTyrThrArgSerAlaPheIleu 82  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGAAGAATTCACCCCGTACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCCGCTAATCTTTCCCACTTTGCCAATTCCTGTACC-----AGACGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCAGAGACCGGACATTTCTGTACTAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTTPProCysAla 141  
Db 429 GAGATTAAACGAGCAACACGTAATCTCTCCAGAGCAGCAACACACAAATACCCATGTGCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTTPAsnTyrAsnTyrGly 161  
Db 489 CCGGAAAAGGCTACTTCGGTCCGATCCAACTATCATGTGAAGTCACTCACTCGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181

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Db 549 CGGTGTGCTCAAGTCTCGGCTTCTTACGCCAGCCGCACTTGTGGTAGCAAC 608
Qy 182 AlaValAlaPheLysAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTCAGGTGCGGTTTGTGTTTGGATGAATAGCGTAAGCGGTTCTG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTATATGGA--ATGGAATGTAAACGGTGT 725
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATCCGGTGCAGTCACGACGAGGATTGGATCTATAGACTATTGTGGACAGCTTGGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGGACCTGCTTAACTTAGTTGC 812

RESULT 14
US-08-455-736-37
; Sequence 37, Application US/08455736
; Patent No. 5880328
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,736
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-1994
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
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; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
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; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-455-736-37

Alignment Scores:
Pred. No.: 4.84e-81 Length: 1079
Score: 830.00 Matches: 148
Percent Similarity: 73.09% Conservative: 34
Best Local Similarity: 59.44% Mismatches: 57
Query Match: 58.95% Indels: 10
DB: 2 Gaps: 5

US-10-692-367-70 (1-250) x US-08-455-736-37 (1-1079)
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTCCGTTACTGTGGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 GATGCATACCTCGGTTGGATGCCGATCCAGTCAGTCTCTGTAGA-----GGTAGTGAACC 206
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyTle 62
Db 207 CCGACCGGAGGG-----TCGGTCGTAGCATTGTGACACAGGTTCTTTAAACATATT 260
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 261 ATCAACCAAGCTGGTATGTTGCGCGGGAAGATTCTACACCGTGACTCTTTTCGTT 320
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207 CCGACCGGAGGG-----TCGGTCGGTAGCATTTGTACACAAGGTTTCTTTAAACAATATT 260
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QY 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
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549 GCGTGTGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608
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669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGGA---ATGGAATGTAACGGTGGT 725
QY 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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QY 242 ValAspProGlyProAsnLeuThrCys 250
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786 GTGGACCTTGGTCTCAACCTTAGTTGC 812
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Job time : 131.74 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:04:03 ; Search time 2237.67 Seconds  
(without alignments)  
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Title: US-10-692-367-70  
Perfect score: 1408

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Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Deiop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2 1/USPTO spool/US10692367/runat 20052005 172255 20018/app query.fasta\_1.846  
-DB=EST -QFMT=fastcap -SUPFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptp -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl1:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1237	87.9	855	4	BG837663
3	1166	82.8	737	6	CD435649
4	1161.5	82.5	958	4	BG837479
5	1160	82.4	767	7	C0524416
6	1099.5	78.1	837	7	CN133023
7	1062.5	75.5	710	6	CD443492
8	1016	72.2	647	6	CA197556
9	994	70.6	628	4	BM736454

10	982	69.7	625	5	BM895383	952073H05
11	980	69.6	978	9	CG328450	CG328450
12	978	69.5	786	6	CA270202	SCQSLB205
13	975	69.2	741	6	CD994869	QBB18D07.
14	973	69.1	578	6	CD994156	QBB13F07.
15	971	69.0	753	6	CD994885	QBB18E05.
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19	965	68.5	578	6	CD994454	QBB15F08.
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21	960	68.2	812	7	CN132942	OX1_9 D11
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26	953	67.7	887	6	CB981996	CB981996
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#### ALIGNMENTS

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AV103546

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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AV103546 Zea mays PC0155066 mRNA sequence. 1179 bp mRNA linear HTC 16-OCT-2002

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AV103546 Zea mays

Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1179)

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,

Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Design of

Maize Mapping Project/DuPont Consensus Sequences for

Overgo Probes

Unpublished (2002)

2 (bases 1 to 1179)

Coe, E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,

these are publicly available from ZmDB and may be found by BLAST

searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

Location/Qualifiers

1..1179

/organism="Zea mays"

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/mol_type="mRNA"
/db_xref="MaizeDB:638921"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Alignment Scores:
Pred. No.: 4,126-120 Length: 1179
Score: 1271.50 Matches: 222
Percent Similarity: 92.16% Conservative: 13
Best Local Similarity: 87.06% Mismatches: 13
Query Match: 90.31% Indels: 7
DB: 3 Gaps: 1
US-10-692-367-70 (1-250) x AV103546 (1-1179)

QY 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
DB 149 CAGAACTGCGGCTGCGACCAAACTTCTGCTGCAGCAAGTTTCGGCTACTGCGGCACGACC 208
QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
DB 209 GACGCTACTGCGGCGAGCGGTGCGAGTCGGGCGCGCTCGGGCGGCGGCGGCGG 268
QY 43 SerGlyGly-----GlyGlyAlaAenValAlaSerValValThr 55
DB 269 GCGCGCGCGCGGAGCGCGGAGCGGAGTGGCGGTGCGAAGTGGCTAATGTGTCACC 328
QY 56 GlySerPheAenGlyIlelyAenGlnalaglySerGlyCysGluGlyLysAenPhe 75
DB 329 GACGCGTTCTTCAACGGCATCAAGAACAGCGCGGAGCGGCGGTGCGAGGGCAAGACTTC 388
QY 76 TyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGly 95
DB 389 TACACCGCGAGCGGCTTCTGAGCGCGCTCAACGGGTACCGCGGCTTCGCCATTCGGCGG 448
QY 96 SerGlnValGlnGlyLysArgGluLeuAlaAlaPheAlaHisAlaThrHisGluThr 115
DB 449 ACGGAGGTGGAGGCAAGCGGAGATCGCGCTTCTTCGCGCAGCTCAGCAGCAGCAGC 508
QY 116 GlyHisPheCysTyrIleSerGluLleSerLysSerAenAlaTyrCysAspProThrLys 135
DB 509 GGACATTTCTGCTACATCAGCGGAGATCAACAGAGCAACGCGCTACTGCGAGCGGCAAC 568
QY 136 ArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 155
DB 569 AGGAGTGGCGGCGTGGCGGCGGCGAGGAGTACTACGGGCGCGCGCGCTCGCATCTCG 628
QY 156 TrpAenTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspPro 175
DB 629 TGGAACTACAACTACGGGCGCGCGGAGGAGACATCGGCTTCAACGGGCTCGCGGACCC 688
QY 176 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMetAen 195
DB 689 AACAGGTTGGCGGAGGAGCGGCTGATCGGTTCAGAGCGGCGCTCTGGTTCTGGATGAC 748
QY 196 AenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyVala 215
DB 749 AACGTGACACGTGTGATGCCCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGGCGC 808
QY 216 LeuGluCysAspGlyAsnAenProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGln 235
DB 809 CTCGAGTGCACAGGGAAACAACCCCGCCAGATGAAGCGCGCGTCTACTACAGGACG 868
QY 236 TyrCysArgGlnLeuGlyValAspProGlyProAenLeuThrCys 250

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Db 869 TACTGCCAGCAGCTTCGGGTGCGACCCAGGCGCCCAACCTCACTTGC 913

RESULT 2
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DEFINITION Zm10_01e10 A Zm10_AAPC_ECORC_Fusarium_graminearum_corn_silk Zea
ACCSSION BG837663
VERSION BG837663.1 GI:14203986
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 855)
Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualifiers
1..855
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="CO388"
/db_xref="taxon:4577"
/clone="Zm10_01e10"
/tissue type="Silk"
/dev stage="4-5 days post-silk emergence"
/clone_lib="Zm10_AAPC_ECORC_Fusarium_graminearum_corn_silk"
/notes="Vector: Bluescript SK+/XhoI-BcoRI; Site_1: EcoRI;
Site_2: XhoI; Field-grown corn was silk channel-inoculated
in the morning (-10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."

ORIGIN
Alignment Scores:
Pred. No.: 9,49e-117 Length: 855
Score: 1237.00 Matches: 228
Percent Similarity: 97.50% Conservative: 6
Best Local Similarity: 95.00% Mismatches: 6
Query Match: 87.86% Indels: 2
DB: 4 Gaps: 0
US-10-692-367-70 (1-250) x BG837663 (1-855)

QY 11 ValCysCysSerLysPheGlyTyrCysGlyThrThrAspGluTyrCysGlyCys 30
DB 854 GTATGCTGAGCAAGTTTGGCTACTGCGGACGACCGAGTACTGCGGCGGCGGTC 795
QY 31 GlnSerGlyProCysArgSerGlyGlyGlySerSerGlyGlyGlyAlaAenVal 50
DB 794 CAGTCGGGCGCGTC-CGCTCGGCGGCGGCGGCGGAGCAGTGGCGGCGGCGGTCG 736
QY 51 AlaserValValThrGlySerPheAenGlyIleLysAenGlnAlaGlySerGlyCys 70
DB 735 GCTAGCGTCGTCAACCGGCTCTCTTCTTCAACGGCATCAAGAGCCGCGGCGGTCG 676

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Qy 71 GluGlyLysAenPheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGly 90
Db 675 GAGGGCAAGAACTTCTACACCGGAGCGGTCTCTGAGCGCGTCAAGGGCTACCCAG- 617

Qy 91 PheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHis 110
Db 616 TTCGCCCATGCGGGTTCAGGTGAGGCAAGCGAGATCGCGCTTCTTCGCGAC 557

Qy 111 AlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyr 130
Db 556 GCCACGCACGAGACCGGGCAFTTCTGTCTACATCAGCGAGATCAACAGAGCAACGCCTAC 497

Qy 131 CysAspProThrLysArgGlnTyrProCysAlaAlaGlnLysTyrTyrGlyArgGly 150
Db 496 TGCACACCGACCAAGAGCGAGTGGCGTGCAGCGCGGCGAGAGTACTACGGCGCGGC 437

Qy 151 ProLeuGlnIleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAsp 170
Db 436 CCGTGTGAGATCTCTGTGGAATCTACATACGGGCGCGGAGGGCCATCGGCTTCGAC 377

Qy 171 GlyLeuGlyAspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeu 190
Db 376 GGGCTCGGGACCCCGGCAGCGTGGCGGACCGTGGTGGCGTTCAAGCGCGCGCTC 317

Qy 191 TrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArg 210
Db 316 TGGTTCGTGGATGAACAGCGTGCAGGGGTGGTGGCGCAGGGGTTCGGCGCCACCCAGG 257

Qy 211 AlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIle 230
Db 256 GCCATCAACGGCGCCCTCGAGTGGCGGGGAACACCCCGCCAGATGAACGGCGCGT 197

Qy 231 GlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
Db 196 GGCTACTACAGCAGTACTGCGCGCAGCTCGCGTTCGACCCCGGCGCCCAACCTCACCTGC 137

RESULT 3
CD435649
LOCUS
DEFINITION EL01N0364B04.b Endosperm_3 Zea mays cDNA, mRNA sequence.
ACCESSION CD435649
VERSION CD435649.1 GI:31351292
KEYWORDS EST.
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 737)
  Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
  Larkins, B., Beecraft, P. and Messing, J.
  Characterization of the maize endosperm transcriptome and its
  comparison to the rice genome
  Genome Res. 14 (10), 1932-1937 (2004)
  Contact: Lai, Jinsheng
  Dr. Joachim Messing's lab
  Wakeman Institute, Rutgers University
  190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
  Tel: 732-445-3801
  Fax: 732-445-5735
  Email: jlai@wakeman.rutgers.edu
  Seq primer: T3.
  Location/Qualifiers
    1..737
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      /cultivar="W22"
      /db_xref="taxon:4577"
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## ORIGIN

Alignment Scores:  
 Pred. No.: 1.59e-109 Length: 737  
 Score: 1166.00 Matches: 211  
 Percent Similarity: 95.96% Conservative: 3  
 Best Local Similarity: 94.62% Mismatches: 4  
 Query Match: 82.81% Indels: 5  
 DB: 6 Gaps: 1

US-10-692-367-70 (1-250) x CD435649 (1-737)

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Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 83 CAGAACTCGCGCTGCCAGCCAAAGCTCTGCTGAGCAAGTTCGGCTACTCGGGACAGACC 142

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 143 GACGAGTACTCGGCGAGCGGTGCCAGTCCGGCCCGTCCGCTCGGGCGGC----- 193

Qy 43 SerGlyGlyGlyAlaAenValAlaSerValValThrGlySerPheAsnGlyIle 62
Db 194 ---GGCGCGGTGGTGGAAACGTGGCTAGCGTCTCACCGCTCTCTTCTTCAACGGCATC 250

Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82
Db 251 AAGAACCCAGCGCGGAGCGGTGGAGGGCAAGAACTTCTACACCCGAGCGCGTTCCTG 310

Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 311 AGCGCGTCAAGGGTATCCAGGGTTCGCCCATCGCGGTTCGAGGTGCAGGGCAAGCGC 370

Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 371 GAGATCGCGCTTCTTCGGCGACGCCACGACGAGACCGGGCATTTCTGCTACATCAGC 430

Qy 123 GluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142
Db 431 GAGATCAACCAAGAGCAACCGCTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCG 490

Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162
Db 491 GGGCAGAAGTACTACGGCGCGCGCGCGCTCGAGATCTCGTGAACACTACACTACGGGCC 550

Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182
Db 551 CGCGGGAGGGCCATCGGCTTCAGCGGTCTGGGACCCCGCGAGGTGGCGGGAGCGCC 610

Qy 183 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHis-ArgValMetPr 202
Db 611 GTGGTGGCGTTCGAAGCGCGCTCTGGTTCCTGGATGAACACCGGTGCACGGGGGTGGTGC 670

Qy 202 oGlnGlyPheGlyAlaThrIleArgAlaIleAAsnGlyValAlaLeuGluCysAspGlyAsnAs 222
Db 671 GCAGGGTTCGGCGCCACCACCGAGGCGCATCAACGGCGCCCTTCGAGTGGCGGGAGCAA 730

Qy 222 nProAla 224
Db 731 CCGCGCC 737

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## RESULT 4

## BG837479

## LOCUS

## DEFINITION

## Zm10\_10h09\_A Zm10 AAFC ECORC Fusarium graminearum\_corn\_silk Zea

## mays cDNA Clone Zm10\_10h09, mRNA sequence.

## ACCESSION

## BG837479

## VERSION

## BG837479.1

## KEYWORDS

## EST.

## SOURCE

## Zea mays

## ORGANISM

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

## clade; Panicoideae; Andropogoneae; Zea.

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REFERENCE
AUTHORS   1 (bases 1 to 958)
           Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
           Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
           Spott,D., and Tinker,N.A.
TITLE     Expressed Sequence Tags from Maize Silk Six Hours After Silk
           Channel Inoculation with Fusarium graminearum
JOURNAL   Unpublished (2001)
COMMENT   Contact: Harris, Linda J.
           Eastern Cereal and Oilseed Research Centre
           Agriculture and Agri-food Canada
           Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
           CANADA
           Tel: (613) 759-1314
           Fax: (613) 759-6566
           Email: harriel@agr.gc.ca.
FEATURES
source    Location/Qualifiers
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           /dev_stage="4-5 days post-silk emergence"
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           /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
           Site 2: XhoI; Field-grown corn was silk channel-inoculated
           in the morning (~10 am) with 1 ml of a macroconidial
           suspension (500,000 spores/ml) of Fusarium graminearum and
           silk channels were collected and immediately frozen in
           liquid nitrogen 6 hours later. RNA was extracted from
           silk tissue between 1 cm below and above the inoculation
           point in the silk channel, RNA from five silk channels was
           pooled."
ORIGIN
Alignment Scores:
Score:      6.6e-109      Length:      958
Percent Similarity: 1161.50      Matches:      212
Best Local Similarity: 89.37%      Conservative: 15
Query Match: 82.49%      Mismatches: 21
DB:          4           Indels:      7
           Gaps:        1
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Qy  3  GlnAsnCysGlyCysGlnProAsnValCysCysSer-LysPheGlyTyrCysGlyThrTh 22
Db  32 CAGAACTCGCGCTGCCAGCCTTAACCTTCTGCTGCAGCAAAAGTYCGGCTACTTCGGCAGCAG 91
Qy  22 rAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGly----- 38
Db  92 CGAGCACTACTGCGCGCAGCGGTGCCAGTGGCGCCCGCTCGCTCGCGCGCGCGCGCG 151
Qy  39 -GlyGlyGlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPh 58
Db  152 CGGCGCGCGGCGCGGAGCAGTGGCGGTGCAGAACGTGCTAACTGTCTACGCGACGGT 211
Qy  58 ePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrAr 78
Db  212 CTTCAAGCGCATCAAGAAACAGCGCGGAGCGGCTGGCGGCAAGAACTTCTACACCCG 271
Qy  78 qSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnVa 98
Db  272 GAGCGCGTTCCTGAGCGCGGTCAACAA-GRACNCCGTTGCGCCATCGCGGAGCGAGGT 330
Qy  98 lGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPh 118
Db  331 GGAGGGCAAGCGCGAGATCGCGCTTCTTCGCGCAGCTCAGCGACGAGCGGACATT 390
Qy  118 eCyTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTr 138
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Db  391 CTGTACTCATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACGCAAGCAACAGCGAGTG 450
Qy  138 pProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTy 158
Db  451 GCCGTGCGCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGCGAGATCTCTGTGGAAC 510
Qy  158 rAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgVa 178
Db  511 CAACTACGGGCGCGCGGAGGACATCGGCTTCAACGGGCTCGCGGACCCCAACAGGGT 570
Qy  178 lAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnValIh 198
Db  571 GGCGCAGGAGCGCGCTGATCGGTTCAAGAGCGGCGCTCTGGTTCTGGATGAACAACGTGCA 630
Qy  198 sArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCy 218
Db  631 CCGTGTGATCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTG 690
Qy  218 sAspGlyAsnAsnProAlaGlnMetAsnAlaAArgIleGlyTyrTyrLysGlnTyrCysAr 238
Db  691 CAACGGGAGAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTACAGCAGTACTGCCA 750
Qy  238 gGlnLeuGlyValAspPro-GlyProAsnLeuThrCys 250
Db  751 GCCMCTCGCGTCSACCCAGGGGCGCCAMCCTCACTTGC 788
RESULT 5
CO524416 767 bp mRNA linear EST 15-JUL-2004
LOCUS     3530.1_161.1_E12.y.1_3530 - Full length cDNA library created by
DEFINITION Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION CO524416
VERSION   CO524416.1 GI:50329290
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 767)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
           Department of Biological Sciences
           Stanford University
           855 California Ave, Palo Alto, CA 94304, USA
           Tel: 650 723 2227
           Fax: 650 725 8221
           Email: walbot@stanford.edu
           Plate: 3530.1_161.1 row: E column: 12.
FEATURES
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           /lab_host="DH10B"
           /clone_lib="3530 - Full length cDNA library created by
           Invitrogen from multiple tissues"
           /note="Organ: silks, husks, ears, pollen, shoot tips,
           leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
           6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
           Project contracted with Invitrogen to produce a
           normalized, full length library in a pSport vector. This
           is a Gateway compatible vector, permitting clone movement
           to new vector backbones for expression in diverse host
           cells using recombination rather than restriction enzymes.
           Details of the vector and sequencing primers are available
           at ZmDB in the EST library description tables. poly(A)+

```

mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.96e-109 Length: 767  
 Score: 1160.00 Matches: 206  
 Percent Similarity: 98.59% Conservative: 4  
 Best Local Similarity: 96.71% Mismatches: 3  
 Query Match: 82.39% Indels: 0  
 DB: 7 Gaps: 0

US-10-692-367-70 (1-250) x C0524416 (1-767)

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 Db 127 CAGAACTCGGCTGCCAGCCAAAGCTATGCTGCAGCAGATTGGCTACTCGGCACGACC 186  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
 Db 187 GACGAGTACTCGGCGACGGGTGCGAGTCGGGCGCGTCCGCTCGGGCGGGCGGCGCAGC 246  
 Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyTle 62  
 Db 247 AGTGGCGCGGTGTGCGAAGCTGGCTAGCGTGTGCTACCGGCTCCTCTTCAACGGGCATC 306  
 Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
 Db 307 AAGAGCCAGGCGGGAGCGGTGCGAGGGCAGAACTTCTACACCCGAGCGCGTCTCTG 366  
 Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
 Db 367 AGCGCGGTCAAGGCGTACCCAGGCTTCGCCCATCGCGGTCGAGGTGCGAGGCAAGCGC 426  
 Qy 103 GluLeAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
 Db 427 GAGATCGCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCATTTCTGCTACATCAGC 486  
 Qy 123 GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142  
 Db 487 GAGATCAACAGACGACGCTTACTGCGACCGGACCAAGAGCGAGTGGCCGTGGCGCGC 546  
 Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162  
 Db 547 GGGCAGAGTACTACGGCGCGCGCGCTGCGAGATCTCTGTGGAACCTACAACTACGGGCC 606  
 Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182  
 Db 607 CGCGGAGGGGCCATCGGCTTTCGACGGGTTCGGGGACCCCGCGAGCGGTGGCGGGACGCC 666  
 Qy 183 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMetPro 202  
 Db 667 GTGTGGCGGTTCAGGCGCGCGCTCTGGTTCTGGATGAACAGCGTGACCGGGGTGTGTCCG 726

Qy 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 215  
 Db 727 CAGGGGTTTCGGCGCCACCACCGGCCCATCAACGGCGCC 765

## RESULT 6

LOCUS CN133023 837 bp mRNA linear EST 01-APR-2004  
 DEFINITION OX1\_9\_D11.g1\_A002 Oxidatively-stressed leaves and roots Sorghum  
 bicolor cDNA clone OX1\_9\_D11\_A002 5', mRNA sequence.

ACCESSION CN133023  
 VERSION CN133023.1 GI:45963543  
 KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor

REFERENCE 1 (bases 1 to 837)  
 Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,  
 Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.  
 An EST database from Sorghum: oxidatively stressed leaves and roots  
 Unpublished (2003)

TITLE Other ESTs: OX1\_9\_D11.bl.A002  
 JOURNAL Contact: Cordonnier-Pratt, MM  
 COMMENT Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
 the Human Genome Center, University of Tokyo Institute of Medical  
 Science; plant material and RNA prepared at Texas A & M University;  
 sequencing done in the Laboratory for Genomics and Bioinformatics,  
 University of Georgia. Sequence ends have been trimmed to exclude  
 vector and regions below Phred quality 16. Three-prime sequences  
 are presented as their reverse complement and have been trimmed to  
 exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTCGG).

FEATURES

1..837

Location/Qualifiers

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/Clones="OX1\_9\_D11.A002"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Oxidatively-stressed leaves and roots"

/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1:  
 XhoI; Site 2: XhoI; The library was prepared from polyA+  
 RNA from oxidatively stressed, hydroponically grown  
 sorghum seedlings. At 8 days of age, growth medium was  
 supplemented with hydrogen peroxide to 0.003% and leaves  
 were misted with 10 uM methyl viologen. Leaves and roots  
 were harvested at 3, 12 and 27 hr after treatment and all  
 tissue pooled. Double-stranded cDNA was cloned  
 unidirectionally into different DraIII sites of the  
 pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,  
 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA  
 insert."

ORIGIN

Alignment Scores:

Pred. No.: 1.33e-102 Length: 837

Score: 1099.50 Matches: 198

Percent Similarity: 87.45% Conservative: 11

Best Local Similarity: 82.85% Mismatches: 25

Query Match: 78.09% Indels: 5

DB: 7 Gaps: 2

US-10-692-367-70 (1-250) x CN133023 (1-837)

```

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 134 CAGAACTACGGCTGCGCAGGCTTACTGTCAGCAAGTTTCGGTTACTGCGGCAGCAGC 193
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 194 GACGAGTACTCGCGCAGCGGTGCGAGTTCGGGCCGCTCGCTCGCGCGCGCAGCAGT 253
Qy 43 SerGlyGlyGlyGlyAlaAenValAlaSerValThrGlySerPhePheAenGlyTle 62
Db 254 -----GAGGTGGAGAGTGGCTGGCTGTTCACCGAGCGCATTTCTTCAACAGCATC 304
Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82
Db 305 AAGAACCGCGCGGAGCGGTGCGAGGCAAGAACTTCTACCGCGAGCGCTTCTCTG 364
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyArg 102
Db 365 AGCGCCGCGCAGCGGTACAAAGGCTTC-----GGTGGCAGTGGTGCAGGGCAAGCGC 418
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 419 GAGATCGCGGCTTCTCGCCACATCAGCGACGAGCGGACATTTCTGTACATCAGC 478
Qy 123 GluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAla 142
Db 479 GAGATCAACAAGAACACCGCTTACTGCGACTCGAGCAACGACGACGAGTGGCGCGC 538
Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162
Db 539 GGTCAAGAGTACTACGGCGCGCGCGCTGCAAAATCTCGTGGAACTACAACTACGGGCT 598
Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyArgProGlyArgValAlaAraAspAla 182
Db 599 GCGGGAGGACATCGGCTTCAGCGGCTTCGGAACCGGACAGGTTGGCGCAAGACGCC 658
Qy 183 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMetPro 202
Db 659 GTGGTGGGTTCAAGACGCGCTCTGTTCTGGACCAACACGTCGACCGGGTGTATGTCG 718
Qy 203 GlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGlyCysAspGlyAenAen 222
Db 719 CAGGGTTTCGGCGCCACCATCAGGCGCCATCAACGGCGCCCTCGAGTGCAACGGCAAGAT 778
Qy 223 ProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 779 ACTGCCAGATGAACGCGCGGTGGCTACTACAGGCAAGTACTGCCAGCAGCTCGGC 835

```

```

RESULT 7
CD443492 710 bp mRNA linear EST 03-JUN-2003
LOCUS EL01N0427B11.b Endosporm_4 Zea mays cDNA, mRNA sequence.
DEFINITION CD443492
ACCESSION CD443492
VERSION CD443492.1 GI:31359135
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 710)
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Larkins, B., Beckett, P. and Messing, J.
Characterization of the maize endosporm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu

```

```

FEATURES
source
Seq primer: T3.
Location/Qualifiers
1..710
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosporm of 7-23DAP"
/clone_lib="Endosporm 4"
/note="Vector: pbluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 6,87e-99 Length: 710
Score: 1062.50 Matches: 189
Percent Similarity: 97.95% Conservative: 2
Best Local Similarity: 96.92% Mismatches: 3
Query Match: 75.46% Indels: 1
DB: 6 Gaps: 1
US-10-692-367-70 (1-250) x CD443492 (1-710)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 126 CAGAACTACGGCTGCGCAGGCTTACTGTCAGCAAGTTTCGGTTACTGCGGCAGCAGC 185
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGly 41
Db 186 GACGAGTACTGTCGCGAGCGGTGCGAGTTCGAGCGCGCTCGCGCGCGCGCGCGC 245
Qy 42 SerSerGlyGlyGlyGlyAlaAenValAlaSerValThrGlySerPhePheAenGly 61
Db 246 GGCAGTGGTGGCGGTGGTGGCAACGTCGTCAGCTGTCACCGCTCTCTTCTTCAACGCGC 305
Qy 62 IleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPhe 81
Db 306 ATCAAGAACACCGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCGTTC 365
Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db 366 CTGAGCGCGGTCAAGGCTTACCCAGGCTTCGCCCATGCGCGGTGCGAGTGCAGGCGAAG 425
Qy 102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIle 121
Db 426 CGCGAGATCGCGCTTCTTCGCGCAGCCAGCAGCAGCGCGGCACTTCTGTACATC 485
Qy 122 SerGluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
Db 486 AGCGAGATCAACAGAGCAACGCCCTACTGCGACCCGACCAAGAGGCAAGTGGCGCGCC 545
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
Db 546 GCGGGCGAGAAAGTACTACGGCGCGCGCGCTGCGAGATCTCGTGGAACTACACTACGGG 605
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAraAsp 181
Db 606 CCGCGCGGAGGGGCATCGGCTTCAGCGGCTCGCGGACCCCGGACGGTGGCGCGCGGAC 665
Qy 182 AlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAen 196
Db 666 GCCGTGGTGGGTTCAAGCGCGCGCTCTGTTCTGGATGAACAGC 710

RESULT 8
CD443492 647 bp mRNA linear EST 25-SEP-2003
LOCUS SCBFAD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11
DEFINITION 5', mRNA sequence.
ACCESSION CA197556
VERSION CA197556.1 GI:35227930
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

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```
Pred. No.: 6.59e-92 Length: 628
Score: 994.00 Matches: 179
Percent Similarity: 94.15% Conservative: 14
Best Local Similarity: 87.32% Mismatches: 12
Query Match: 70.60% Indels: 1
DB: 4 Gaps: 0

US-10-692-367-70 (1-250) x BM736454 (1-628)

Qy 46 GlyGlyAlaAanValAlaSerValThrGlySerPhePheAenGlyIleIyAenGln 65
Db 3 GGGCGGGGGAACGTGGCTAAGCTGGC-AGCGACGGCTTCTTCAACGGCATCAAGAACCG 61
Qy 66 AlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeuSerAlaVal 85
Db 62 GCGGCGGAGGGTGGCAGGGCAAGAACTTCTACACCGGAGCGGCTTCTGAGCGCGCTC 121
Qy 86 LysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyLysArgGluIleAla 105
Db 122 AACAACTACCGGGCTTCGCCATGGCGGAGCGGAGGTGGAGGGCAAGCGCGAGATGCC 181
Qy 106 AlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSer 125
Db 182 GCCTTCTTTCGGCGCAGCTCACCGACGAGACCGGACATTTCTGCTACATCAGCGAGATCAAC 241
Qy 126 LysSerAenAlaTyrCysAspProThrLysArgGlnTTrpProCysAlaAlaGlyGlnLys 145
Db 242 AAGAGCAACGCTACTGCGAGCAAGCAACAGGCGGTGGCGCGCGGGCGGAGAG 301
Qy 146 TyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyProAlaGlyArg 165
Db 302 TACTACGGCGCGCGCGCTCGATCTCGTGGAACTACAACTACCGGCGCGCGGGAGG 361
Qy 166 AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAla 185
Db 362 GACATCGCTTCAACGGGCTCGCGACCCCAACAGGGGTGGCGAGGACCGCGTATCGCG 421
Qy 186 PheLysAlaAlaLeuTTrpPheTrpMetAenAenValHisArgValMetProGlnGlyPhe 205
Db 422 TTCAAGACGGCGCTCTGCTTCTGGATGAACAACTGCAACCGTGTGATCGCGCGGCTTC 481
Qy 206 GlyAlaThrIleArgAlaAlaAenGlyAlaLeuGlyCysAspGlyAenAenProAlaGln 225
Db 482 GCGCGCACCATCAGGGCCATCAACGGCGCCCTCGAGTCAACAGCGGAAACAAACCGCGCCAG 541
Qy 226 MetAenAlaArgIleGlyTyrLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
Db 542 ATGAACGCGCGCTCGGCTACTTACAAGCAGTACTGCGCAGAGCTCCGCGTCGACCCAGGG 601
Qy 246 ProAenLeuThrCys 250
Db 602 CCCAACCTCACTTGC 616

RESULT 10
LOCUS BM895383
DEFINITION 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
ACCESSION BM895383
VERSION BM895383.1 GI:19350851
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 625)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
JOURNAL
COMMENT Contact: Walbot V
Department of Biological Sciences
```

Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 952073 row: H column: 05.

FEATURES  
Location/Qualifiers  
1..625  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.13e-90 Length: 625  
Score: 982.00 Matches: 178  
Percent Similarity: 91.04% Conservative: 15  
Best Local Similarity: 83.96% Mismatches: 13  
Query Match: 69.74% Indels: 7  
DB: 5 Gaps: 1

US-10-692-367-70 (1-250) x BM895383 (1-625)

Qy 35 CysArgSerGlyGlyGlySerSerGlyGlyGlyAlaAanValAlaSerValVal 54  
Db 7 TGTGCG-----GGAGGCGAGTGGCGGTGCGAACGTGGCTTAACGG-GTC 47  
Qy 55 ThrGlySerPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAen 74  
Db 48 AGCAGCGGCTTCTTCAACGGCATCAGACAGCGCGGAGCGGTGCGAGGGCAAGAAC 107  
Qy 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94  
Db 108 TTCTACACCGGAGCGCGTTCCTGAGCGCGCTCAACAAGTACCGGGCTTCGCCCATGGC 167  
Qy 95 GlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114  
Db 168 GGGACGGAGGTGGAGGCAAGCGGAGATCGCGCTTCTTTCGGCGCAGCTCACCGCAG 227  
Qy 115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThr 134  
Db 228 ACCGACATTTCTGCTACATCAGCGAGATCAACAGAGCAACCGCTACTCTGCGAGCGCAGC 287  
Qy 135 LysArgGlnTTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154  
Db 288 AACAGGCGAGTGGCGTTCGCGCGGGCGGAGAGTACTACGGCGCGCGCGCTCGCAGATC 347  
Qy 155 SerTrpAenTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174  
Db 348 TCGTGAACATCACTACCGGCGCGCGGGAGGAGACATCGGCTTCAACGGGCTCGCGCAC 407  
Qy 175 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTTrpPheTrpMet 194  
Db 408 CCCAACAGGGTGGCGAGGACCGCGTATCGGCTTCAAGAGCGGCGCTCTGGTTCTGATG 467  
Qy 195 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaAlaAenGly 214



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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCOSLB2051F10"
/lab_host="DH10B"
/clone_lib="Lb2"
/note="Organ: Lateral buds from plants adult plants
growing in greenhouse; Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucet.lad.ic.unicamp.br/public"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3,97e-90 Length: 786
Score: 978.00 Matches: 182
Percent Similarity: 86.34% Conservatives: 14
Best Local Similarity: 80.18% Mismatches: 23
Query Match: 69.46% Indels: 8
DB: 6 Gaps: 2

US-10-692-367-70 (1-250) x CA270202 (1-786)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 117 CAAAACTCGCGCTGCACCAAACTACTGTCTGCAGCAAGTTTCGGGTACTCGGCACGACC 176
Qy 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 177 GACGACTACTGTGGCAGCGGTGCGAGTCCGGCCGCTCGGGCGGGCGGAGCCCA 236
Qy 43 SerGlyGly-----GlyGlyAlaAsnValAlaSerValValThrGlySerPheAsn 60
Db 237 GCGGTGCGCAGCAGTGGTGGTGGGAACGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 296
Qy 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
Db 297 GGCATCAAAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGTGGC 356
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
Db 357 TTCTGAGCGCGCGGACTCGTACAAGGTTTC-----GGTGGCGGTGCGTGGAGGCG 410
Qy 101 LysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 411 AAGCGGAGATCGCGCGCTTCTTCGGCAGCTCAGCAGCAGAGCGGACATTTCTGCTAC 470
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
Db 471 ATCAGCGAAATCAACAAGAACAGCCCTACTTCGCACTCGAGCAACAGCAGTGGCGGTGC 530
Qy 141 AlaAlaGlyLysLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 531 CCGCGGAGACAGAGTACTACGGCGCGCGCGCTGTCAGATCTCTGTGAATCAACACTAC 590
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 591 GGGCTCGCGGAGGAGACATCGGCTTCAACGGGTTCGGGAACCCCGCAGGTTGGCGCAG 650
Qy 181 AspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 651 GACCGCGTATCGCGCTTCAAGACGCGCGCTCTGGTCTTGTGATGAACAACTTGCACCGG 710
Qy 201 -MetProGlnGlyPheGlyAlaThr-1leArgAlaIle-AsnGlyAla-LeuGluCysAs 219
Db 711 AATGTCNCGGGGTTCGAGACCCATTCAGGCTATTAAACGGAACCCCTCGAGTGCAG 770
Qy 219 pGlyAsnAsnPro 223

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Db 771 AGGAAACCAACCC 783

```

## RESULT 13

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CD994869
LOCUS QBB18407.xg QBB Zea mays cDNA clone QBB18407, mRNA sequence.
DEFINITION CD994869
ACCESSION CD994869
VERSION CD994869.1 GI:32855188
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

```

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 741)

```

## REFERENCE

```

AUTHORS Genoplatte.
TITLE Genoplatte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte

```

```

Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

```

This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (<http://www.genoplatte.com> and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

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Location/Qualifiers
source
1..741
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QBB18407"
/tissue_type="embryo"
/clone_lib="QBB"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 7,47e-90 Length: 741
Score: 975.00 Matches: 173
Percent Similarity: 97.81% Conservatives: 6
Best Local Similarity: 94.54% Mismatches: 4
Query Match: 69.25% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994869 (1-741)

Qy 68 SerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuSerAlaValLysAla 87
Db 1 AGCGGGTTCGAGGGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGTCAAGGCG 60
Qy 88 TyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhe 107
Db 61 TACCCAGGCTTCGCCACCGCGGTCGAGGTGCGAGGCAAGCGCGAGATCGCGCGCTTC 120
Qy 108 PheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSer 127
Db 121 TTCGGCGACCCACGACGAGACCGGGCATTTCTGTACTACGCGAGATCAACAGAGC 180
Qy 128 AsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyr 147
Db 181 AACGCCTACTCGACCCGCAAGAGGACGTGGCGGTGCGCTGCGGGGCAAGAGTACTAC 240
Qy 148 GlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIle 167
Db 241 GGGCGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACCGGCGCGCGGAGCGGCATC 300
Qy 168 GlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaValAlaPheLys 187
Db 301 GGGTTCAGCGGGTTCGGGGACCCCGGAGGCGTGGCGGAGCGCGGTGGGTTCAG 360
Qy 188 AlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAla 207

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Db      361 GCGGCGCTCTGTTCTGATGAACAGCGTGCACGGGGTGGTCCCGACAGGGTTGCGGCC 420
Qy      208 ThrileArgAlaileAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsn 227
Db      421 ACCACCGGCGCATCAACGGCGCCCTCGAGTGGCGGGAAACAACCCCGCCAGATGAAC 480
Qy      228 AlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsn 247
Db      481 GCGCGCGTGGCTACTACAGGCGAGTACTGCGCGCAGTCTCGGCGTGCAGCCCGGGGCCAAC 540
Qy      248 LeuThrCys 250
Db      541 CTCACCTGC 549

RESULT 14
LOCUS      CD994156 578 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA sequence.
ACCESSION  CD994156
VERSION     CD994156.1 GI:32854475
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 578)
AUTHORS   Genoplante, a major partnership french program in plant genomics
TITLE     Unpublished (2003)
JOURNAL   Contact: Genoplante
COMMENT   Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.inbio.gen.fr).
FEATURES   Location/Qualifiers
            source
              1..578
                /organism="Zea mays"
                /mol_type="mRNA"
                /cultivar="F2"
                /db_xref="taxon:4577"
                /clone="QBB13f07"
                /tissue_type="embryo"
                /clone_lib="QBB"

ORIGIN
Alignment Scores:
Pred. No.: 8.55e-90 Length: 578
Score: 973.00 Matches: 172
Percent Similarity: 97.28% Conservative: 7
Best Local Similarity: 93.48% Mismatches: 5
Query Match: 69.11% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994156 (1-578)

Qy      67 GlySerGlyCysGluGlyValAsnPheTyrThrArgSerAlaPheLeuSerAlaVallys 86
Db      1 GGGAGCGGGTCGAGGGGCAAGAACTTCTACACCGGAGCGGTCTCTGAGCGCGTCAAG 60
Qy      87 AlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyValArgGluIleAlaAla 106
Db      61 GCGTACCCAGAGTTCCGCCACCGCGGGTCGAGGTGCGAGGCGAAGCGCGAGATCGCCGCC 120
Qy      107 PhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLys 126
Db      121 TTCTTCGCGCGCCACGACGAGACCGCGGATTTCTGTTCTTCAGCGAGATCAACAAG 180
Qy      127 SerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyr 146

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Db      181 AGCAACGCCCTACTCGGACCCGAGCAAGAGCGAGTGGCCGTCGCGCGGGCGAGAGTAC 240
Qy      147 TyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAsp 166
Db      241 TACGGCGCGCGCGCTCGAGATCTCGTGGAACTACAACTACGGGCGCCCGCGGAGGCGCC 300
Qy      167 IleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAlaPhe 186
Db      301 ATCGGCTTCGACGGGCTCGGGACCCGCGCAGGGTGGCGGGACGCGCGTGGTGGCGTTC 360
Qy      187 LysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGly 206
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Qy      207 AlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMet 226
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RESULT 15
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DEFINITION QBB18e05.xg QBB Zea mays cDNA clone QBB18e05, mRNA sequence.
ACCESSION  CD994885
VERSION     CD994885.1 GI:32855204
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 753)
AUTHORS   Genoplante, a major partnership french program in plant genomics
TITLE     Unpublished (2003)
JOURNAL   Contact: Genoplante
COMMENT   Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.inbio.gen.fr).
FEATURES   Location/Qualifiers
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ORIGIN
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Score: 971.00 Matches: 172
Percent Similarity: 97.27% Conservative: 6
Best Local Similarity: 93.99% Mismatches: 5
Query Match: 68.96% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994885 (1-753)

Qy      68 SerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuSerAlaVallysAla 87

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Db 61 TACCCAGGGCTTCGCCACGCGGGTCGAGGGTGGAGGCAAGCGGAGATCGCGCCCTTC 120
Qy 108 PheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSer 127
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Qy 128 AsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyr 147
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